Appendix A: Estimates of model parameters used in stochastic population model.

General modeling approach

By assuming that the fecundity in state $k$ of individual $i$ in year $j$ is $F_{kij} \sim \text{Poisson}(f_{kij})$ and survival is $S_{kij} \sim \text{Binomial}(s_{kij})$, the temporal variation in fecundity and survival was decomposed into components due to demographic variation, climatic and other environmental variables, density effects and residual unexplained environmental (co)variation using the following statistical model:

$$
\begin{align*}
\log f_{Lij} &= \beta_{f_{ij}0} + \beta_{f_{ij}Z} Z_{ij} + \beta_{f_{ij}N} N_{ij} + u_{f_{ij}0j} \\
\log f_{Hij} &= \beta_{f_{ij}0} + \beta_{f_{ij}Z} Z_{ij} + \beta_{f_{ij}N} N_{ij} + u_{f_{ij}0j} \\
\log s_{oij} &= \beta_{s_{ij}0} + \beta_{s_{ij}Z} Z_{ij} + \beta_{s_{ij}N} N_{ij} + u_{s_{ij}0j} \\
\log s_{tij} &= \beta_{s_{ij}0} + \beta_{s_{ij}Z} Z_{ij} + \beta_{s_{ij}N} N_{ij} + u_{s_{ij}0j} \\
\log s_{2ij} &= \beta_{s_{ij}0} + \beta_{s_{ij}Z} Z_{ij} + \beta_{s_{ij}N} N_{ij} + u_{s_{ij}0j} \\
\log s_{Nij} &= \beta_{s_{ij}0} + \beta_{s_{ij}Z} Z_{ij} + \beta_{s_{ij}N} N_{ij} + u_{s_{ij}0j} \\
\log s_{Lij} &= \beta_{s_{ij}0} + \beta_{s_{ij}Z} Z_{ij} + \beta_{s_{ij}N} N_{ij} + u_{s_{ij}0j} \\
\log s_{Hij} &= \beta_{s_{ij}0} + \beta_{s_{ij}Z} Z_{ij} + \beta_{s_{ij}N} N_{ij} + u_{s_{ij}0j}
\end{align*}
$$

where $Z_{ij}$ is a column vector of climatic and other environmental variables (e.g., winter temperature, food) and $N_{ij}$ is a column vector of conspecific densities (e.g., $N_{pop}$, $N_L$) observed during the study period. The beta’s ($\beta_{f_{ij}0}$, $\beta_{s_{ij}0}$, and row vectors $\beta_{f_{ij}Z}$, $\beta_{s_{ij}N}$, etc.) are constants estimated by the statistical model. We specifically considered interactions between climate and density effects ($Z_{ij}N_{ij}$). In addition, we estimated the
residual environmental process variance and covariance in demographic rates that was not explained by $Z_j$ or $N_j$, by including random intercepts ($u_{0j}$) that vary between years.

Due to data limitations we were forced to constrain $u_{e0j} = u_{s0j} = u_{sN0j}$. Based on preliminary data exploration it seemed reasonable to assume that $u_{f0j}$ and $u_{s0j}$ can be approximated by a multivariate normal distribution (MVN) with mean zero and a between-year variance-covariance matrix $\Omega_u$:

$$
\begin{bmatrix}
u_{f0j} \\
u_{f0j} \\
u_{s0j} \\
u_{s0j} \\
u_{sN0j}
\end{bmatrix} \sim MVN(0, \Omega_u)
= \begin{bmatrix}
\sigma^2_{u_{f0j}} & \sigma^2_{u_{f0j}u_{s0j}} & \sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{f0j}u_{sN0j}} \\
\sigma^2_{u_{f0j}u_{s0j}} & \sigma^2_{u_{f0j}u_{s0j}} & \sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{f0j}u_{sN0j}} \\
\sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{s0j}u_{sN0j}} & \sigma^2_{u_{s0j}u_{sN0j}} \\
\sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{s0j}u_{sN0j}} & \sigma^2_{u_{s0j}u_{sN0j}} \\
\sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{f0j}u_{sN0j}} & \sigma^2_{u_{s0j}u_{sN0j}} & \sigma^2_{u_{s0j}u_{sN0j}} \\
\end{bmatrix}
$$

Note that we assume a multivariate normal distribution of (co)variances of vital rates on the transformed log and logit scale (with base $e$). Between-year covariances between fecundity and survival were based on fecundity in the breeding season and survival during the preceding period (and not survival during the following period).

**Model without climatic, density and other environmental covariates**

We first fitted a multivariate model that only included an intercept and a separate year random effect for each vital rate with a fully specified between-year variance covariance matrix. All parameter estimates are given with standard errors between parentheses. The model can be described by the following multivariate regression equation:
Note that in this model \( \Omega_u \) describes the variance within vital rates and covariances between vital rates, which also includes (co)variation due to density dependence and climatic or environmental variables.

**Model with climatic, density and other environmental covariates**

Below we give the final model that included three climatic/environmental variables explaining a substantial amount of the temporal variation in vital rates (see Fig. 3 in the main text). Models that included various density and other environmental variables were not better supported by the data as determined by model selection procedures based on information theoretic criteria (all \( \Delta \text{DIC}>1 \)). The model can be described by the following multivariate regression equation:
with three environmental variables winter temperature $w$ (°C), ragworm abundance $r$ (individuals/m²) and flooding event $q$ (0 or 1) included. These variables were standardized to mean 0 by subtracting the normalization constants $w^*=3.67$, $r^*=107.2$ and $q^*=0.375$ as determined over the study period 1983-2007. Ragworm abundance was subsequently modeled as a function of the variable winter temperature (Fig. 3I):

$$r = 153.04(15.0) - 12.8(3.6)w + e_{r_j}.$$ 

Winter temperature was modeled as a random variable described by a transformed lognormal process $w \sim 10 - \lognormal(\mu - 10, \sigma)$, with $\mu$ and $\sigma$ chosen such that $E(w) = 3.67(0.44)$ and $\sigma_w = 1.71(0.49)$ as in the study period 1983-2007 (see Fig. 2C). In this paper we focus on temperature effects (as this is the only variables for which we have evidence that it will change systematically in the future) and therefore residual ragworm process variance ($e_{r_j}$) and flooding events were modeled as random variables part of the residual environmental stochasticity:
with ragworm process variance $e_{eq} \sim N(0, \sigma_{eq}) \; : \; \sigma_{eq} = 31.5(9.1)$, flooding variance $e_{eq} \sim (Bin(\pi) - \pi) \; : \; \pi = 0.375(0.049)$ and residual environmental (co)variances:

\[
\begin{pmatrix}
\begin{bmatrix}
0.114(0.117) & -0.114(0.083) & 0.513(0.148) \\
-0.078(0.076) & -0.116(0.057) & 0.143(0.074) \\
0.010(0.087) & -0.163(0.069) & 0.221(0.091) \\
-0.030(0.132) & -0.119(0.095) & 0.239(0.130) \\
\end{bmatrix} & 0.617(0.178) & 0.021(0.088) & 0.300(0.087) & 0.010(0.087) & -0.163(0.069) & 0.221(0.091) & -0.030(0.132) & -0.119(0.095) & 0.239(0.130) & 0.124(0.082) & 0.108(0.094) & 0.674(0.195) \\
\end{pmatrix}
\]

The contribution of variance component of environmental variable $Z$ (or density variable $N$) to total process variance in vital rate $x_i$ was calculated using the formula:

\[
R^2_{Z,x_i} = \frac{\sigma^2_{\text{model without Z}} - \sigma^2_{\text{model with Z}}}{\sigma^2_{\text{model without Z}}}
\]