

Text S1. The available data

Demographic data

Since 2003, we collect capture-mark-recapture data, population counts and productivity data for the black-browed albatross (*Thalassarche melanophris*, hereafter BBA) population in New Island, Falkland/Malvinas Island. However, due to gaps in the chicks ringing data in 2004/05 (hereafter, 2004/05 will be referred to as the 2004 season, and so on and so forth) this study spans from the 2005 to the 2019 season. Birds ringed in 2003 and 2004 were assumed to enter the monitored study plots when they were first encountered after the 2004 season. Every year, we recorded all breeding birds nesting in 5 discrete sub-colonies and ringed every unringed breeder. The fate of each egg and chick was recorded daily (during the incubation and brooding phase) and weekly (during the post-brooding phase). Each chick surviving to the 60th day of age was ringed and considered as successfully fledged, as very few chicks die between this age and fledging. Chicks were weighed on the 58th and 60th day of age to obtain a robust estimate of their mass at 59 days old (average between the 58 and 60 days measurements). For each breeding season t , we calculated a yearly average chick mass (figure S1), which was significantly positively correlated with probability of breeding and breeding success in the same season (t) and survival from the current (t) to the subsequent ($t+1$) breeding season (see the main text).

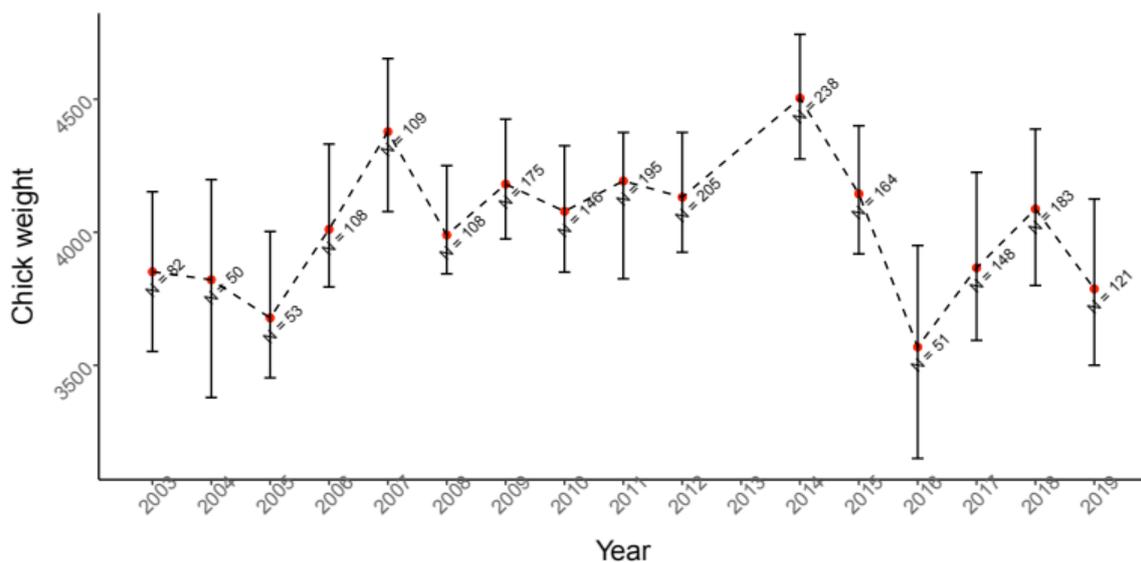


Figure S1. The yearly average chick mass at 59 days of age. The red circle represents the mean, the whiskers indicate the 25%-75% quantiles. Chick mass variability was positively correlated with probability of breeding and breeding success in the same breeding season, and with survival from the current to the following breeding season.

Throughout each study season, we recorded the identity of the ringed non-breeding birds seen inside and outside of our study patches; we also identified the ringed birds breeding outside the study colonies that were ringed as chicks in the study plots. Every year, we counted the number of individuals in each age-stage defined in the IPM; recorded the total number of breeders (dividing them into "local" breeders, ringed as chicks in our monitored plots, and "immigrant" breeders, which entered the study cohort as breeding adults); and

the total number of fledglings produced. The input data for the IPM is presented in table S1.

Table S1. Description of data input for the Integrated Population Model

Data Type	Description
Capture Mark Recapture	3173 individual encounter histories across 15 years. At each encounter event, each individual was assigned to one of the twelve age-stage classes defined in the IPM.
Population counts	Matrix 15 (years) × 12 (age-stage classes), storing the number of individuals recorded in each stage per year.
Productivity	Separate matrices for first-time-breeders and adult breeders. Each matrix is a 15 (years) × 2 (N fledglings, N breeding pairs) storing the number of fledglings produced per breeding pairs each year.

GPS tracking data

We collected GPS tracking data from breeding BBA on New Island during incubation (2009, 2013, 2017, 2018, 2019) and brooding (2008, 2009, 2010, 2013, 2015, 2016, 2017, 2018, 2019). GPS loggers were attached to the mantle and scapular feathers or to the tail feathers and set to record the bird location at a resolution of 7 or 14 minutes. The tracks were cleaned and the on-land and erroneous locations were removed. After processing, we obtained 735 foraging trips (157 and 578 during incubation and brooding, respectively). This represents the most comprehensive tracking dataset available for breeding BBA in the Falkland Islands.

Text S2. The explanatory variables

Estimate of space use for variables extraction

To reduce the computational burden of our dataset and make it treatable for the analysis, we adopted a resampling protocol. For each trip, we randomly resampled N points, separated from each other by at least 30 minutes, where N was equal to $2/3$ of the total trip duration in hours. In so doing, we reduced the intrinsic temporal autocorrelation of the dataset whilst rewarding longer trips with higher number of data points. Making use of the kernelUD function in the R package adehabitatHR (Calenge 2019), we calculated Kernel Utilisation Distributions (UD) based on the resampled tracks. The appropriate UD bandwidth was set as 30 km. The overall UD, estimated on a Lambert azimuthal grid centred in New Island, depicted the overall BBA space use (figure S2). The 90% contour of the overall UD was used to determine the spatial extent of the local oceanographic explanatory variables subsequently included in our IPMs (see below).

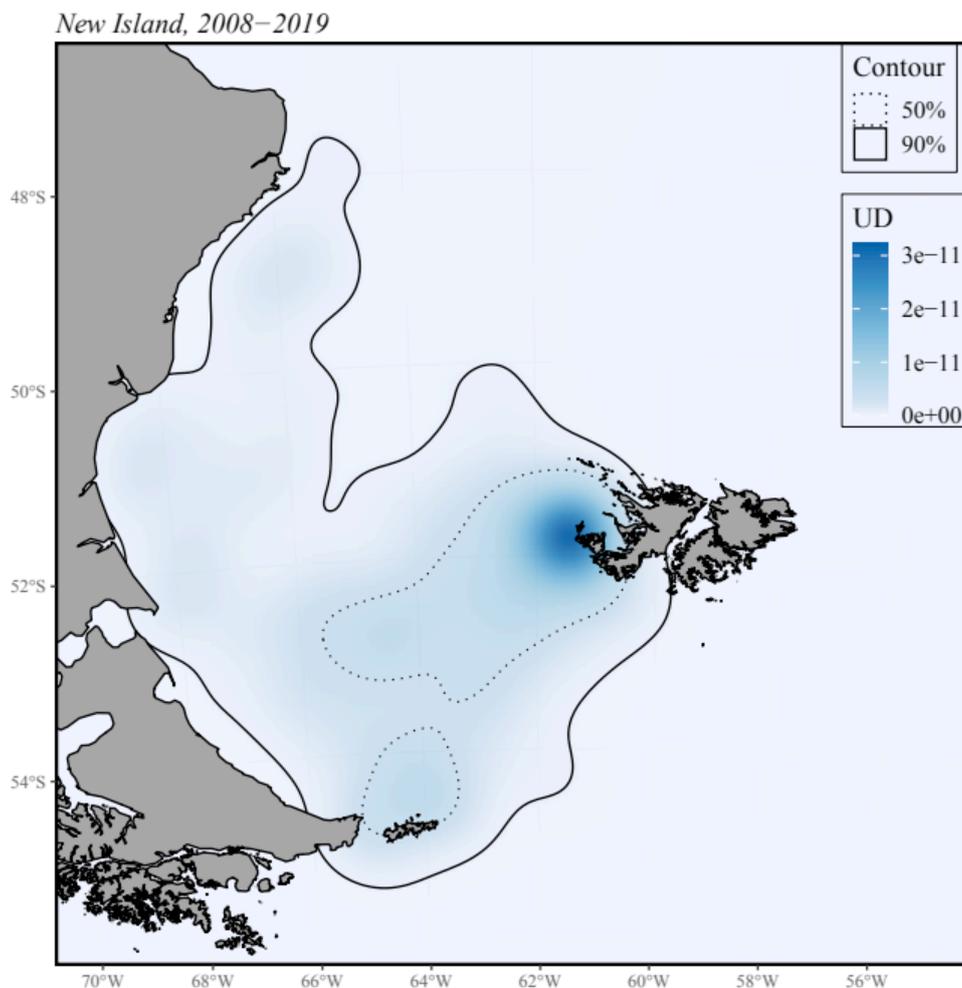


Figure S2. The overall Utilisation Distribution of black-browed albatross from the colony in New Island, Falkland/Malvinas Islands. Darker areas represent areas most intensely used by albatrosses. The 50% and 90% contours are showed with a dotted and solid line, respectively.

Explanatory variables extraction

We considered local oceanographic variables (sea surface temperature anomaly, "SSTA"; net primary production, "NPP"; wind intensity, "WIND"), extracted from the 90% contour of the overall UD; and large-scale climatic indices (Southern Annular Mode, "SAM"; Southern Oscillation Index, "SOI"). We hypothesised that local ocean variables could affect BBA adult survival (ϕ_a) and productivity ($\text{breed}_{\text{adult}}$, $\text{succ}_{\text{adult}}$) processes. As adult survival is the most sensitive trait in longevous species, we hypothesised that the variability in this parameter was influenced by deeper ecosystem changes, captured by large-scale indices. Hence, we included SAM and SOI as predictors for adult survival (ϕ_a).

The local oceanographic variables were Monthly Multi-scale Ultra-high Resolution SSTA ($^{\circ}\text{C}$), downloaded from NOAA at a spatial resolution of 0.01° (<https://coastwatch.pfeg.noaa.gov/erddap/griddap/jplMURSST41anommday.html>). Remotely sensed NPP (mg/m^2) rasters, produced by Copernicus Marine Environment Monitoring Services (<https://oceandata.sci.gsfc.nasa.gov/MODIS-Aqua>), were downloaded at a spatial resolution of 0.04° and daily temporal resolution, but were subsequently summarised as monthly averages for every month in the study. WIND (m/s) was calculated from wind meridional and zonal components reanalysis available from the ECMWF ERA-5 database (<https://cds.climate.copernicus.eu/cdsapp>), at a spatial and temporal resolution of 0.25° and 6 hours. Monthly mean WIND rasters were calculated for each month in the study.

The SAM index, available on the British Antarctic Survey database (<http://www.nerc-bas.ac.uk/icd/gjma/sam.html>) is the atmospheric pressure difference between the latitudes 40°S and 65°S . SAM is the main mode of inter-annual climate variability in the Southern Hemisphere, deeply influencing the circulation (winds, sea surface temperatures and chlorophyll concentration) on the Patagonian Shelf and in the Southern Ocean (Lovenduski & Gruber 2005). SOI was downloaded from <http://www.cpc.ncep.noaa.gov/data/indices/soi>. It is calculated as the difference in surface air pressure between Tahiti and Darwin and captures large-scale fluctuations in air pressure across the tropical Pacific. Negative SOI phases indicate El Niño years, with anomalously warm ocean waters and a dramatic reduction in nutrients availability across the eastern tropical Pacific (Barber & Chavez 1983, Cai et al. 2014).

Both local oceanographic variables and large-scale indices were averaged across three observation windows (figure S3), considered the relevant time spans during which the explanatory variables affected the demographic parameters in exam. For $\text{breed}_{\text{adult}}$, the variables were averaged across the wintering season (i.e. from april to september) prior to the focal breeding season; for $\text{succ}_{\text{adult}}$, the selected window comprised the focal breeding season, from october to march; for ϕ_a , the variables were averaged from october (i.e. the beginning of the focal breeding season) to september (i.e. the end of the subsequent wintering season). For the large-scale indices, we hypothesised that a lag was required for their effects to reach the upper trophic levels and affect BBA demography, particularly for the El Niño anomalies that need to propagate and be transferred to the South Atlantic

(Stenseth et al. 2003). We therefore tested their inclusion under different temporal lags: 6, 12, 24 and 36 months for SAM; and 12, 24 and 36 months for SOI. The temporal lags were applied to the survival temporal window (october to september). The only large-scale index retained as significant in our IPMs was SAM, with a lag of 12 months (figure S4).

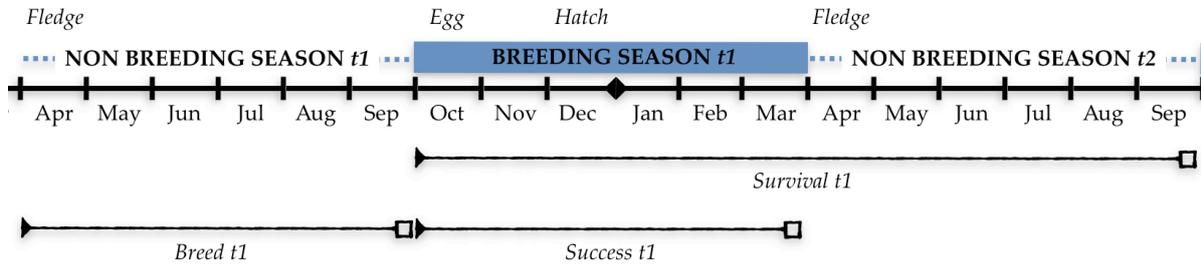


Figure S3. The observation windows considered for the extraction of the explanatory variables in our models. For the focal season $t1$, the relevant time-span for the probability of breeding was the non-breeding season before (*Breed t1*, april to september $t1$). For breeding success, the selected time-span was the focal breeding season (*Success t1*, october to march $t1$). The observation window considered for adult survival was the focal breeding season to the end of the subsequent non-breeding season (*Survival t1*, october $t1$ to september $t2$).

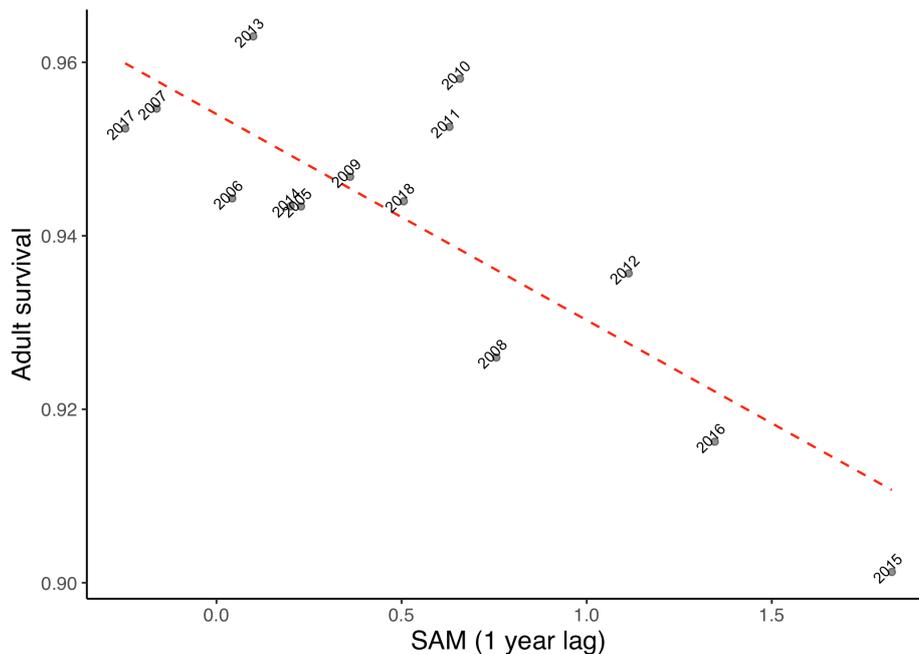


Figure S4. The correlation between adult survival and SAM averaged across the survival temporal window (October to September) with a time-lag of 1 year. Adult survival was strongly negatively correlated with SAM (Pearson's correlation, $r_{12} = -0.82$, $P = 0.0003$). SAM with a lag of 1 year was the only variable retained in the survival IPM.

Text S3. The Integrated Population Modelling framework

Background

Changes in population size over time are driven by demographic rates. The link between population processes (parametrised by demographic rates) and the outcome of these processes (i.e. the population abundance) is straightforward:

$$N_{t+1} = N_t * f(S, P),$$

where N is the population size and f is a generic function of survival (S) and productivity (P). Time-series datasets on abundance therefore intrinsically contain information about the underlying demographic processes. However, traditionally, studies focusing on population dynamics often estimate abundance, survival, fecundity and other demographic rates by separately analysing different type of datasets. In turns, this hampers our understanding of the whole set of processes shaping the changes in population size.

The integrated population models (IPMs) are a novel, powerful tool developed to simultaneously analyse various type of demographic data into a unified modelling framework (Abadi et al. 2010, Schaub & Abadi 2011, McCaffery & Lukacs 2016). IPMs jointly analyse time series of counts; data on demographic rates such as individual based capture-mark-recapture datasets; and data on productivity. In so doing, IPMs capitalise on the strengths of each dataset to yield better estimates of population trajectories. Furthermore, by extracting information for a parameter of interest from multiple data sources, IPMs estimate demographic rates with increased precision compared to conventional models applied to separate datasets. In particular, IPMs proved to be particularly effective in estimating critical parameters difficult to quantify due to the lack of explicit information. Moreover, the flexibility of the IPM formulation allows for modelling the effects of candidate covariates of interest on specific demographic parameters.

IPM formulation

We constructed an age-stage structured IPM with twelve age-stage classes (described in the "Materials and Methods" section in the main text). We adopted a state-space modelling formulation to model the population count (Kéry & Schaub 2012b a) component of the IPM. Since in the IPM population counts inform demographic rates and vice-versa, failing to capture emigration would lead to underestimates in the survival parameters. Conversely, not accounting for the immigration process (through which immigrating successful or failed breeders first enter into the study cohort) would yield inflated estimates of breeding parameters and adult survival. To account for emigration, we incorporated the *BreedOut* stage into the IPM using data on birds ringed as chicks in our study plots that were subsequently recaptured outside. To capture the immigration process, we used data on local (i.e. which were born in the study cohort) and immigrant adults (i.e. which entered into our monitored plots as breeders). The number of immigrant breeders was simply added to the state equations describing the successful and failed

breeders dynamics; in so doing, the demographic parameters only shaped the local component of the breeding population.

The following set of state equations was used to describe the dynamics of the true, but unknown, age-stage population sizes over time. In order to account for stochasticity, we used the Poisson (Po) and Binomial (bin) statistical distributions. To model the number of chicks at each time-step t , we used a Poisson distribution with rate equal to $0.5 \cdot N_{S,t}$ (i.e. half of the total number of successful breeders at the same time-step).

$$N_{J0,t+1} \sim \text{Po}(0.5 \cdot N_{S,t+1})$$

$$N_{J1,t+1} \sim \text{Po}(N_{J0,t} \cdot \phi_1)$$

$$N_{J2,t+1} \sim \text{bin}(\phi_j, N_{J1,t})$$

$$N_{J3,t+1} \sim \text{bin}(\phi_j, N_{J2,t})$$

$$N_{\text{Imm},t+1} \sim \text{bin}(\phi_j, N_{J3,t})$$

$$N_{\text{PreB1},t+1} \sim \text{bin}(\phi_a, N_{\text{Imm},t})$$

$$N_{\text{PreB2},t+1} \sim \text{bin}(\phi_a, N_{\text{PreB1},t} \cdot (1 - \text{recr}_{6-7y}))$$

$$N_{\text{PreB3},t+1} \sim \text{bin}(\phi_a, (N_{\text{PreB2},t} \cdot (1 - \text{recr}_{6-7y}) + N_{\text{PreB3},t} \cdot (1 - \text{recr}_{8+y})))$$

$$N_{\text{BreedOut},t+1} \sim \text{bin}(\phi_a, (N_{\text{PreB1},t} \cdot \text{recr}_{6-7y} \cdot \text{emig} + N_{\text{PreB2},t} \cdot \text{recr}_{6-7y} \cdot \text{emig} + N_{\text{PreB3},t} \cdot \text{recr}_{8+y} \cdot \text{emig}))$$

$$N_{S,t+1} \sim \text{bin}(\phi_a, (N_{\text{PreB1},t} \cdot \text{recr}_{6-7y} \cdot (1 - \text{emig}) \cdot \text{succ}_{\text{CPB}} + N_{\text{PreB2},t} \cdot \text{recr}_{6-7y} \cdot (1 - \text{emig}) \cdot \text{succ}_{\text{CPB}} + N_{\text{PreB3},t} \cdot \text{recr}_{8+y} \cdot (1 - \text{emig}) \cdot \text{succ}_{\text{CPB}} + (N_{S,t} + N_{F,t} + N_{\text{NonB},t}) \cdot \text{breed}_{\text{adult}} \cdot \text{succ}_{\text{Cadult}})) + N_{\text{SImmig},t+1}$$

$$N_{F,t+1} \sim \text{bin}(\phi_a, (N_{\text{PreB1},t} \cdot \text{recr}_{6-7y} \cdot (1 - \text{emig}) \cdot (1 - \text{succ}_{\text{CPB}}) + N_{\text{PreB2},t} \cdot \text{recr}_{6-7y} \cdot (1 - \text{emig}) \cdot (1 - \text{succ}_{\text{CPB}}) + N_{\text{PreB3},t} \cdot \text{recr}_{8+y} \cdot (1 - \text{emig}) \cdot (1 - \text{succ}_{\text{CPB}}) + (N_{S,t} + N_{F,t} + N_{\text{NonB},t}) \cdot \text{breed}_{\text{adult}} \cdot (1 - \text{succ}_{\text{Cadult}}))) + N_{\text{FImmig},t+1}$$

$$N_{\text{NonB},t+1} \sim \text{bin}(\phi_a, (N_{S,t} + N_{F,t} + N_{\text{NonB},t}) \cdot (1 - \text{breed}_{\text{adult}}))$$

The observation equations linked the true states to the observed data by accounting for age-stage specific probability of detection: p_C (i.e. nestlings detection probability); p_J (juveniles); p_{ImmPB} (immatures and pre-breeders); p_{BreedOut} (birds that emigrated and recruited outside of the study colonies); p_{AdultB} (adult breeders, both successful and failed); $p_{\text{AdultNonB}}$ (adult non breeders).

$$Y_{J0,t} = N_{J0,t} \cdot p_C$$

$$Y_{J1,t} = N_{J1,t} \cdot p_J$$

$$Y_{J2,t} = N_{J2,t} \cdot p_J$$

$$Y_{J3,t} = N_{J3,t} \cdot p_J$$

$$Y_{\text{Imm},t} = N_{\text{Imm},t} \cdot p_{\text{ImmPB}}$$

$$Y_{\text{PreB1},t} = N_{\text{PreB1},t} \cdot p_{\text{ImmPB}}$$

$$Y_{\text{PreB2},t} = N_{\text{PreB2},t} \cdot p_{\text{ImmPB}}$$

$$Y_{\text{PreB3},t} = N_{\text{PreB3},t} \cdot p_{\text{ImmPB}}$$

$$Y_{\text{BreedOut},t} = N_{\text{BreedOut},t} \cdot p_{\text{BreedOut}}$$

$$Y_{S,t} = N_{S,t} \cdot p_{\text{AdultB}}$$

$$Y_{F,t} = N_{F,t} \cdot p_{\text{AdultB}}$$

$$Y_{\text{NonB}, t} = N_{\text{NonB}, t} * p_{\text{AdultNonB}}$$

The likelihood for the age-stage population count data is the product of the likelihood of the observation and process equations, and is denoted as:

$$L_{\text{COUNT}}(y \mid \phi_a, \phi_j, \text{recr}_{6-7y}, \text{recr}_{8+y}, \text{succ}_{\text{CPB}}, \text{breed}_{\text{adult}}, \text{succ}_{\text{adult}}, \text{emig}, N_{J0}, N_{J1}, N_{J2}, N_{J3}, N_{\text{Imm}}, N_{\text{PreB1}}, N_{\text{PreB2}}, N_{\text{PreB3}}, N_{\text{BreedOut}}, N_{\text{S}}, N_{\text{F}}, N_{\text{NonB}}, p_{\text{C}}, p_{\text{J}}, p_{\text{ImmPB}}, p_{\text{BreedOut}}, p_{\text{AdultB}}, p_{\text{AdultNonB}})$$

For the CMR component of our IPM, the individual capture histories were modelled using a multi-event framework with a state-space modelling formulation (Kéry & Schaub 2012c a). This allowed for the estimation of age-stage specific survival and productivity rates accounting for age-stage specific probability of detection. In the capture histories, each individual bird was assigned one of the twelve possible states described above, with the state assignment assumed to be exact. The likelihood of the CMR data is hereby denoted as:

$$L_{\text{CMR}}(m \mid \phi_a, \phi_j, \text{recr}_{6-7y}, \text{recr}_{8+y}, \text{succ}_{\text{CPB}}, \text{breed}_{\text{adult}}, \text{succ}_{\text{adult}}, \text{emig}, p_{\text{C}}, p_{\text{J}}, p_{\text{ImmPB}}, p_{\text{BreedOut}}, p_{\text{AdultB}}, p_{\text{AdultNonB}})$$

For the productivity data, we modelled the number of fledglings recorded each year produced by first-time breeders (FTB) and adult birds (AB, i.e. second time breeders or more) using a binomial distribution with probability equal to succ_{CPB} and $\text{succ}_{\text{adult}}$ and size equal to the total number of first time and adult breeding pairs, respectively. The likelihood is:

$$L_{\text{P}}(J0, \text{FTB}, \text{AB} \mid \text{succ}_{\text{CPB}}, \text{succ}_{\text{adult}}).$$

Assuming independence between each dataset, the joint IPM likelihood is the product between each component likelihood:

$$L_{\text{IPM}}(y, m, 0, \text{FTB}, \text{AB} \mid \phi_a, \phi_j, \text{recr}_{6-7y}, \text{recr}_{8+y}, \text{succ}_{\text{CPB}}, \text{breed}_{\text{adult}}, \text{succ}_{\text{adult}}, \text{emig}, N_{J0}, N_{J1}, N_{J2}, N_{J3}, N_{\text{Imm}}, N_{\text{PreB1}}, N_{\text{PreB2}}, N_{\text{PreB3}}, N_{\text{BreedOut}}, N_{\text{S}}, N_{\text{F}}, N_{\text{NonB}}, p_{\text{C}}, p_{\text{J}}, p_{\text{ImmPB}}, p_{\text{BreedOut}}, p_{\text{AdultB}}, p_{\text{AdultNonB}}).$$

We specified vague priors for all recapture, survival and breeding parameters, using uniform distributions bounded between 0 and 1: parameter $\sim U(0,1)$. The only exception was the prior for p_{J} , which was instead a uniform distribution bounded between 0 and 0.1: $p_{\text{J}} \sim U(0, 0.1)$.

The priors for all age-stages population sizes were set as Poisson distribution with mean $\lambda = 100$, with the exception of the prior of N_{J0} , which was set as $\lambda = 70$.

Analysis of temporal variability

We modelled the temporal variability of productivity ($\text{breed}_{\text{adult}}$ and $\text{succ}_{\text{adult}}$) and survival (ϕ_a) by including each breeding season (i.e. each recapture occasion) as a temporal random effect. Because of the complex formulation and the large number of parameters in the IPM, the inclusion of temporal random effects on both survival and productivity parameters (which are multiplied by each other to define the transition probabilities) resulted in lack of model convergence. Therefore, we separately included temporal random effects on $\text{breed}_{\text{adult}}$, $\text{succ}_{\text{adult}}$ and ϕ_a in three different IPMs. The inclusion of the random effect in the model was specified using the formula:

$$\text{logit}(\text{breed}_{\text{adult}, t}) = \zeta + \epsilon_{\text{breed}, t} \quad \epsilon_{\text{breed}, t} \sim N(0, \sigma^2_{\text{breed}})$$

$$\text{logit}(\text{succ}_{\text{adult},t}) = \eta + \varepsilon_{\text{succ},t} \quad \varepsilon_{\text{succ},t} \sim N(0, \sigma^2_{\text{succ}})$$

$$\text{logit}(\phi_{a,t}) = \theta + \varepsilon_{\phi^a,t} \quad \varepsilon_{\phi^a,t} \sim N(0, \sigma^2_{\phi^a})$$

where ζ, η, θ are the overall mean probabilities of breeding, success and adult survival (on the logit scale); $\varepsilon_{\text{breed},t}, \varepsilon_{\text{succ},t}, \varepsilon_{\phi^a,t}$ are the temporal random effects, drawn from a Normal distribution with temporal variance (on the logit scale) equal to $\sigma^2_{\text{breed}}, \sigma^2_{\text{succ}}, \sigma^2_{\phi^a}$, respectively. The prior distributions for $\sigma^2_{\text{breed}}, \sigma^2_{\text{succ}}$ and σ_{ϕ^a} were set as uniform distributions bounded between 0 and 2.

Effect of candidate covariates

Due to the IPMs complexity and the impossibility to test for the effect of every variable on each parameter, we adopted the following protocol. Starting from the baseline model formulation (i.e. without random effects), we created a set of IPMs including either local oceanographic variables or large-scale climatic indices. Prior to modelling, we ensured that the explanatory variables were not collinear using variance inflation factors (VIFs) from the AED package (Zuur et al. 2009), with a threshold value of 3. All variables were standardised before model fitting.

We used univariate logistic regression to separately investigate the effect of the candidate covariates on $\phi_a, \text{breed}_{\text{adult}}, \text{succ}_{\text{adult}}$ as follows:

$$\text{logit}(\phi_{a,t}) = \beta_0 + w_1 * \beta_1 * X_{1,t} + w_2 * \beta_2 * X_{2,t} + \dots$$

$$\text{logit}(\text{breed}_{\text{adult},t}) = \beta_0 + w_1 * \beta_1 * X_{1,t} + w_2 * \beta_2 * X_{2,t} + \dots$$

$$\text{logit}(\text{succ}_{\text{adult},t}) = \beta_0 + w_1 * \beta_1 * X_{1,t} + w_2 * \beta_2 * X_{2,t} + \dots$$

where β_0 is the intercept; β_1 is the slope of variable 1; $X_{1,t}$ is the candidate explanatory variable 1, indexed by timestep; w_1 is a parameter quantifying the inclusion probability of covariate 1, thus representing its importance in the model (O'Hara & Sillanpää 2009).

As we considered lagged climatic indices and we did not know in advance what was the relevant lag for each variable, we created two IPMs separately testing for the effect of each climatic variable, considering all lags. In the end, based on their inclusion probability, all SOI indices were discarded and only SAM with a 12 month temporal lag was selected.

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