setscaling()

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Inputs

The scale invariant size spectrum model generated by *set_scaling_model()* depends upon the following inputs:

- The number of species $no\_sp = s$. By default this is 11.

- The minimum asymptotic size $min\_w\_inf = W_\infty^L = \min\{W_{\infty.i} : i \in \{1,..,s\}\}$. By default this is 10

- The maximum asymptotic size $\max\_w\_\inf = W_\infty^H = \max\{W_{\infty.i} : i \in \{1,..,s\}\}$. By default this is 10^3

- The minimum egg size $min\_egg = w_e^L = \min\{w_{e.i} : i \in \{1,..,s\}\}$. By default this is 10^{-4}

- The minimum maturity weight $min\_w\_mat = w_*^L = \min\{w_{*i} : i \in \{1,..,s\}\}$. By default this is $10^{0.4}$

- The number of weight bins $no\_w = K$. By defaulr this is $1+100\log_{10}\left(\frac{W_\infty^H}{w_e^L}\right)$

- The minimum weight of plankton modeled, W_{min}^P min_w_pp is set to $\frac{\min\{w_{e.i} : i \in \{1,...,s\}\}}{\beta e^{5\sigma}}$ by default.

- The maximum weight of modeled plankton $w\_pp\_cutoff = w_{cut}$. By default this is W_∞^L. [We ensure that the plankton's carrying capacity $c_p(w)$ has the feature that $w > w_{cut}$ implies $c_p(w) = 0$.]

- The exponent of the maximum consumption rate (also known as the 'the scaling of intake'), n . By default this is 2/3.

- The scaling of standard metabolism, q. By default this is 3/4

- The exponent λ of the background spectrum. By default this is $2 + q - n$

- The growth rate of the primary produc- tivity (the background spectrum), $r\_pp = r_0$. By default this is 0.1.

- The premultiplier of the community spectrum power law κ. By default this is 0.005.

- The assimilation efficiency α. By default this is 0.4

- Multiplicative constant for std. metabolism and activity, k_s.By default this is 4

- Multiplicative constant for max. food intake, h. By default this is 30.

- Preferred predator prey mass ratio β. By default this is 100.

- Width of prey size preference σ. By default this is 1.3.

- Initial feeding level f_0. By default this is 0.6

- The size beyond which the knife edge gear catches (if that is what is setup for fishing), knife_edge_size. The default for this is 100 [I think this is a weight, and not a length, any may not be relevant depending on the gear names].

- The na,e of the gear, gear_names. By default this is "knife_edge_gear", indicating to mizer to setup the fishing selectivity using knife edge gears.

- The factor R_{fac} such that $R_{max.i} = R_i R_{fac}$, for each species i. Here R_{max} is the maximum recruitment allowed and R_i is the steady-state recruitment. [Thus the larger R_{fac} the less the impact of the non-linear stock-recruitment curve.] By default this is ∞.

- A boolean variable 'perfect'. By default perfect=FALSE. If perfect=TRUE then parameters are set so that the community abundance, growth before reproduction and death are perfect power laws.

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Procedure

Tidy up inputs and check validity

- If community exponent λ was given as an input then the exponent for volumetric search rate q is rewritten so $q := \lambda - 2 + n$, where n is the exponent for max. food intake.

- If $R_{fac} \leq 1$ then $R_{fac} := 1.01$.

- The number of weight bins K is replaced with the nearest integer to K

- Let $T := round\left(5 \log_{10}\left(\frac{W_{\inf}^H}{w_e^L}\right) + 1\right)$. If $K < T$ then $K := T$ [this is done so there are at least 5 bins in the interval from w to $10w$ [is this true for any w, or only w=w_e etc. ?].

- Check that $K \leq 10,000$ and $W_\infty^L < W_\infty^H$ and $w_e^L < w_*^L$ and $s \geq 2$ and n, q, r_pp, kappa, alpha, h, beta, sigma, ks, f0, knife_edge_size>0 If any of these conditions are false then give a warning message, and halt.

- If perfect=TRUE then let $w_{cut} := \infty$

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Define variables

- Set the exponent of standard metabolism to be $p := n$

- $\lambda := 2 + q - n$

- Define the smallest weight we model fish at to be $W^L := w_e^L$.

- Define the largest weight we model fish at to be $W^H := W_\infty^H$

- To round the minimum maturity weight w_*^L up to a grid point we let $\delta = \frac{\log_{10}(W^H) - \log_{10}(W^L)}{K-1}$ and $j = 1 + \left\lceil \frac{\log_{10}(w_*^L) - \log_{10}(W^L)}{\delta} \right\rceil$ and $v = 10^{\log_{10}(W^L) + (j-1)\delta}$ and we round the minimum maturity weight up by letting $w_*^L := v$.

- To round the minimum asymptotic weight w_∞^L to the nearest grid point we and $J = 1 + \left\lceil \frac{\log_{10}(W^H) - \log_{10}(W_\infty^L)}{\delta(s-1)} \right\rceil$ where s is the number of species. We let $W_\infty^L := 10^{\log_{10}(W^H) - J(s-1)\delta}$. [actually is a round() function used here instead ? maybe we should use the same approach in more places].

- Prepare to setup egg weights: Let $I[e, i] \in \{1, .., K\}$ denote the index of the weights that corresponds with the weight such that $w_{I[e,i]} = w_{e.i}$. We set $(I[e, 1], I[e, 2], .., I[e, s]) := (1, J + 1, 2J + 1, .., (s - 1)J + 1)$.

- We set the maximum egg size to be $w_e^H = w_e^L \left(\frac{W^H}{W_\infty^L} \right)$.

- Determine logarithmic spacing of egg weights $\Delta = \frac{\log_{10}(w_e^H) - \log_{10}(w_e^L)}{s-1}$.

- Let $(x_{e.1}, x_{e.2}, .., x_{e.s}) = (\log_{10}(w_e^L), \log_{10}(w_e^L) + \Delta, .., \log_{10}(w_e^L) + (s - 1)\Delta)$. The egg weight of background species i is set to $w_{e.i} := 10^{x_{e.i}}$.

- The asymptotic weight of background species i is set to $W_{\infty.i} := w_{e.i} \left(\frac{W_\infty^L}{w_e^L} \right)$.

- The maturity weight of background species i is set to $w_{*i} := w_{e.i} \left(\frac{w_*^L}{w_e^L} \right)$.

- The value of the reproduction effeciciency is set to $\epsilon = 0.1$, although it is overwritten later.

Setting up the data structure

- A dataframe $\mathbb{F}$ is made holding the species-specific information, together with a declaration that $z_0 = 0$, [where z_0 is the pre-multiplier of mizer's traditional background death term I presume], however we do use a different type of background death term that is described later. The other information included in the data frame are the names of the species, $1, .., s$ and w_min, w_inf, w_mat, w_min_idx, h, ks, beta, sigma, alpha, erepro, sel_func = "knife_edge", knife_edge_size = knife_edge_size, gear = gear_names.

- A mizer params object $\mathbb{P}$ is made by using $\mathbb{F}$ and $p, n, q, \lambda, f_0, \kappa, W^L, W^H, K, W^P_{min}, w_{cut}, r_0$ as inputs to MizerParams(). Here W^P_{min} is the minimum weight of plankton modeled, and r_0 is the replenishment rate of the plankton. The values of γ, w and dw are (re)computed by calling MizerParams(), and we use such updated values.

Steady state solution for species one

- Compute coefficient of predation death rate that would be induced by a power law spectrum of background species: $\mu_0 := (1-f_0)\sqrt{2\pi}\kappa\gamma\sigma\beta^{n-1}\exp\left(\sigma^2(n-1)^2/2\right)$

- Compute coefficient of energy available for reproduction and growth, at power law state $\hbar := \alpha h f_0 - k_s$. If $\hbar < 0$ then halt.

- We define pow=$B := \frac{\mu_0}{\hbar(1-n)}$, and if $B < 1$ then an error message is displayed about how at steady state the ratio of death rate to growth rate is too small, leading to an accumulation of fish at their largest size.[check the 1-n really goes on the denominator].

- The death rate at steady state is $\mu(w) := \mu_0 w^{n-1}$

- The growth rate of species 1 at steady state is $g(w) := \hbar w^n(1 - \psi_1(w))$, where $\psi_1(w)$ is the fraction of their energy that a weight w member of species 1 diverts to reproduction.

- Let $I[\infty, i]$ denote the index such that $w_{I[\infty,i]} = W_{\infty.i}$, that gives the asymptotic weight of the ith species. Let $\mathbb{I} = \{1, 2, .., I[\infty, 1] - 1\}$

- The unscaled steady state abundance $\widehat{N_1}(w)$ of species 1 is such that $\widehat{N_1}(w_1) = 1$, and for each $j \in \{2, .., K\}$ we have that $\widehat{N_1}(w_j) = 0$ if $j > I[\infty, 1]$ and otherwise, $(\widehat{N_1}(w_1), \widehat{N_1}(w_2), \widehat{N_1}(w_3), .., \widehat{N_1}(w_K))$ is set equal to $(1, H[1], H[2], .., H[I[\infty, 1]-1], 0, 0, .., 0)$. Here $H[k] == \Pi_{u=1}^{k} \frac{g(w_u)}{g(w_{u+1})+\mu(w_{u+1})dw_{u+1}}$ [This is to match with the steady state of the upwind difference scheme, but I'd better check I've got the indices correct, etc., and simplify].

- Rescale the abundance of species 1 so it lies on a power law. Let $M = \kappa / \sum_{j=1}^{I[\infty,1]} \widehat{N_1}(w_j)w_j^{\lambda-1}dw_j$ be the multiplier, and generate the properly scaled abundance of species 1, which we set to be $N_1^*(w) := \widehat{N_1}(w)(10^{\Delta(1-\lambda)/2}-10^{-\Delta(1-\lambda)/2})M/(1-\lambda)$. [I am not sure where the $(10^{\Delta(1-\lambda)/2}-10^{-\Delta(1-\lambda)/2})$ renormalization factor comes from]

Finish computing steady state solution

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- Initially set $N_i(w_j) = 0$

- For each species $i \in \{1, .., s\}$ let $I[e, i]$ be the egg weight index, so $w_{I[e,i]} = w_{e.i}$