

Appendix S1. Supporting Information to:

“Mechanistic description of population dynamics using dynamic energy

budget theory incorporated into integral projection models”

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1. Modelling growth and reproduction from the Kooijman-Metz model

The Kooijman-Metz energy budget model (Kooijman & Metz 1984) assumes that individual organisms are isomorphic which means that body weight W is proportional to the cubed length of an individual. Individuals are born at length L_b and mature at length L_p . The rate at which individuals ingest food, I , is assumed to be proportional to body surface area and hence to the squared length of an organism:

$$I = I_{max}YL^2$$

where L is length of an individual, Y is the experienced feeding level at time t , I_{max} is the proportionality constant relating maximum food ingestion rate to L^2 . Ingested food is assimilated with a constant efficiency ε .

Of the energy assimilated by individuals, a fraction κ is allocated to somatic growth and maintenance (respiration energy) and the remainder to reproduction (reproduction energy). Juveniles do not produce young and instead reproduction energy is assumed to be allocated to the development of the reproductive apparatus. Respiration energy is divided into (i) energy for maintenance, which is assumed proportional to body weight and thus scales with the cubed length of an individual following ξL^3 (where ξ is the proportionality constant relating maintenance energy to cubed length), and (ii) energy spent on tissue growth. Individuals therefore change in weight W at a rate that is proportional to the difference between the respiration energy and energy required for maintenance:

$$\frac{dW}{dt} = \psi^{-1}(\kappa \varepsilon I_{max} Y L^2 - \xi L^3)$$

where ψ represents the energetic requirements to grow one unit in body weight. We substitute the weight-length relationship $W = \beta L^3$ (where β is a weight-length scaling constant) which leads to the following change in length over time (Kooijman & Metz 1984):

$$\frac{dL}{dt} = \dot{r}_B (L_m \cdot Y - L)$$

where maximum length at abundant food $L_m = \kappa \varepsilon I_{max} / \xi$ and $\dot{r}_B = \xi / (3\beta\psi)$ is the von Bertalanffy growth rate. After rearrangement this becomes:

$$\frac{dL}{dt} = -\dot{r}_B (L - YL_m) \Leftrightarrow \frac{dL}{L - YL_m} = -\dot{r}_B dt$$

After integration from time t to time $t + 1$, this results in:

$$\ln(L(t + 1) - YL_m) - \ln(L(t) - YL_m) = -\dot{r}_B a \Leftrightarrow \frac{L(t + 1) - YL_m}{L(t) - YL_m} = e^{-\dot{r}_B t}$$

which leads to (assuming individuals can shrink under starvation conditions):

$$L(t + 1) = L(t)e^{-\dot{r}_B} + (1 - e^{-\dot{r}_B})L_m \cdot Y,$$

which is Eqn 3 in the main text.

The remaining fraction $1 - \kappa$ of consumed food energy is allocated to reproduction (or, in case of juveniles, to the development of reproductive organs and tissue) and hence the reproduction energy equals $(1 - \kappa)\varepsilon I_{max} Y L^2$. Dividing this energy by the energy investment per single offspring, βL_b^3 , leads to the number of offspring per unit time from a female with length $L(t)$ at time t (assuming individuals can shrink under starvation conditions):

$$R(t) = \frac{(1 - \kappa)\varepsilon I_{max} Y L^2(t)}{\beta L_b^3}$$

Defining $R_m = (1 - \kappa)\varepsilon I_{max} L_m^2 / (\beta L_b^3)$ as the maximum reproduction rate of an individual reared at the highest feeding level, the reproduction rate can also be expressed as:

$$R(t) = \frac{Y \cdot R_m \cdot L^2(t)}{L_m^2}$$

2. Consequences of variable von Bertalanffy growth rate in mites

Growth of bulb mites is highly plastic and shows great variation with food availability, as shown in Fig. S1 for mites raised on ad lib access to yeast, the high feeding level (Fig. S1: black squares), and ad lib access to filter paper, the low feeding level (Fig. S1: grey triangles). The Kooijman-Metz DEB model, and hence the DEB-IPM, assumes a constant von Bertalanffy growth rate \dot{r}_B . Fitting the von Bertalanffy growth rate equation $L_t = L_\infty - [L_\infty - L_b]e^{-\dot{r}_B t}$ against the growth data of mites on the low and high feeding level (keeping L_b fixed at 0.166 mm) returns a value of $L_\infty = 0.756$ mm and $\dot{r}_B = 0.015$. Inputting these values in the von Bertalanffy growth rate equation to predict body length as a function of age results in a good fit against the growth data of mites on the low feeding level (Fig. S1: red line versus grey squares), but completely underestimates the growth of mites on the high feeding level (Fig. S1: red line versus black triangles). For this reason we decided to linearly relate \dot{r}_B to feeding level and ultimate length following $\dot{r}_B = 1/(\beta + \alpha L_\infty)$ (Eqn 15 in the main text), where the coefficient α is related to energy conductance and the coefficient β to somatic maintenance (Kooijman *et al.* 2008). Fitting the von Bertalanffy growth rate with different \dot{r}_B values for the two different feeding levels significantly improves predictions on mite growth on the low feeding level data (Fig. S1: grey line versus grey symbols). Had we assumed a constant value of $\dot{r}_B = 0.015$ for all feeding levels, this would have resulted in a great mismatch between predicted and observed population growth rate, lifetime reproductive success and generation time for nearly all feeding levels (Fig. S2).

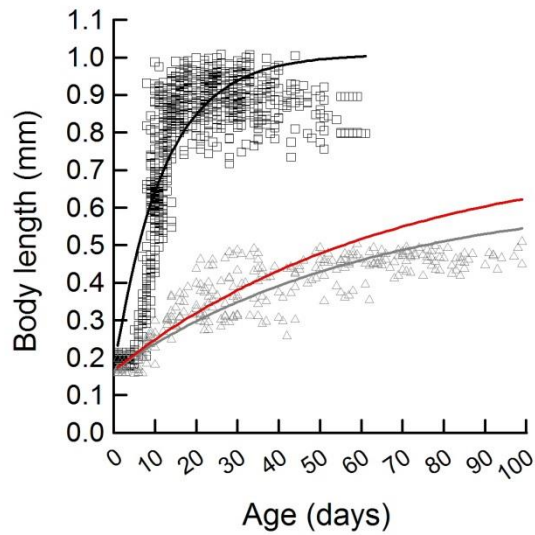


Figure S1. Observed and predicted body length (mm) of bulb mites raised on ad lib access to yeast (high feeding level: black squares) and ad lib access to filter paper (low feeding level: grey triangles) in relation to age (days). Lines are predicted body lengths using the von Bertalanffy growth rate equation $L_t = L_\infty - [L_\infty - L_b]e^{-\dot{r}_B t}$. In this equation, L_∞ and L_b are measured directly from data (Table 1 in the main text) and \dot{r}_B is estimated by fitting the latter equation against empirical data on body length versus age of mites (see main text). Three predictions are shown where \dot{r}_B is estimated using only the yeast data (black line, with $L_\infty = 1.008$, $L_b = 0.166$ and $\dot{r}_B = 0.083$); using only filter paper data (grey line, with $L_\infty = 0.642$, $L_b = 0.167$ and $\dot{r}_B = 0.016$) and using both data sets (red line, with $L_\infty = 0.756$, $L_b = 0.166$ and $\dot{r}_B = 0.015$).

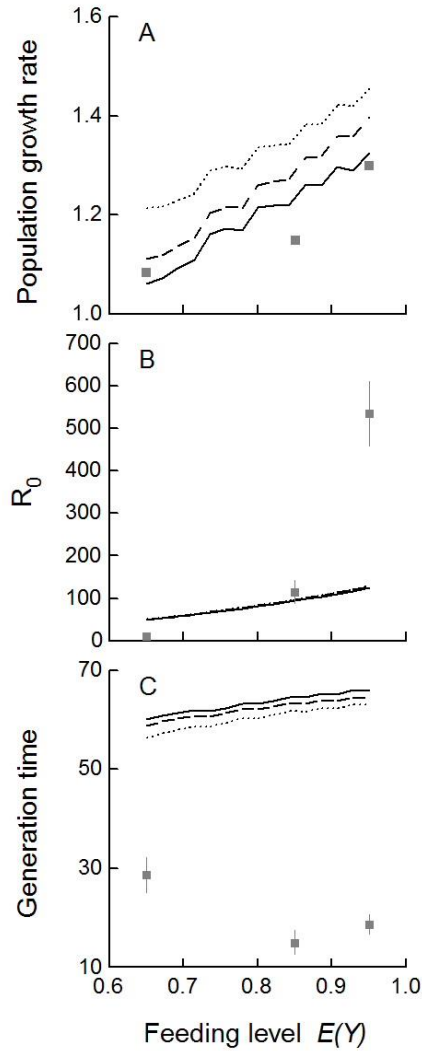


Figure S2. Population growth rate λ (A [d^{-1}]), lifetime reproductive success R_0 (B), and generation time T (C [days]) in relation to feeding level $E(Y)$ as predicted for three values of $\sigma(Y)$: $\sigma(Y) = 0.1$ (solid lines); $\sigma(Y) = 0.3$ (dashed lines) and $\sigma(Y) = 0.5$ (dotted lines) for bulb mites, assuming a constant value of $\hat{r}_B = 0.015$. All other parameter values are as described in the main text and Table 1. Grey symbols are observed values on a low [$E(Y) = 0.64$], intermediate [$E(Y) = 0.85$] and high feeding level [$E(Y) = 0.95$] (see Fig. 2 in the main text). Vertical lines through the symbols in (B) and (C) are 95% confidence intervals.

3. Additional assumptions of the DEB-IPM: when individuals do not shrink

When individuals do not shrink under starvation conditions, then some further assumptions have to be introduced into the equations describing growth and reproduction. To stop individuals from decreasing in length, growth in body size stops when the individual length is larger than $L_m \cdot Y$ as the default allocation to growth and maintenance, the fraction κ of assimilated energy (= respiration energy) is not sufficient to cover maintenance costs alone.

Eqn 3 in the main text then becomes:

$$L(t+1) = \begin{cases} L(t)e^{-r_B} + (1 - e^{-r_B})L_m \cdot Y & \text{for } L \leq L_m Y \\ L(t) & \text{otherwise} \end{cases}, \quad \text{eqn S1}$$

which is Eqn 4 in the main text. Using this equation, the expected length $E(L)$ and variance in length $\sigma^2(L)$ at time $t+1$ for a cohort of individuals of length L is then given by:

$$E(L(t+1)) = \begin{cases} L(t)e^{-r_B} + (1 - e^{-r_B})L_m \cdot E(Y) & \text{for } L \leq L_m E(Y) \\ L(t) & \text{otherwise} \end{cases} \quad \text{eqn S2}$$

and

$$\sigma^2(L(t+1)) = \begin{cases} (1 - e^{-r_B})^2 L_m^2 \sigma^2(Y) & \text{for } L \leq L_m E(Y) \\ 0 & \text{otherwise} \end{cases}, \quad \text{eqn S3}$$

which are respectively Eqn 7 and Eqn 8 in the main text.

Reproduction

When the respiration energy (the fraction κ of all assimilated energy) is not sufficient to cover maintenance costs, ingested energy is rechannelled from reproduction to cover maintenance, which occurs for $L > L_m \cdot Y$ (see also main text). For $L > L_m \cdot Y/\kappa$, an individual is assumed to die instantaneously (see also main text). The rate of reproduction of a cohort of individuals of length L is then given by:

$$R(L(t)) = \begin{cases} 0 & \text{for } L_b \leq L < L_p \\ E(Y)R_m L(t)^2 / L_m^2 & \text{for } L_p \leq L \leq L_m E(Y) \\ \frac{R_m}{1 - \kappa} \left[E(Y)L(t)^2 - \frac{\kappa L(t)^3}{L_m} \right] & \text{for } L_m E(Y) < L \leq L_m E(Y)/\kappa \end{cases} \quad \text{eqn S4}$$

These extra conditions for growth and reproduction do not necessarily affect model outcome, as is illustrated in case of bulb mites in Fig. S3.

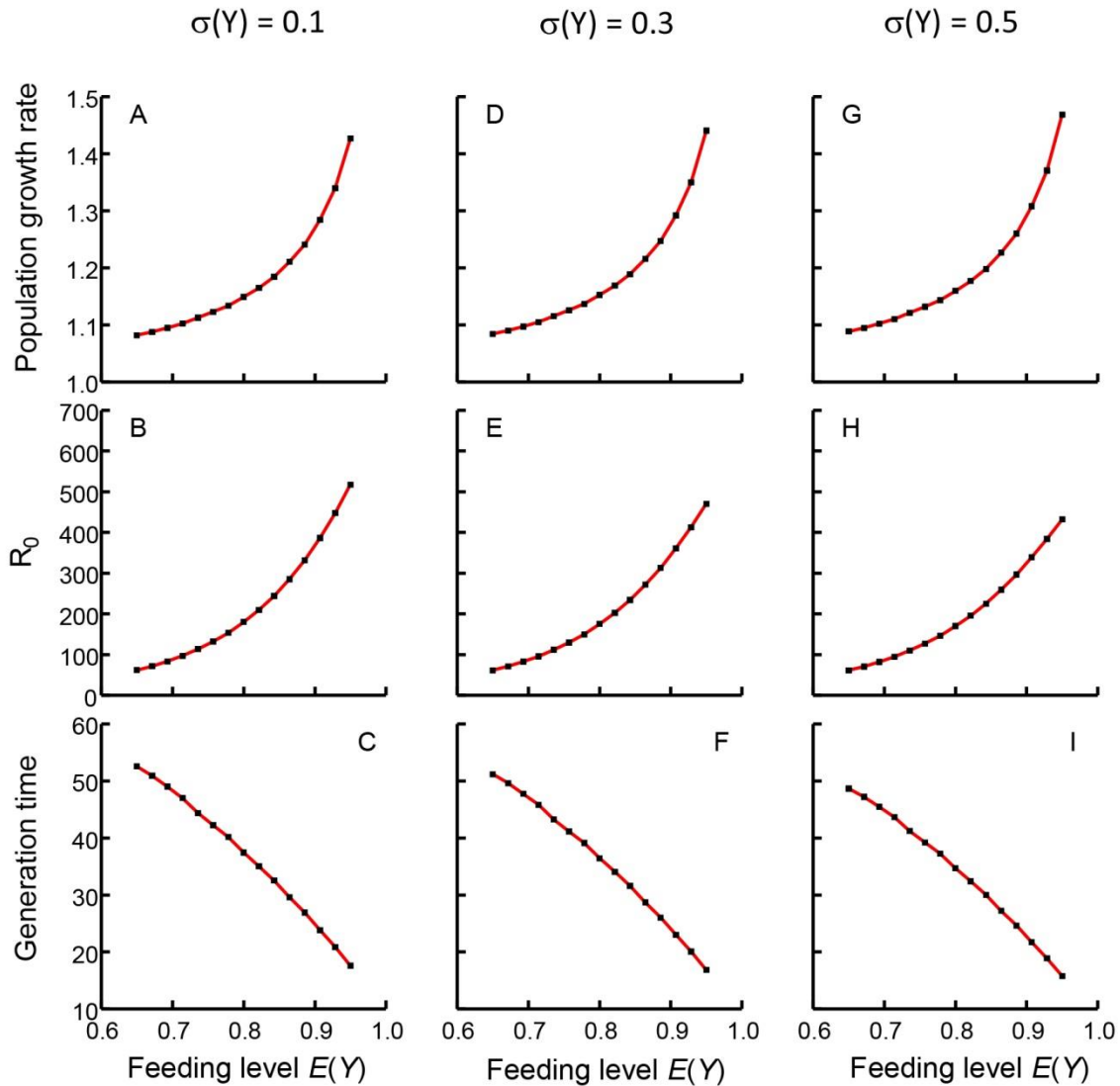


Figure S3. Population growth rate λ (top row), lifetime reproductive success R_0 (middle row), and generation time (T , days) (bottom row) as predicted for the bulb mite in relation to feeding level $E(Y)$ for three values of $\sigma(Y)$: $\sigma(Y) = 0.1$ (left-hand column); $\sigma(Y) = 0.3$ (middle column) and $\sigma(Y) = 0.5$ (right-hand column). Two scenarios are shown that have the same outcome. The red lines denote the scenario where individuals can shrink under starvation conditions (using Eqn 5, Eqn 6 and Eqn 10 of the main text to describe growth and reproduction), whereas the black symbols denote the scenario where individuals do not shrink under starvation conditions (using Eqns S4 – S6 to describe growth and reproduction). Parameter values are $\alpha = -137.8$, $\beta = 151.0$, $\kappa = 0.082$, $L_b = 0.166$, $L_m = 1.008$, $\mu = 0.03$, and $R_m = 32$. The parameter L_p depends on feeding level (see main text).

4. Building the DEB-IPM: a detailed explanation and toy example

The integral projection model projects a distribution of body length at time t to a new distribution at time $t + 1$ (Easterling et al. 2000). To understand how this works it is easiest to follow the fate of a cohort of bulb mite individuals with body length L at time t that experience a feeding level of $E(Y) = 0.95$ with $\sigma(Y) = 0.5$. We use all default parameter values for bulb mites: $\kappa = 0.082$, $L_b = 0.166$, $L_m = 1.008$, $\mu = 0.03$, $r_B = 0.083$, and $R_m = 32$ (Table 1 of the main text), and assume individuals can shrink in response to starvation conditions. Suppose that this cohort of bulb mites is of length $L = 0.6$ mm. The probability that this cohort survives from time t to $t + 1$ is calculated using Eqn 12 of the main text: $S(0.6) = e^{-0.03} = 0.97$ (see Table 1 for parameter values); hence 97% of this cohort survives. The surviving part of the cohort then grows. To generate the distribution of body lengths among survivors, one calculates $G(L', 0.6) \times 0.97$. The function $G(L', 0.6)$ generates a Normal distribution with mean $E(L(t + 1)) = L(t)e^{-r_B} + (1 - e^{-r_B})L_m \cdot E(Y) = 0.6 \cdot e^{-0.083} + (1 - e^{-0.083}) \cdot 1.008 \cdot 0.95 = 0.63$ (Eqn 5 of the main text), and standard deviation $\sigma^2(L(t + 1)) = (1 - e^{-r_B})^2 L_m^2 \sigma^2(Y) = (1 - e^{-0.083})^2 \cdot 1.008^2 \cdot 0.5^2 = 1.6 \cdot 10^{-3}$ (Eqn 6 of the main text), which should then be multiplied by 0.97. The next step is to consider reproduction. Our cohort of individuals is larger than $L_p = 0.564$ and hence reproduction rate equals $E(Y)R_m L(t)^2 / L_m^2 = 0.95 \cdot 32 \cdot 0.6^2 / 1.008^2 = 10.77$ eggs per day (Eqn 10 of the main text). The distribution of body lengths among these offspring is calculated by using $D(L', 0.6) \times 10.77$ (Eqn 13 of the main text). The function $D(L', 0.6)$ generates a Normal distribution with mean $E(\overline{L}_b(t)) = 0.166$ and standard deviation $\sigma_{L_b}^2 = 0$ (as we assumed

that parents of all sizes are equally likely to produce offspring of a constant size L_b), which should then be multiplied by the total number of offspring produced, 10.77.

The distribution of body lengths L' generated by a cohort of individuals of length $L = 0.6$ mm is then obtained by summing the distributions $D(L', 0.6) \times 10.77$ and $G(L', 0.6) \times 0.97$: $N(L'|0.6, t + 1) = D(L', 0.6)R(0.6) + G(L', 0.6)S(0.6)$, where $N(L'|0.6, t + 1)$ is the expected distribution of body lengths at time $t + 1$ produced by a cohort of individuals of length 0.6 mm at time t . When considering cohorts of individuals all possible lengths, i.e. any length between the shortest and longest length observed in a population, the distribution of body lengths at time t can be written as $N(L, t)$. The expected distribution for cohorts of all possible lengths L at time $t + 1$ is $N(L'|L(t), t + 1)$; multiplying this distribution by the number of cohorts of individuals of length L at time t , and summing across all these distributions, generates the distribution of body lengths at time $t + 1$:

$$N(L', t + 1) = \int_{\Omega} [D(L', L(t))R(L(t)) + G(L', L(t))S(L(t))]N(L, t)dL$$

which is Eqn 1 of the main text.

Predictions on population growth rate (λ), lifetime reproductive success (R_0) and generation time (T) are calculated by discretising the IPM. This is done by choosing a sequence of closely spaced body lengths that starts below the shortest observed body length and ends above the longest observed body length. In the bulb mite study case, we worked with a sequence of 200 numbers long. In general, the discrete approximation of the continuous IPM is better with a shorter bin interval (interval between consecutive length values), but this trades off against an increase in calculation time. The preferred way is to explore a range of bin sizes and choose a number where results are no longer noticeably

affected by decreasing bin size (Easterling et al. 2000). Once the range of body lengths number of bins are chosen, the next step is to calculate the midpoint value of each bin, and then evaluate each of the four fundamental functions at each midpoint value. All calculated values are then stored in a matrix for further analysis.

A matrix is a square or rectangular array of numbers. Matrix approximations of IPMs are always square matrices. Each column in the matrix approximation of the IPM represents the midpoint of a body length bin at time t ; each row represents the midpoint of a body length bin at time $t + 1$. Each individual item, or entry, in the matrix represents the transition rate of a cohort of individuals from a body length bin at time t to a body length bin at time $t + 1$. To create the matrix approximation of the DEB-IPM, four matrices were calculated: **S**, **R**, **G**, and **D**. The matrix **S** is a diagonal matrix, which means that the only matrix entries that can have values that are not zero are those that lie on the diagonal (running from the top-left corner to the bottom right corner); all other entries in the matrix are zero. The entries on the diagonal are the survival rate values for cohorts in each body length bin and represent cohorts of individuals that do not move from one body length to another between time t and time $t + 1$. Likewise, **R** is also a diagonal matrix, but here, values on the diagonal describe the expected number of offspring produced by a cohort of individuals of length L at time t . **D** and **G** are not diagonal matrices as cohorts of individuals can move between body length bins either by growing (or shrinking), **G**, or by producing offspring with a body length different from their own, **D**. Each column in **D** and **G** sums to one because surviving individuals must express a body length value at time $t + 1$ (**G**) and offspring must express a body length value when they enter the population (**D**). The final step is to create a discretised version of $N(L, t)$, which is typically called $\mathbf{n}(t)$ and which describes the number of cohorts of individuals within each body length bin.

To give a toy example of how to construct these matrices, as before, we take the values: $E(Y) = 0.95$, $\sigma(Y) = 0.5$, $\kappa = 0.082$, $L_b = 0.166$, $L_m = 1.008$, $\mu = 0.03$, $r'_B = 0.083$, and $R_m = 32$. We take a shortest body length of 0.10 mm and a longest body length of 1.10 mm, and divide this range into ten body length bins: 0.1 – 0.2 mm; 0.2 – 0.3 mm; 0.3 – 0.4 mm; etc. The midpoints of these bins respectively are: 0.15, 0.25, 0.35,...,1.05 mm. Using Eqn 12 of the main text we calculate $S(L(t)) = e^{-0.03} = 0.97$ (see above), which leads to:

$$\mathbf{S} = \begin{bmatrix} 0.97 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.97 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.97 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.97 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.97 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.97 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0.97 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.97 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.97 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.97 \end{bmatrix}$$

To fill in \mathbf{G} , we need to calculate $G(L', L(t))$, where $L(t)$ equals 0.15, 0.25, 0.35,..., 1.05 mm, which results in:

$$\mathbf{G} = \begin{bmatrix} 0.787 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0.213 & 0.889 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0.111 & 0.945 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.055 & 0.974 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0.026 & 0.988 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0.012 & 0.994 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.006 & 0.997 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0.003 & 0.999 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.001 & 0.999 & 0.001 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0.001 & 0.999 \end{bmatrix}$$

Using Eqn 10 of the main text we can calculate $R(L(t))$ for each midpoint value, which results in:

$$\mathbf{R} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 9 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 13 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 17 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 22 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 27 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 33 \end{bmatrix}.$$

Finally, we use Eqn 13 of the main text to calculate $D(L', L(t))$, which results in:

$$\mathbf{D} = \begin{bmatrix} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

The fact that there are only ones on the first row of \mathbf{D} and zeros elsewhere is explained by the fact that we assumed that all parents are equally likely to produce offspring of a size L_b with $\sigma_{L_b}^2 = 0$, which means that all offspring produced are 0.166 mm and always fall in the first body length bin of 0.1 – 0.2 mm.

5. Consumer-resource DEB-IPM: construction and a bulb mite application

Construction of a consumer-resource DEB-IPM

The DEB-IPM presented in the main text can be extended to include resource dynamics and population feedback on resource dynamics. In the absence of consumers, we assume that the resource grows according to:

$$H(X(t), t + 1) = (1 - \rho)X(t) + \rho X_{max}, \quad (\text{eqn S5})$$

where ρ is the fraction of resource that is replenished every time step and X_{max} equals the resource abundance in the absence of consumers. This form of resource growth in discrete time is analogous to resource growth following semi-chemostat dynamics in continuous time. An individual consumer is assumed to forage on the shared resource following the scaled Holling type II functional response so that the intake rate of an individual consumer of length L equals $I_{max}L^2Y$ with maximum ingestion rate I_{max} (see above). Resource consumption of a cohort of individuals of length L between time t and time $t + 1$ then equals (assuming that resource density available for consumption stays constant within the time interval):

$$\begin{aligned} C(L(t), t) &= \int I_{max}L^2N(L, t)Yf(Y)dY \\ &= I_{max}L^2N(L, t) \int Yf(Y)dY \\ &= I_{max}L^2N(L, t)E(Y) \end{aligned} \quad (\text{eqn S6})$$

As explained in the main text, Y is assumed to follow a probability distribution $f(Y)$ at the individual level with mean $E(Y) = X/(K + X)$. Change in resource density between time t and $t + 1$ in the presence of consumers is the difference between resource growth and consumption by the whole population between time t and $t + 1$:

$$X(t + 1) = (1 - \rho)X(t) + \rho X_{max} - I_{max} \frac{X}{K + X} \int L^2 N(L, t) dL \quad (\text{eqn S7})$$

The number length distribution of the population is determined by the four functions $S(L(t))$, $G(L', L(t))$, $R(L(t))$, and $D(L', L(t))$, described in the main text, from which consumer density is calculated following Eqn 1 of the main text. In contrast to the DEB-IPM presented in the main text, expected feeding level, $E(Y)$, is now directly related to resource density X . For a cohort of individuals of length L , this means that an increase in resource density X increases their experienced feeding level, and hence their growth and reproduction rates.

Parameterisation of consumer-resource DEB-IPM

We parameterised the consumer-resource DEB-IPM for bulb mites to study model dynamics as a function of ρ and I_{max} and adopted the default values of $\rho = 0.1$ and $I_{max} = 0.1$, and assumed that individuals can shrink in response to starvation conditions. The half-saturation constant was set at $K = 5$ and maximum resource density equals $X_{max} = 4$. To prevent too small individuals from reproducing we introduced a minimum length for reproduction of

0.314 mm (equal to L_p on the low feeding level diet [Table 1 of the main text]). This means that in Eqn 10 and in Eqn 13 of the main text, the critical length at puberty above which individuals reproduce equals $L_p = \max(0.314, 0.539L_\infty)$. Using the bifurcation analysis method of de Roos & Persson (2013, p. 70-71), we carried out a single numerical simulation over a very long time period to study model dynamics as a function of ρ . We subdivided this entire period into intervals during which the value of ρ was constant, while from one interval to the next, the value of ρ was increased or decreased by a small amount. This stepwise increase or decrease of ρ means that we used the final values of the model variables obtained for a particular value of ρ as initial values of the model variables for the following value of ρ . As a result, we explored the full range of values of ρ from low to high and vice versa. The same approach was taken to explore the consequences of varying I_{max} . It is important to note that, in the Kooijman-Metz model, the parameters L_m and R_m are proportional to I_{max} (see above under “Modelling growth and reproduction”). This means that, for a cohort of individuals of length L , an increase (decrease) in I_{max} increases (decreases) the growth rate $G(L', L(t))$ through an associated increase (decrease) in L_m (see Eqn 5 of the main text). Furthermore, a change in I_{max} affects the reproduction rate $R(L(t))$ through associated changes in L_m and R_m (see Eqn 10 of the main text). While studying model dynamics as a function of I_{max} , we therefore used the derived values $L'_m = I'_{max}/I_{max_default} \cdot L_{m_default}$ and $R'_m = (I'_{max}/I_{max_default})^3 \cdot R_{m_default}$. Here, I'_{max} is the changed value of I_{max} , and $L_{m_default}$ and $R_{m_default}$ are the values of L_m and R_m , respectively, at the default value for I_{max} , $I_{max_default} = 0.1$. Because a change in L_m affects the length domain Ω (Eqn 1 in the main text) over which the DEB-IPM is discretised, we adjusted the number of bins that the length domain was divided into for each simulation

run, keeping bin size the same between runs. As a result, matrix size differed between simulation runs and we could not use the above bifurcation analysis method. Instead, we carried out consecutive, independent numerical simulations of the resource and consumer dynamics, and, between consecutive runs, increased the value of I_{max} by a small amount, starting with a very low value of $I_{max} = 0.05$. Each run was started with the initial conditions

$$\int_{L_b}^{L_m} N(L, t = 0) dL = 2 \text{ and } X(0) = X_{max}.$$

Consumer-resource DEB-IPM dynamics

Fig. S4 illustrates the dynamics of the consumer-resource DEB-IPM. For both the resource (Fig. S4A), expected feeding level (Fig. S4B), juvenile density (Fig. S4C) and adult density (Fig. S4D), the consumer-resource DEB-IPM predicts a rapid approach to their respective equilibrium values. At equilibrium, the consumer population is dominated by juveniles and only a small proportion of consumers are adults (Fig. S4C-D), which is typical of bulb mite population structures (Smallegange & Deere 2014). Fig. S5 illustrates the long-term dynamics predicted by the consumer-resource DEB-IPM as a function of resource replenishment rate ρ . With increasing values of ρ , resource (Fig. S5A) and feeding level (Fig. S5B) remain constant but both juvenile density (Fig. S5C) and adult density (Fig. S5D) increase linearly until maximum values are reached at the maximum resource replenishment rate of $\rho = 1$. Fig. S6 illustrates the long-term dynamics predicted by the consumer-resource DEB-IPM as a function of maximum ingestion rate I_{max} . At low values of I_{max} , resource (Fig. S6A) and feeding level (Fig. S6B) are at their maximum values as adult and juvenile density are close to zero (Fig. S6C, D). As I_{max} increases, both juvenile and adult

density increase and resource and feeding level decrease, until consumers deplete the whole resource within one time step and go extinct (Fig. S6).

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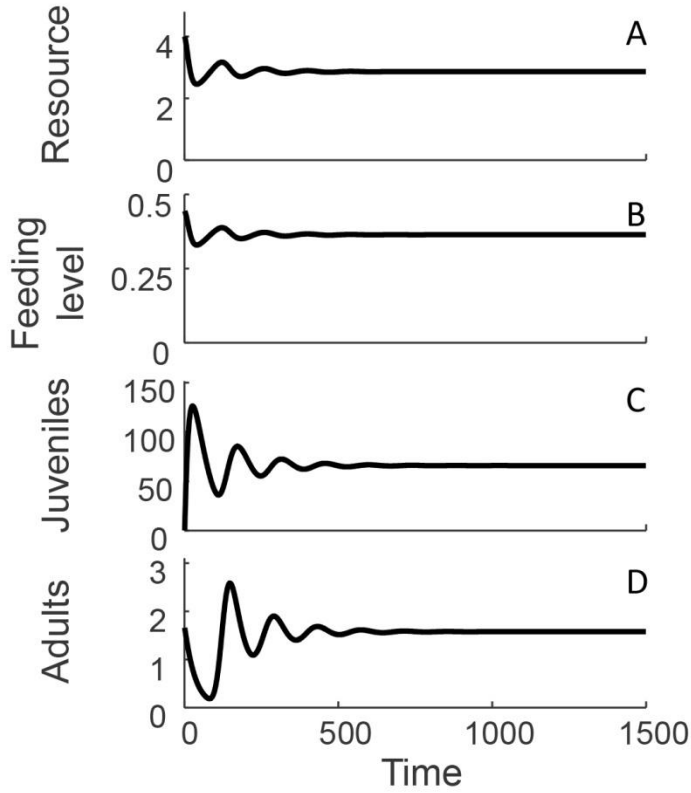


Figure S4. Dynamics of the resource X (A), expected feeding level $E(Y)$ (B), juvenile consumer density $\int_{L_b}^{L_p} N(L, t) dL$ (C) and adult consumer density $\int_{L_p}^{L_m} N(L, t) dL$ (D) as predicted by the consumer-resource DEB-IPM starting from the initial conditions $\int_{L_b}^{L_m} N(L, t = 0) dL = 2$, $X(0) = X_{\max}$ and other parameters at default values: $K = 5$, $I_{\max} = 0.1$, $\rho = 0.1$, $X_{\max} = 4$, $\sigma(Y) = 0.3$, and (DEB parameters) $\alpha = -137.8$, $\beta = 151.0$, $\kappa = 0.082$, $L_b = 0.166$, $L_m = 1.008$, $\mu = 0.03$, $R_m = 32$. The DEB parameter L_p depends on feeding level (see main text).

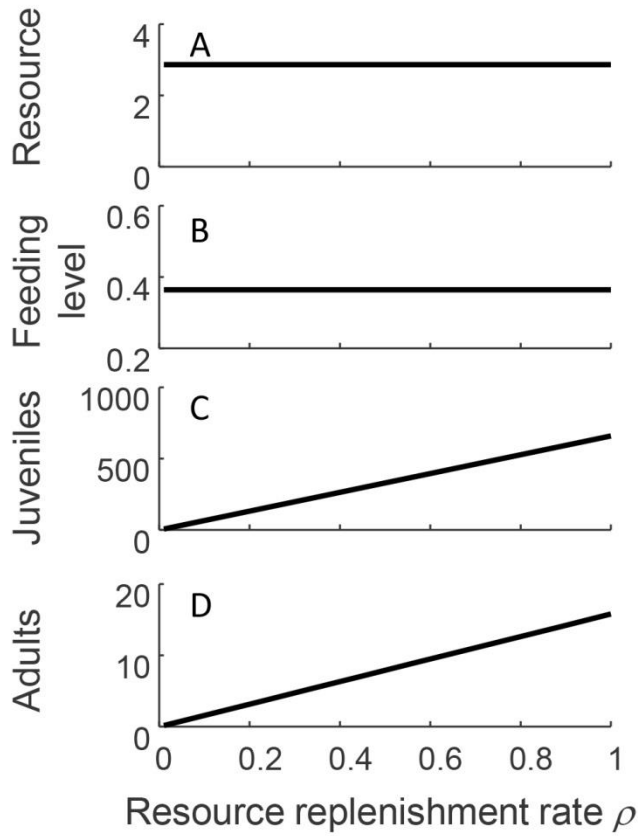


Figure S5. Dynamics of the resource X (A), expected feeding level $E(Y)$ (B), juvenile consumer density $\int_{L_b}^{L_p} N(L, t)dL$ (C) and adult consumer density $\int_{L_p}^{L_m} N(L, t)dL$ (D) for different values of ρ . Results plotted are the final values obtained within each interval of the entire simulation period, within which the value of ρ was kept constant (all other parameters have default values: see legend Fig. S4).

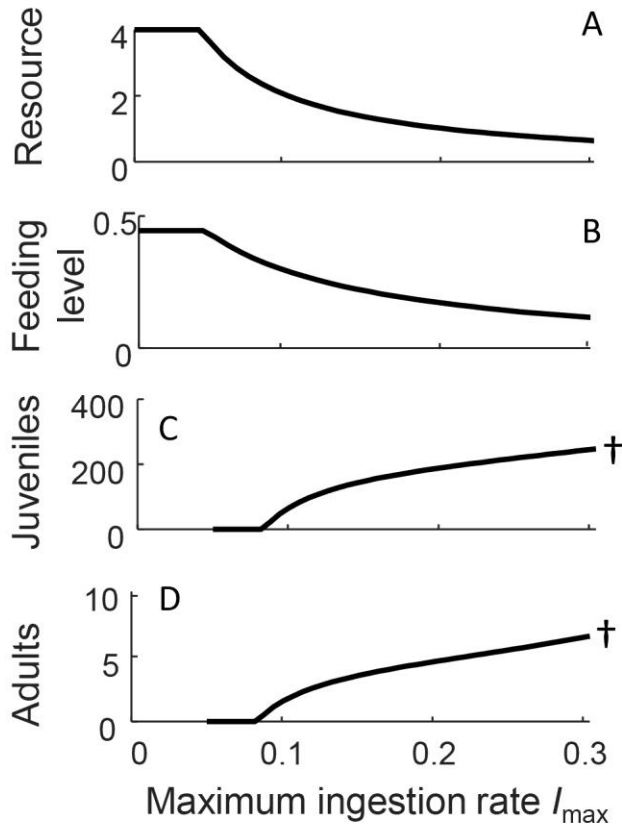


Figure S6. Long-term values of the resource X (A), expected feeding level $E(Y)$ (B), juvenile consumer density $\int_{L_b}^{L_p} N(L, t) dL$ (C), and adult consumer density $\int_{L_p}^{L_m} N(L, t) dL$ (D) for different values of the maximum ingestion rate I_{\max} . The values of L_m and R_m depends on I_{\max} (see text here in SI) and all other parameters have default values (see legend Fig. S4). At the highest value of I_{\max} , consumers deplete the resource within one time step and go extinct (indicated by †).