

Linking climate variability, productivity and stress to demography in a long-lived seabird

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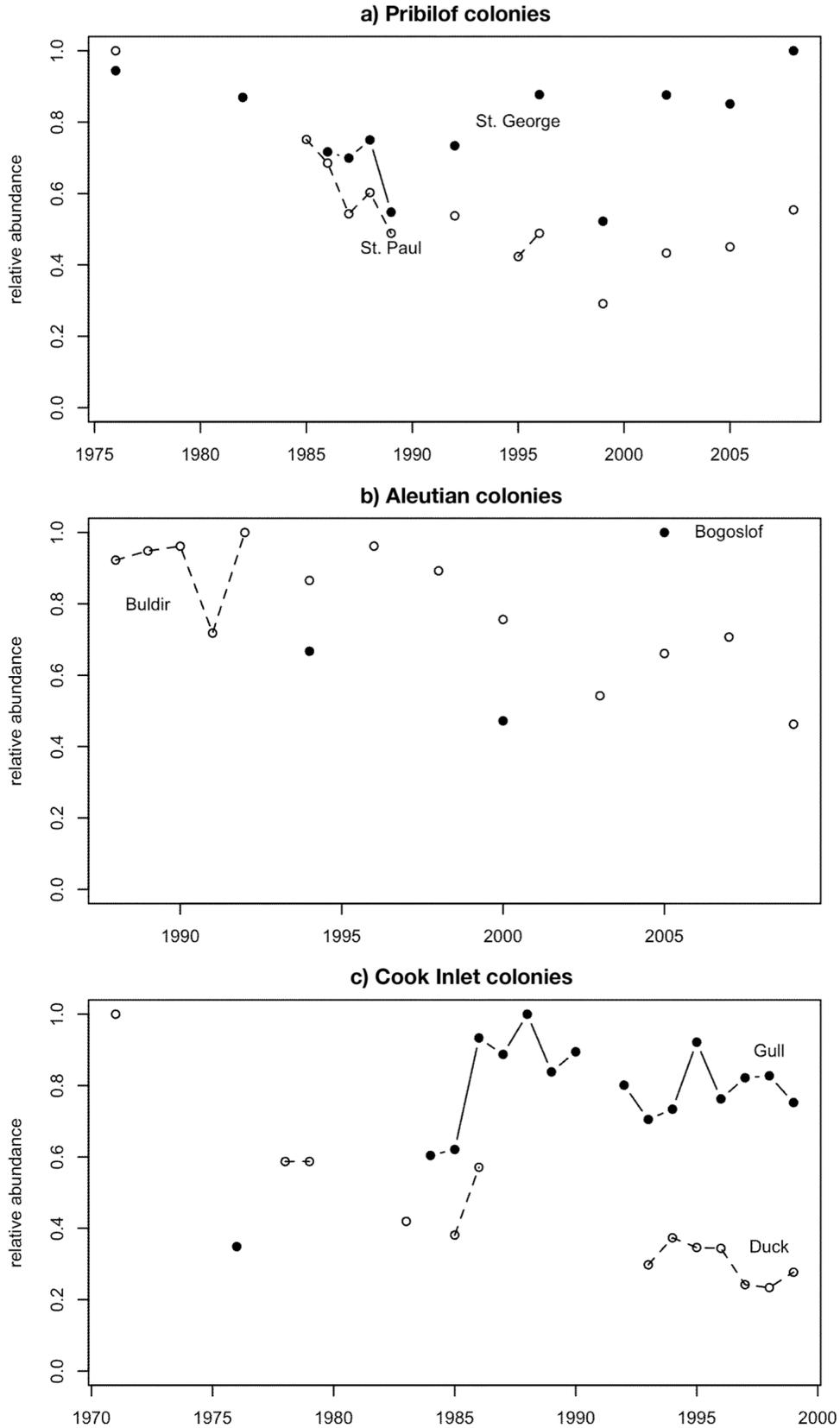
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Supplement 1. In this supplement, we summarize the annual sample sizes used to measure stress hormones at each colony (Table S1) and present temporal trends in abundance (Fig. S1).

Table S1. Numbers of birds sampled for corticosterone for each colony–year combination

	Duck	Gull	Saint Paul	Saint George	Bogoslof	Buldir
1996	5	11	–	–	–	–
1997	24	25	–	–	–	–
1998	38	97	–	–	–	–
1999	29	67	13	–	11	–
2000	32	63	35	30	45	–
2001	9	38	–	–	–	–
2002	8	–	9	–	20	–
2003	–	–	30	31	–	32
2004	–	–	31	29	15	46
2005	–	–	15	26	10	–
2006	–	–	–	–	–	–
2007	–	–	–	–	–	–
2008	–	–	43	62	20	–
2009	–	–	47	55	25	–

Fig. S1. Trends in relative abundance as determined by counts on reference plots divided by the maximum for each colony in the (a) Pribilof colonies (●: St. George; ○: St. Paul), (b) Aleutian colonies (●: Bogoslof; ○: Buldir), and (c) Cook Inlet colonies (●: Gull; ○: Duck). Note different timespans of data availability and thus different x-axes for the different regions



Supplement 2. Quantifying uncertainty in demographic predictions

Here, we quantify the effects of uncertainty due to sampling size by estimating a long-term mean value for R_0 for kittiwakes *Rissa tridactyla* on Bogoslof, Buldir, Saint George, and Saint Paul Islands. We cannot evaluate the uncertainty arising from the potential for differential CORT responses across space or time, or borrowing juvenile survival estimates from Prince William Sound, and do not estimate or evaluate the effects of temporal variability per se.

Given these assumptions, we calculate the expected value of R_0 as:

$$R_0 = \frac{1}{2} s \frac{1}{m(x)} f \quad (\text{S1})$$

where s is survival from fledging to age of first reproduction, f is the average number of chicks fledged per reproductive event, and $m(x)$ is the annual adult survival associated with CORT level x as described in the main text (section ‘Estimating adult survival from stress data’ of ‘Materials and methods’). Multiplying by one-half corrects for the sex ratio.

If r represents the vector of the parameter making up $m(x)$, we then calculate the probability that R_0 takes a particular value R_0^* :

$$p\left(R_0 = R_0^* = \frac{1}{2} s^* \frac{1}{m^*(r^*, x^*)} f^*\right) = p\left(s = s^* \ \& \ r = r^* \ \& \ x = x^* \ \& \ f = f^*\right) \quad (\text{S2})$$

where s^* , $m^*(r^*, x^*)$, and f^* are the quantities that yield R_0^* when plugged into Eq. (S1), with r the parameters for the function $m(x)$. For compactness, we write probabilities like $p(z = z^*)$ as $p(z^*)$ from now on.

Logically consistent statements about probability in this context require a Bayesian approach, albeit one in which we can use entirely uninformative priors. Then we can calculate the probability of a particular value of R_0^* given data y (to be further described later) as follows:

$$p(R_0^* | y) = p(s^*, r^*, x^*, f^* | y) \quad (\text{S3})$$

We estimated s , r , x , and f from separate datasets which we define as y_s , y_r , y_x , and y_f , respectively; thus, $p(s)$, $p(r)$, $p(x)$, and $p(f)$ are independent and can be multiplied to give their joint probabilities:

$$p(R_0^* | y) = p(s^* | y_s) p(r^* | y_r) p(x^* | y_x) p(f^* | y_f) \quad (\text{S4})$$

By Bayes’ theorem:

$$p(R_0^* | y) = \frac{p(y_s | s^*)}{p(y_s)} \frac{p(y_r | r^*)}{p(y_r)} \frac{p(y_x | x^*)}{p(y_x)} \frac{p(y_f | f^*)}{p(y_f)} \quad (\text{S5})$$

where $p(a^*)$ is a prior probability, $p(y_a/a^*)$ is likelihood, and $p(y_a)$ is a (generally unknowable, but constant) probability of the data. In theory, calculating the value of Eq. (S5) yields a complete description of the posterior probability of R_0^* . In practice, this direct calculation may be prohibitively difficult (and depend on unknowable probabilities of data), but in practice we can use Markov Chain Monte Carlo (MCMC sampling; Gelman et al. 2003) to fully describe the relative posterior probability corresponding to any set of parameters (s, r, x, f) and thus any R_0 to any desired level of precision. In calculating these relative posterior probabilities, the unknowable constant probabilities of the data drop out since they are constant regardless of the proposed parameter values or observed data. We can then use quantile analysis of all the values of R_0 calculated for each set of parameter estimates retained in the MCMC chain to estimate credible intervals on R_0 .

To implement MCMC sampling of Eq. (S5), we first note that each component term of the multiplication is independent and can thus be sampled independently (i.e. we propose a jump in s , accept or reject it, then propose a jump in r , accept or reject it, and so on for x and f for each iteration of the chain and then repeat the chain for a large number of iterations).

We estimated s from Suryan et al. (2000), but do not have direct access to that data. Therefore, we do not calculate prior probabilities or likelihoods involving s directly; instead, we assign a posterior probability for $p(s^*)p(y_s/s^*)/p(y_s)$ by assuming it follows a normal distribution with a mean of 0.567 and a SD of 0.026, as reported in Suryan et al. (2000). For the remaining terms, we assumed uniform priors [$p(r^*)$, $p(x^*)$, and $p(f^*)$ drop out as constants].

We calculated likelihoods for r as:

$$p(r | y_r) = \prod_s \frac{e^{r_1 + r_2 x_s}}{1 + e^{r_1 + r_2 x_s}} \prod_m \left(1 - \frac{e^{r_1 + r_2 x_m}}{1 + e^{r_1 + r_2 x_m}} \right) \quad (\text{S6})$$

where x_s are the CORT measurements for all surviving birds and x_m are the CORT measurements for all lost birds in Satterthwaite et al. (2010). To calculate likelihoods for f , we assumed each year's f was estimated perfectly (since sample sizes to estimate productivity were relatively large) and assumed the yearly values followed a scaled beta distribution with a maximum value of 2.0 (since fecundity cannot be negative, and kittiwakes in this system almost never lay >2 eggs). For the Pribilof colonies, productivity data were transformed by adding 0.0001 to avoid numeric difficulties introduced by calculating the density of a beta distribution at 0. We then subtracted

0.0001 from the emergent estimates of mean f . To calculate likelihoods for x , we assumed that a lognormal distribution described the measurements for each individual within a year (since CORT levels cannot be negative and follow an approximately lognormal distribution as plotted in Satterthwaite et al. 2010). We thus generated an MCMC chain with estimates of the median, standard deviation, and mean value of x for each year in the dataset, and when converting the chain of parameter estimates to an estimate of R_0 we used the mean of yearly mean (arithmetic scale) CORT values to estimate survival. We did not make direct use of our estimates for the standard deviations in f or x . However, in addition to credible intervals on R_0 , we can generate credible intervals on individual components of the life cycle or composite parts of it (e.g. fledging times expected survival from fledging to first reproduction).

For each colony, we ran the chain for 630 000 iterations and discarded the first 30 000 as burn in, then thinned the chains to every 30th replicate. We conducted MCMC sampling using customized code or the MCMCmetrop1R command in the library MCMCpack (Martin et al. 2011) of R (R Development Core Team 2009). We examined plots and key diagnostics for convergence and proper mixing. This led to 95% credible intervals on R_0 of 1.01 to 3.5 for Bogoslof, 0.18 to 0.65 for Buldir, 0.24 to 0.97 for St George, 0.28 to 1.08 for St Paul, 1.03 to 5.28 for Gull, and 0.02 to 0.36 for Duck.