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METHODS

Antarctic fur seal study population. Long-term population monitoring of Antarctic fur seals at Bird Island, South Georgia (54°00'S, 38°02'W) began in 1982 on a specially designated study beach where an aerial scaffolding walkway provides safe access while minimising disturbance to the animals. Female fur seals were identified using cattle ear tags fitted to the fore flippers since 1982 and subcutaneous electronic chips (Passive Integrated Transponder tags, PIT-tags) fitted since 1996. Tags were fitted either to pups of approximately six weeks of age or to breeding adults, captured following standard methodologies[1] and reliably aged by counting the number of annuli within sectioned post-canine teeth. A genetic sample was collected upon capture and body weight (kg) was recorded for pups and adult females, together with dorsal (standard) body length (cm) for breeding females. Each breeding season, from November to January, all females encountered were examined for presence of tags and their breeding status and performance were recorded during twice-daily surveys. As a measure of adult female breeding success, early pup survival was estimated through the recovery of dead pups during each breeding season. Once established as breeders, females were highly philopatric[2] and came ashore to breed almost every year.

Krill, sea surface temperature and climate data. Antarctic krill availability was determined from a long-term dietary analysis of Antarctic fur seals based on scat samples collected weekly since 1989[3]; the raw data are available on request from the British Antarctic Survey, UK. Median krill body size is a reliable proxy of krill availability and biomass[4, 1]. Sea Surface Temperature (SST), representative of oceanographic conditions off South Georgia, was selected and analysed as in Forcada *et al.*[5], using dataset number ds277.0 (NCEP Version 2.0 OI Global SST and NCDC Version 3.0 Extended Reconstructed SST Analyses[6], which is available at http://dss.ucar.edu. The main environmental effect tested was the Southern

Annular Mode index (SAM) because this is the primary mode of climate variation at higher latitudes of the Southern Hemisphere. It has a direct component of local forcing which affects the Scotia Sea oceanography and ecosystem[4, 7] and also interacts with global climate, as measured by ENSO (El Niño Southern Oscillation[7]). The SAM index positively correlates with sea surface temperature off South Georgia and inversely correlates with krill biomass and Antarctic fur seal pup production (**Fig.** 1A). The SAM thus effectively integrates inter-annual climate forcing on fur seals and their main food supply, krill. The monthly SAM index[8] was obtained from http://www.nerc-bas.ac.uk/icd/gjma/sam.html.

Generation of genetic data. Total genomic DNA was extracted from tissue samples and genotyped at nine highly polymorphic dinucleotide microsatellite loci (Extended Data **Table** 3) as described in detail by Hoffman and Amos[9]. All of these loci are in Hardy-Weinberg and linkage equilibrium, and map to different chromosomes in the dog, *Canis familaris*[10-12]. Any reactions yielding uncertain genotypes (e.g. with faint or unclear bands) were repeated, allowing the genotyping error rate to be driven down to 0.001–0.007 per reaction[9]. Individual multilocus heterozygosity was calculated using the measure homozygosity weighted by locus, HL[13]. HL weights heterozygosity by the variability of each locus at which an individual is homozygous and tends to outperform other measures when allelic diversity is high[14].

Models for standard body length at age

Mixed effects Gompertz models of body length at age were fitted to compare female growth between periods (Fig. 1 D). The best model, fitted with REML and with lowest BIC, was

$$y(\mathrm{x}) = (\varepsilon A + a_i)\exp\left\{-\left[B_0 B_1 p\right]^x\right\} + \quad _{ij}$$

where y is standard length, x is age, the fixed effect estimates are A=127.69 (s. e. m. = 0.37), B_o = 1 (s. e. m. = 0.23) and B_1 = -0.50 (s. e. m. = 0.14); p is a factor which identifies periods 1983–1992 and 2003–2012 respectively; a_i =0.002 is a random effect for period A-The period

specific variance structure was estimated as $Var(\varepsilon_{ij}|u_i) = \sigma^2 \delta^2_{P_{83-92},j}$ where $\delta^2_{P_{83-92},j} = 1.129$ and $\sigma^2 = 4.32$.

Population trends. State-space models[15] were used to analyse the trajectory of the study population from 1981 to 2012 and to investigate the main components of variability in observed inter-annual change, $\log(\lambda_t)$ for season t, in number of breeders N. The observed number of breeders y_t and its corresponding standard error in each season was obtained from the long term monitoring of this population[5]. The state process part of the models assumed an exponential growth of N on the log scale, with $\log(N_{t+1}) = \log(N_t) + \log(\lambda_t)$, where $\log(\lambda_t) \sim Normal\left[\log\left(\bar{\lambda}\right), \sigma_t^2\right]$. The observation process related population numbers to observed counts of seals y_t at season t, as $y_t = N_t + \tau_t$, with seasonal observation error $\tau_t \sim Normal\left(0, \sigma_y^2\right)$. The inter-annual population change was treated as a linear model of several potential covariates X_t, including the SAM index, South Georgia SST and median krill size as $\log\left(\lambda_t\right) = \alpha + \sum_j \beta_j X_t + \varepsilon_t$, where ε_t are seasonal random effects. We used Bayesian methods and MCMC updating within the program WinBUGS[16] to obtain parameter estimates. We used non-informative uniform and Gaussian priors to update the posterior distributions of error parameters and coefficients of the linear models of $\log(\lambda_t)$ respectively. The model with best set of predictors of $\log(\lambda_t)$ was selected according to lowest DIC[17]. The best model included SAM and krill (**Fig**. 1, black line) and seasonal random effects; large krill size correlates with low krill biomass ($\hat{\rho}_{SAM,krill} = 0.54$, $P < 0.01$; this study). This model predicted population trajectories (**Fig.** 1A) and estimated the linear long-term decline as a derived parameter; the annual decline is estimated at 1.6% (95% CI: 0.3, 3.4).

Modelling the Antarctic fur seal life cycle. We used an Antarctic fur seal female life cycle (Extended Data **Fig**. 1A) with a combined age structure for pre-breeders and stage structure

for breeders. The life cycle is defined by transition probabilities between stages and fertilities (f), which are the female weanlings contributed by females breeding at t+1.

Stages:

P - Pre-breeder: an immature female, from weaning until it starts breeding.

B - Breeder: a mature female already recruited into the population which pups.

S - Successful breeder: pupping female whose pup survives for at least 6 weeks.

F - Failed breeder: pupping female whose pup dies before 6 weeks of age.

N - Non-breeder: mature female that skips breeding in a given season.

D - Dead: female that dies (or emigrates permanently).

Transitions*:*

In the life cycle (Extended Data **Fig**. 1A), transitions combine probabilities of survival and stasis, or movement between stages, combined in parameters ϕ_{ij}. These transitions are further decomposed in the following vital rates of biological interest:

ϕ_i - apparent survival: probability of being in state e_i and surviving from occasion k to k+1.

α_i - recruitment: probability that an as yet inexperienced female starts pupping at age I on occasion k+1 [40].

β_i - breeding probability or fecundity: probability to pup on occasion k+1, conditional upon survival.

ς_i - breeding success: probability that a pup survives at least 6 weeks conditional on its mother surviving and pupping between occasions k and k+1.

As an example, for an immature female (stage *P*) to recruit and pup successfully (stage *S*) between consecutive occasions, she had to: survive with probability ϕ_P^k, produce a pup with probability α^k and the pup had to survive the first 6 weeks of life with probability ς_P^k. A female pup would have a PIT-tag implanted at birth and, if it survived for 6 weeks, it would

be subsequently tagged and become part of the study. Once recruited, and conditional on surviving ($\phi_{\cdot}^{k}$), a female would breed with probability $\beta_{\cdot}^{k}$, or skip breeding ($1-\beta_{\cdot}^{k}$), in which case it could be observed as a non-breeder (*N*).

Multi-event capture-mark-resighting models. We used age and time-dependent multi-event models *sensu* Pradel[18] to parameterize the life cycle. Models assumed that female fur seals moved independently among sets of stages $\mathbb{E}^{(l)}$ over $K = 12$ occasions or breeding seasons. Successive stages followed a Markov chain and could not be observed directly with certainty, but a set of *events* Ω was observed at each encounter occasion *k*, and these depended on the underlying stage of the individual at that occasion. The sets of intermediate stages were $\mathbb{E}^{(0)}=\{P,S,F,N,D\}$, $\mathbb{E}^{(1)}=\{P,S,F,N,D\}$, and $\mathbb{E}^{(2)}=\{P,B^1,B^2,B^3,B^4,N,D\}$, including pre-breeder (*P*), breeder (*B*), successful breeder (*S*), failed breeder (*F*), non-breeder (*N*), and dead (*D*). Connections and transition probabilities (vital rates) between stages are represented in Extended Data **Fig**. 1B.

Estimation of multi-event models. Female fur seal breeding histories were organised in encounter occasions, for $k = 1$ to *K*, and at each occasion the encounter was defined by an observed event (*P*, *S*, *F* or *N*). On each occasion (breeding season), known individuals were given temporary individually distinctive paint marks and were scanned for PIT-tags when first seen. If they pupped, the pup was given a PIT-tag, temporarily marked with hair dye, sampled for genetic analysis, and its early survival was determined either through recovery of the corpse in case of death, or by subsequent inspection after 6 weeks, when plastic tags were applied to the fore flippers. At this point, an event (*S* or *F*) was assigned to the mother for that occasion.

Multiple models were fitted using maximum likelihood estimation in the program ESURGE V.1.8.5[19], applying the transition and event probabilities to individual encounter histories. This provided ML estimates of relative deviance, model rank accounting for

parameter redundancy (*np*), statistical parameters (ϑ), and $QAIC_c$, which was used for model comparisons and biological hypothesis testing. Transition and event probabilities (θ) were logit functions of estimated parameters $\hat{\vartheta}$, obtained as $\hat{\theta} = logit^{-1}(\mathbf{X}\hat{\vartheta})$. The approximate variance-covariance parameter matrix, $\hat{\mathbf{V}} = -\hat{\mathbf{H}}^{-1}$, was obtained from the Hessian of the log-likelihood $\hat{\mathbf{H}} = (\partial^2 \log \ell / \partial\vartheta_i \partial\vartheta_j)$; standard errors were derived as $SE(\hat{\vartheta}) = \sqrt{\text{var}(\hat{\vartheta})\hat{c}}$, where $\hat{c}$ is the variance inflation factor obtained from the goodness-of-fit testing. A multivariate normal distribution $\mathbf{\Theta}_b^* \sim N(\hat{\mathbf{\Theta}}, \hat{\mathbf{V}})$, where $\hat{\mathbf{\Theta}}$ was the vector of mean estimates of $\hat{\vartheta}_{ij}$, was used to generate parameter deviates for subsequent matrix population models.

Without a specific goodness-of-fit testing framework for multi-event models, we used by approximation the tests developed for Arnason-Schwarz models developed by Pradel *et al.*[20], as implemented in the program U-CARE V.2.3.2[21]. We designated an umbrella model to reflect the demography of the study population. Typical effects of transience observed in these complex models were structurally incorporated into the multi-event models as age structure, and further overdispersion was approximated as $\hat{c} = \chi^2 / df$ from the test-statistics. Multi-model comparisons were based on the $\Delta QAIC_c$, where $QAIC_c$ was *Rdev*/$\hat{c}$+2*np*+2*np*(*np*+1)/(*ess*-*np*-1) where *np* was the model rank or number of estimable parameters and *ess* the effective sample size.

Models with covariates affecting various transitions were fitted to test the biological hypotheses formulated. Covariates were incorporated as fixed-effects only of linear or quadratic form, given the complexity of the fitted models and the long computation times required to fit individual covariate models. Temporal variation accounted for by covariates (R^2) was evaluated as [*Rdev*(M)- *Rdev*(M_{Cov})]/ [*Rdev*(M)- *Rdev*(M_t)], where *Rdev* is the relative deviance of a model of the transition of interest with the covariate (M_{Cov}), with temporal variation (M_t), or without temporal variation[22].

When the stage in a specific year was uncertain because an individual seal was not detected, we used the method of Pledger *et al*.[23] implemented in E-SURGE for posterior state allocation. This allowed stage uncertainty to be carried over when population mean trait and HL values at each year were required for subsequent inference and comparisons over time.

Population projection models. We used stage structured matrix population models with $n(t+1) = A_t n(t)$, where $n(t)$ gives the number of females in each stage, and

$$A_t = \begin{pmatrix} 0 & 0 & f^3 & f^4 & f^5 & f^6 & f^7 & f^S & f^F & f^N \\ \phi_0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \phi_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \phi_{23} & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \phi_{34} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi_{45} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \phi_{56} & \phi_{67+} & 0 & 0 & 0 \\ 0 & 0 & \phi_{2S} & \phi_{3S} & \phi_{4S} & \phi_{5S} & \phi_{6S} & \phi_{SS} & \phi_{FS} & \phi_{NS} \\ 0 & 0 & \phi_{2F} & \phi_{3F} & \phi_{4F} & \phi_{5F} & \phi_{6F} & \phi_{SF} & \phi_{FF} & \phi_{NF} \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \phi_{SN} & \phi_{FN} & \phi_{NN} \end{pmatrix}$$

expressed in terms of transition probabilities and fertilities, where A_t corresponds to the life cycle graph (Extended Data **Fig**. 1A) and projects the population from year t to t+1. The model assumes a birth-pulse post-breeding census; a female in stage N at t may contribute f^N offspring at t+1. The projection matrix $\mathbf{A}_t$ in terms of lower level parameters or vital rates is given by

$$A_t = \begin{pmatrix} 0 & 0 & 0.5\phi_2\alpha_3\varsigma_3 & 0.5\phi_3\alpha_4\varsigma_4 & 0.5\phi_4\alpha_5\varsigma_5 & 0.5\phi_5\alpha_6\varsigma_6 & 0.5\phi_6\alpha_7\varsigma_7 & 0.5\phi_S\beta_S\varsigma_S & 0.5\phi_F\beta_F\varsigma_F & 0.5\phi_N\beta_N\varsigma_N \\ \phi_0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \phi_1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \phi_2(1-\alpha_3) & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \phi_3(1-\alpha_4) & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi_4(1-\alpha_5) & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \phi_5(1-\alpha_6) & \phi_6(1-\alpha_7) & 0 & 0 & 0 \\ 0 & 0 & \phi_2\alpha_3\varsigma_3 & \phi_3\alpha_4\varsigma_4 & \phi_4\alpha_5\varsigma_5 & \phi_5\alpha_6\varsigma_6 & \phi_6\alpha_7\varsigma_7 & \phi_S\beta_S\varsigma_S & \phi_F\beta_F\varsigma_F & \phi_N\beta_N\varsigma_N \\ 0 & 0 & \phi_2\alpha_3(1-\varsigma_3) & \phi_3\alpha_4(1-\varsigma_4) & \phi_4\alpha_5(1-\varsigma_5) & \phi_5\alpha_6(1-\varsigma_6) & \phi_6\alpha_7(1-\varsigma_7) & \phi_S\beta_S(1-\varsigma_S) & \phi_F\beta_F(1-\varsigma_F) & \phi_N\beta_N(1-\varsigma_N) \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \phi_S(1-\beta_S) & \phi_F(1-\beta_F) & \phi_N(1-\beta_N) \end{pmatrix}$$

Vital rates are defined as the parameters in the state transition matrices of the multi-event models. Fertility terms include 0.5 to account for females only, as there were no observed significant departures from a 1:1 sex ratio.

We parameterised transition matrices for each year from 2002 to 2012 using parametric bootstrap deviates of MEMR parameter estimates to evaluate changes in population growth rate (λ) over this period. A decomposition analysis was then used to evaluate the contributions (δ_l) of temporal variation in homozygosity (HL) and SAM to changes in λ. Contributions assumed small gradual changes in covariates. For instance, the contribution of changes in SAM were calculated as

$$\frac{d\lambda}{dSAM} = \frac{\partial\lambda}{\partial SAM} + \frac{\partial\lambda}{\partial HL}\frac{\partial HL}{\partial SAM} = \sum_l \sum_{ij} \frac{\partial\lambda}{\partial a_{ij}} \frac{\partial a_{ij}}{\partial \theta_l} \left(\frac{\partial \theta_l}{\partial SAM} + \frac{\partial \theta_l}{\partial HL}\frac{\partial HL}{\partial SAM} \right),$$

Where θ_l are vital rates and the a_{ij} are matrix model elements, which is equivalent to a life-table response experiment [17]. We used the line integral model of decomposition of Horiuchi *et al.*[24], whereby inter-annual changes in λ were

$$\lambda(t_2) - \lambda(t_1) = \sum_{i=1}^{n} \int_{x_i(t1)}^{x_i(t_2)} \frac{\partial\lambda(t)}{\partial x_i(t)} dx_i(t)$$

for years t_1 and t_2 and n covariates $\mathbf{x}= [x_1, x_2,\ldots,x_n]$, which were the effects of HL and SAM on different vital rates. This method takes into account any interactions between covariate effects and allows straightforward calculation through numerical integration over the period 2002–2012, $\Delta\lambda_T$.

Scaled covariate (SAM, and HL) contributions (δ) through θ_i to Δλ were expressed as $100*\delta/\Delta\lambda$ where δ is the estimated contribution of HL or SAM, to Δλ and to the mean ($\delta_{\overline{\Delta\lambda}}$) of inter-annual differences.

Elasticities - scaled sensitivities of $\log\lambda_s$ to vital rates - were estimated with Tuljapurkar's[25] approximation. Environmental stochasticity affects populations matrices $\mathbf{A}_t$ by small perturbations, $\mathbf{A}_t.+\varepsilon\mathbf{C}_t$ and the matrix $\mathbf{C}_t$ determines elements of $\mathbf{A}_t$ to be perturbed.

After a small perturbation $\log \lambda_s(\varepsilon) = \log \lambda_s + \varepsilon \lim_{n\to\infty} \frac{1}{\mathrm{T}} \sum_{t=0}^{\mathrm{T}-1} \frac{v'(t+1)\mathbf{C}_t w(t)}{R_t v'(t+1) w(t+1)}$, where $v'(t)$ are reproductive value vectors transposed; $w(t)$ are stage distribution vectors; and $R(t)$ a sequence of population growth rates. The elasticity to mean vital rates and their process variance were obtained replacing $\mathbf{C}_t$ with $\frac{\theta_t \partial \mathbf{A}_t}{\partial \theta}$ and $\frac{\theta_t \partial \mathbf{A}_t}{\partial \theta} - \frac{\bar{\theta} \partial \bar{\mathbf{A}}}{\partial \theta}$ respectively, where $\bar{\mathbf{A}}$ is the mean population matrix.

Vital rate variance contributions to σ_λ were obtained using a random design life table response experiment[26], with $\sigma_\lambda \approx \sigma_{\theta_i} \left(\frac{\partial \lambda}{\partial \theta_i} \right)^2 + \sum_{i \neq j} \sigma(\theta_i, \theta_j) \frac{\partial \lambda}{\partial \theta_i} \frac{\partial \lambda}{\partial \theta_j}$, where the first term corresponds to the variance and the second to covariance contributions.

Integral projection models. We constructed models for a female population structured by age as a discrete variable[27, 28], and by HL as a continuous individual-level state variable. HL was associated with three main functions describing survival (S), fertility (F) and inheritance (H), defined as the probability that a female of homozygosity value h in year t produced a pup with homozygosity h' at time t+1. The distribution of female homozygosity h and age a in year t was defined as $n_a(h, t)$ and the general model structure was

$$n_0(h',t+1) = \sum_{a=0}^{8} \int_{h_L}^{h_U} H(h' \mid h,t) F_a(h,t) n_a(h,t) dh$$

$$n_a(h,t+1) = \int_{h_L}^{h_U} S_{a-1}(h,t) n_{a-1}(h,t) dh, \qquad 1 \le a < 8$$

$$n_8(h,t+1) = \int_{h_L}^{h_U} \left[S_7(h,t) n_7(h,t) + S_8(h,t) n_8(h,t) \right] dh, \qquad a = 8$$

where a = 1, .., 8, and 8 was an absorbing age class representing females aged 8 or older; $S_a(h, t)$ was a survival kernel (probability density function) representing age a females of homozygosity value h surviving to age a+1; $F_a(h, t)$ was a fertility kernel representing female pups produced by mothers of age a and homozygosity h; $H(h'|h, t)$ was the inheritance kernel

or probability distribution of pups of HL value *h*' produced by a mother of homozygosity *h*; subscripts *L* and *U* delimited intervals of HL values.

Survival and fertility functions were parameterised with estimated age and HL-specific vital rate estimates. Inheritance was parameterised combining the parameters of a linear model of the pups' HL in year *t*+1 against the values of their mothers in year *t*, and parameters defining the variance around this association[27, 28]. The statistical models and parameter estimates are described in the Supplementary Information.

We used parametric bootstrap replicates of the vital rate variance matrix ($\hat{\boldsymbol{V}}$) in simulations of the IPMs to estimate the stochastic λ, mean homozygosity ($\overline{HL}$), evaluated as $\sum_a \int_h h\, n_a(h,t)\, dh \Big/ \int_h n_a(h,t)\, dh$, and strength of viability (*VS*) and fertility (*FS*) selection on homozygosity, evaluated as $\sum_a \left[\int_h S_a(h,t) n_a(h,t) h dh \Big/ \int_h S_a(h,t) n_a(h,t) dh \right] - \overline{HL}$ for viability, and similarly for fertility. For each of 400 simulations, we generated a random value of SAM within the range of values observed since 2000.

The comparative effect of small changes in statistical coefficients of vital rates ϑ_i in λ, $\overline{HL}$ and *VS* was investigated with a sensitivity analysis. For asymptotic λ, and similarly for the other parameters, $s_{\vartheta_i} = \Delta\lambda / \Delta\vartheta_i$, where $\Delta\vartheta_i$ was a 1% change in ϑ_i (Extended Data **Figs.** 3–5).

Statistical functions in the Integral Projection Models.

Survival functions (S = ϕ), for ages $a = 0, ..., \geq 8$

$$\phi_0 = \text{logit}\left[-0.469(0.203) - 1.608(0.316)SAM - 1.164(0.819)HL\right] \qquad a = 0$$

$$\phi_a = \text{logit}\left[2.055(0.369) - 1.454(0.518)SAM - 1.164(0.819)HL\right] \qquad 0 < a \leq 2$$

$$\phi_a = (1-\gamma_a)\phi_a^P + \gamma_a \phi_a^B \qquad 2 < a \le 7$$

$$\begin{cases} \phi_a^P = \text{logit}\left[2.055(0.369) - 1.454(0.518)SAM - 1.164(0.819)HL\right] \\ \phi_a^B = \text{logit}\left[0.924(0.583) + 0.267(0.255)Age - 1.082(0.469)SAM\right] \\ \gamma_a = \left(1 - \prod_{j<a}(1-\alpha_j)\right) \Big/ \left(1 - \prod_{j<a+1}(1-\alpha_j)\right) \\ \alpha_j = \text{logit}\begin{bmatrix} -1.084(0.251) + 1.198(0.212)Age - 0.482(0.105)Age^2 \\ -0.663(0.317)SAM - 2.581(1.928)HL \end{bmatrix} \end{cases}$$

$$\phi_a = \beta\phi^B + (1-\beta)\phi^N \qquad a \ge 8$$

$$\begin{cases} \phi^B = \text{logit}\left[1.946(0.179) - 0.876(0.359)SAM - 0.982(0.409)SAM^2\right] \\ \phi^N = \text{logit}\left[3.403(1.523)\right] \\ \beta = 0.5\left\{\begin{matrix} \text{logit}\left[1.977(0.514) - 1.735(0.857)SAM\right] + \\ \text{logit}\left[1.497(0.17) - 0.049(0.301)SAM - 1.101(0.447)SAM^2\right] \end{matrix}\right\} \end{cases}$$

Fertility functions (F), for ages a=2, ..., ≥8

$$F_a = 0 \qquad a < 2$$

$$F_a = 0.5\,\phi_a\,\alpha_a\,\vartheta_a \qquad a = 2$$

$$\begin{cases} \phi_a = \text{logit}\left[2.055(0.369) - 1.454(0.518)SAM - 1.164(0.819)HL\right] \\ \alpha_a = \text{logit}\begin{bmatrix} -1.084(0.251) + 1.198(0.212)Age - 0.482(0.105)Age^2 \\ -0.663(0.317)SAM - 2.581(1.928)HL \end{bmatrix} \\ \vartheta_a = \text{logit}\left[0.019(0.310) + 0.603(0.182)Age - 3.812(2.155)HL\right] \end{cases}$$

$$F_a = 0.5\left[(1-\gamma_a)\phi_a^P \alpha_a + \gamma_a \phi_a^B \beta_a\right]\vartheta_a \qquad 2 < a \le 7$$

$$\begin{cases} \phi_a^P = \text{logit}\left[2.055(0.369) - 1.454(0.518)SAM - 1.164(0.819)HL\right] \\ \phi_a^B = \text{logit}\left[0.924(0.583) + 0.267(0.255)Age - 1.082(0.469)SAM\right] \\ \gamma_a = \left(1-\prod_{j<a}(1-\alpha_j)\right) \Big/ \left(1-\prod_{j<a+1}(1-\alpha_j)\right) \\ \alpha_j = \text{logit}\begin{bmatrix} -1.084(0.251) + 1.198(0.212)Age - 0.482(0.105)Age^2 \\ -0.663(0.317)SAM - 2.581(1.928)HL \end{bmatrix} \\ \beta_a = \text{logit}\left[1.977\ 0.514 - 1.735\ 0.857SAM\right] \\ \vartheta_a = \text{logit}\left[0.019(0.310) + 0.603(0.182)Age - 3.812(2.155)\,\text{HL}\right] \end{cases}$$

$$F_a = 0.5\phi_a\beta_a\vartheta_a \qquad a \ge 8$$

$$\begin{cases} \phi_a = 0.5\left\{\begin{matrix} \text{logit}\left[1.946(0.179) - 0.876(0.359)SAM - 0.982(0.409)SAM^2\right] + \\ \text{logit}\left[3.403(1.523)\right] \end{matrix}\right\} \\ \beta_a = 0.5\left\{\begin{matrix} \text{logit}\left[1.977(0.514) - 1.735(0.857)SAM\right] + \\ \text{logit}\left[1.497(0.17) - 0.049(0.301)SAM - 1.101(0.447)SAM^2\right] \end{matrix}\right\} \\ \vartheta_a = \text{logit}\left[2.079(0.303) - 3.165(1.58)HL\right] \end{cases}$$

In the equations, *Age* is a standardised variable, with ages 3 to 7 being -2, -1, 0, 1, 2, 3. SAM is also a standardised index, with observed range from -0.73 to 1.19.

Inheritance function (H)

$$H(\text{HL}'\,|\,\text{HL}) = \frac{1}{\sqrt{2\pi\sigma(HL)}}\exp\left\{\frac{-\left[HL' - \mu(HL)\right]^2}{2\sigma(HL)^2}\right\}$$

$$\begin{cases} \mu(HL') = 0.177 + 0.049HL \\ \sigma(HL')^2 = 0.008 - 0.005HL \end{cases}$$

The slopes (0.049 and -0.005; both $P > 0.25$) were obtained using a linear model of pup HL against maternal HL, and a model of the estimated residuals using the previous model against mother HL, respectively. Both were not significantly different from zero. Similarly, the heritability of HL, estimated as the squared slope of a linear model of pup HL against mother HL ($h^2 = 0.09$; 95% CI: -0.05, 0.232; $P = 0.27$) was not significantly different from zero.

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