Parameter defaults

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Predation kernel

log-normal kernel

- `beta` = 30 for Multispecies and `beta` = 100 for Trait and Community.
- `sigma` = 2.0 for Multispecies and Community and `sigma` = 1.3 for Trait

NEW: still need to discuss, but ideally the same for all types of model

Ken: I would say:

- `beta` = 400. This follows the analysis in Andersen (2019, p. 26 and figure 2.6).
- `sigma` = 1.0 for following Ursin et al (1973). For the trait-based and community models we can increase to `sigma` = 1.3 to represent that each size or trait-group represent a range of species with various values of `beta`.

Search volume

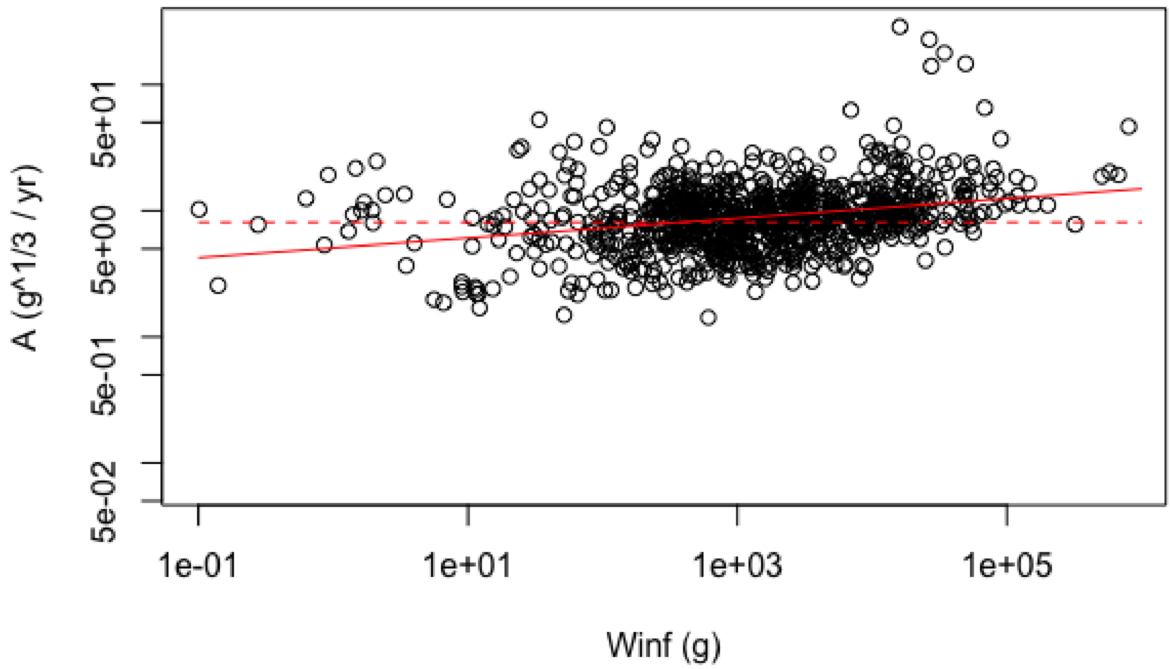
- `q` = `lambda` - 2 + `n` **NEW: if no `lambda` is specified, then `q` = 0.8** See discussion in Andersen (2019; p.22-23 and Fig. 2.4),
- `gamma` is determined from `f0 = 0.6`, `h`, `kappa`, `lambda` and the predation kernel so that if the prey abundance was described by the power law $\kappa w^{-\lambda}$ then the encounter rate would lead to the feeding level`f0`.

Maximum intake rate

- `n` = 2/3
- `h` for `n`=2/3. `h` represents the factor of the maximum consumption rate. It can be calculated from the growth rate coefficient A as:

$$h = \frac{A}{\alpha(f_0 - f_c)}$$

(eq. 3.31), where `alpha`=0.6 is the assimulation efficiency and `f0`=0.6 and `fc`=0.2. We can find the growth coefficient from von Bertalanffy growth parameters (eq.3.9): $A = 3c^{1/3}KL_\infty$ where c is the coefficient in the length-mass relation $c \approx 0.01$ g/cm. An analysis of von Bertlanffy growth from fish base (only used bony fish and estimates where $|t_0| < 1$) gives:



The fit is (red line): $A = \exp(1.62) W_\infty^{0.078}$. The geometric mean (dashed red) is $A \approx 8$ g$^{1/3}$/yr. Using the geometric mean gives:

$$h \approx 33 \text{ g}^{1/3}/\text{yr}$$

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- In multispecies model `h` is determined so that with feeding level `f0 = 0.6` and under the assumption `p` = `n` the species reaches maturity size `w_mat` at the age predicted by the von Bertalanffy growth curve parameters `k_vb` and `t0` = 0. The calculation uses `w_min`, `w_inf`, `n`, `b = 3`, `fc = 0.2`.
- trait: `h` = 40 **NEW value from Ken**
- community: `h` = 10

Metabolic rate

- `p`
  - trait: `p` = `n`, `n` = 2/3
  - multispecies `p` = 0.7 **NEW: `p` = 2/3**

    NEW: issue warning about poor default when user chooses p different from n.
- `k` = 0
- `ks` determined from `fc`, `alpha`, `h`, `n`, `p`
  - trait: set so that `fc` = 0.25 **NEW: `fc` = 0.2**
  - multispecies: set so that `fc` = 0.2 at `w_mat`.
  - community: `ks` = 0

External mortality

- Multispecies: scales with `w_inf`
  - `z0pre` = 0.6
  - `z0exp` = `n - 1`
- Trait: proportional to predation mortality
  - `ext_mort_prop` = 0
- Community: `z0` = 0.1

Reproduction

- `w_mat` = `w_inf` / `eta` with multispecies `eta` = 0.25, trait `eta` = 10^(-0.6) ~ 0.25.
- `w_mat25` = `w_mat * 3^(-0.1)` (corresponds to U = 10)

  NEW: `w_mat25` = `w_mat * 3^(-0.2)` (corresponds to U = 5)
- `m` = 1
- `w_min` = 0.001
- `erepro` = 1 **NEW: `erepro` = 0.01 (thus slightly higher than 0.0066)? Increase for some species if needed but issue warning.**
- `R_max` chosen to achieve desired biomass.

Fishing

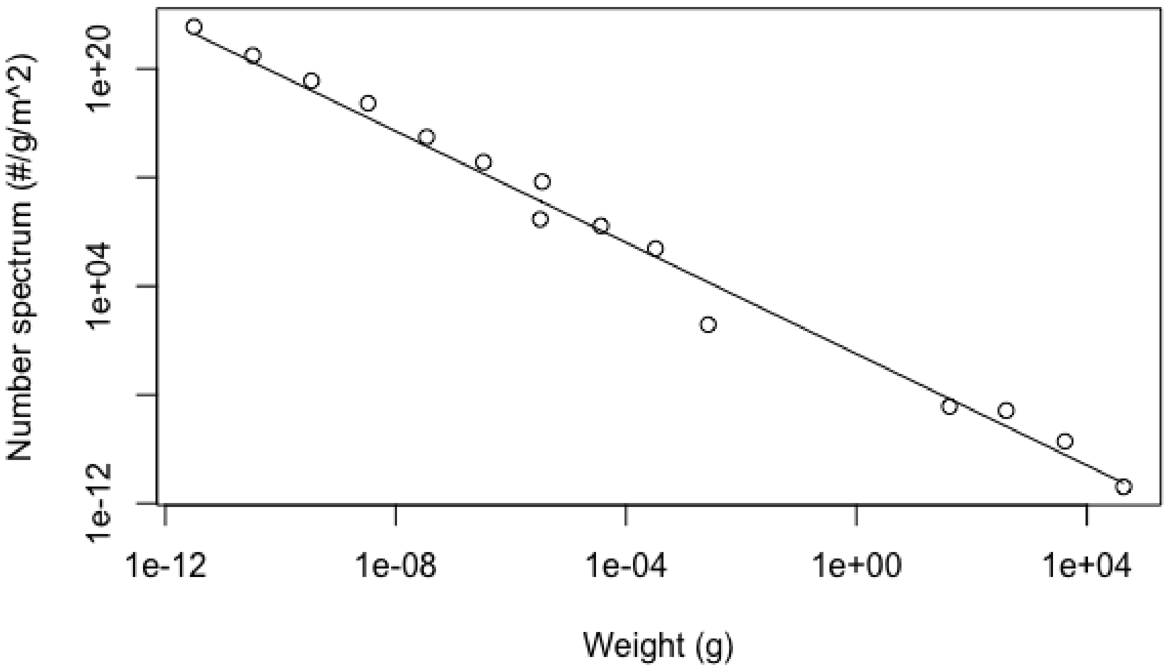
single knife_edge gear, catching all species,

- `catchability` = 1
- `knife_edge_size`
  - Multispecies: `knife_edge_size` = `w_mat`
  - Trait and community: `knife_edge_size` = 1000

Resource

- `r_pp`
  - Multispecies `r_pp` = 10 **NEW: `r_pp` = 4**
  - Trait `r_pp` = 0.1 **NEW: determined by new parameter `resource_level` = 1/2**
  - Community: r_pp = 10
- `kappa`
  - Multispecies `kappa` = 1e+11 **NEW: Use value per m^2, same as Trait**
  - Trait `kappa` = 0.005
  - Community = 1000

  Ken: In the absence of other information we use a "per area" specification of the resource spectrum. Below is the abundance spectrum as observed on the Scotian shelf from Boudreau and Dickie (1992):



The fit is made with `kappa` = 0.1 g^{1.05} (assuming that ´q´=0.8 and ´n´=3/4; for `n`=2/3 the value is simular but different units: `kappa` = 0.1 g^{1.14})

- `lambda` = 2.05 **NEW: `lambda` = `q` + 2 - `n` if the user specified a `q` (and this `q` is the same for all species), otherwise `lambda` = 2.05**

Other

- `alpha`
  - Multispecies: `alpha` = 0.6
  - Trait: `alpha` = 0.4
  - Community: `alpha` = 0.2

NEW: still need to discuss, but ideally the same for all types of model

Ken: Suggest to use `alpha`=0.6 for trait-based and multi-species models (Andersen (2019, p.50)).

Ken: For the community model `alpha` does not represent the assimilation efficiency, but the it represents the average growth efficiency (see Andersen et al (2009), RPSLB (209) 109-114, section "average growth efficiency"). The average growth efficiency depends upon the physiological parameters and the predator-prey interaction parameters in a rather complex way. A value of 0.2 for beta=400 is reasonable (figure 4b).