

Text S1. Main DEB model equations

This appendix summarizes the main equations used in the DEB model according to Rosland *et al.* [6] and Saraiva *et al.* [13]. DEB symbols and notations are the same as in [1] where brackets [] denote quantities per unit structural volume and braces { } denote quantities per unit surface area of the structural volume.

In Saraiva's implementation, feeding mechanisms are described in four steps: water is cleared (1), its content is then filtered (2), ingested (3) and assimilated (4).

$$\dot{C}_R = \frac{\{ \dot{C}_{Rm} \}}{1 + \sum_i \frac{\lambda_i F_i \{ \dot{C}_{Rm} \}}{\{ \dot{J}_{FiFm} \}}} V^{2/3} \quad (1)$$

$$\dot{J}_{FiF} = \dot{C}_R \lambda_i F_i \quad (2)$$

$$\dot{J}_{FiI} = \frac{\rho_i \dot{J}_{FiF}}{1 + \sum_j \frac{\rho_j \dot{J}_{FjF}}{\dot{J}_{FiIm}}} \quad (3)$$

$$\dot{p}_A = C \cdot AE \cdot \dot{J}_{FiI} \quad (4)$$

where C_R is the amount of cleared water, $\{ \dot{C}_{Rm} \}$ is the maximum clearance rate, λ_i is a conversion factor from food units to mol C, F_i is the food proxy (in our model, two variables were used: a classical food proxy such as chl a or phytoplankton abundance and a fixed fraction of TPM to account for inorganic material). $\{ \dot{J}_{FiFm} \}$ and \dot{J}_{FiIm} are the maximum filtration and ingestion rate for food type i ,

respectively while, \dot{J}_{FiF} and \dot{J}_{FiI} are the actual filtered and ingested food. ρ_i is the food binding probability. \dot{p}_A is the assimilation rate, depending on a conversion factor (from mol to J), and AE is the ingestion rate.

In Rosland's implementation, used for functional response assessment, assimilation \dot{p}_A is proportional to the surface of the structural body $V^{2/3}$ and to the maximum ingestion rate $\{ \rho_{Xm} \}$, corrected for thermal effects.

$$\dot{p}_A = AE \left\{ \dot{p}_{X_m} \right\} f V^{2/3} \quad (5)$$

with

$$f = \frac{F}{F + X_k} \quad (6)$$

where f is the functional response to ambient food F standardized with the half-saturation coefficient X_k .

In all cases, energy input leads to a change in the reserve compartment.

$$\frac{dE}{dt} = \dot{p}_A - \dot{p}_C \quad (7)$$

where \dot{p}_C is the catabolic flux due to growth and maintenance costs.

$$\dot{p}_C = \frac{[E]}{[E_G] + \kappa[E]} \left(\frac{[E_G] \{p_{X_m}\}^\gamma V^{2/3}}{[E_m]} + \left[\dot{p}_M \right] V \right) \quad (8)$$

where $[E]$ is the energy density ($[E]=E/V$), $[E_G]$ represents the volume-specific costs of structural growth, κ is the allocation coefficient and $[E_m]$ is the maximum storage density.

Energy is then redistributed to structural growth and reproduction.

$$\frac{dV}{dt} = \frac{(\kappa \dot{p}_C - \dot{p}_M)}{[E_G]} \quad (9)$$

$$\frac{dE_R}{dt} = (1 - \kappa) \dot{p}_C - \frac{1 - \kappa}{\kappa} \dot{p}_M \quad (10)$$

When energy input is not sufficient for structural costs, lysis is possible.

$$\frac{dE_R}{dt} = \kappa \dot{p}_C - \dot{p}_M \quad (11)$$

When the reproductive buffer is empty, structural meat can be decreased.

$$\frac{dV}{dt} = \frac{(\kappa \dot{p}_C - \dot{p}_M)}{C} \quad (12)$$

Finally, energy buffers and length can be related with a shape coefficient δ .

$$L = \frac{\left(\frac{E}{[E_G]} \right)^{1/3}}{\delta} \quad (13)$$