*Mass- and temperature dependence of growth, consumption and metabolism below peak temperatures*

Peak temperatures (optimum in the case of growth), refers to the temperature at which the rate was maximized, by size group. For data below peak temperatures, we assumed that individual growth, maximum consumption rate and metabolism scale as a generalized version of the Arrhenius fractal supply model (Gillooly *et al.* 2001; Brown *et al.* 2004). The mass exponent was not assumed a priori but estimated simultaneously with the temperature coefficient. We thus assumed the natural log of rate (growth, maximum consumption or metabolism) scales with mass and temperature as:

|  |  |  |
| --- | --- | --- |
|  |  | (1) |

where is the intercept, is the mass scaling exponent on a linear scale when () and is the interaction coefficient. On a linear scale, this becomes:

|  |  |  |
| --- | --- | --- |
|  |  | (2) |

We fit hierarchical models with different combinations of group (species)-varying coefficients. This is in contrast to the Arrhenius fractal supply model, which assumes only the intercept varies between taxa. The species-varying coefficients are thus estimated with shrinkage, which reduces the influence of outliers which could occur in species with small samples sizes (Gelman & Hill 2007; Harrison *et al.* 2018). The full model with uncorrelated species-varying coefficients can be written as:

|  |  |  |
| --- | --- | --- |
|  |  | (3) |
|  |  | (4) |
|  |  | (5) |

where is the th observation for species of the natural log of the rate (growth, consumption or metabolism), is the standard deviation and are coefficients. Species-level coefficients, (where ) follow a normal distribution with hyperparameters (global mean) and (between-species standard deviation). In Eq. 4, is the natural log of body mass and is Arrhenius temperature ( in unit ), both variables are mean-centred when fitting. Body mass is the mass in , specific growth rate has unit , consumption rate , and metabolic rate . We use resting or routine metabolism (mean oxygen uptake of a resting unfed fish only showing some spontaneous activity) and standard metabolism (resting unfed and no activity, usually inferred from extrapolation or from low quantiles of routine metabolism, e.g. lowest 10 % of measurements) to represent metabolic rate (Beamish 1964; Ohlberger *et al.* 2007). Routine and resting metabolism constitute 58% of the data used and standard metabolism constitutes 42%. We accounted for potential differences between these metabolic rate measurements by using a random species effect and a single study per species.

*Mass- and temperature dependence of consumption including beyond peak temperatures*

To characterize the decline in consumption rates beyond peak temperature, we fit second and third degree polynomial regressions (with and without in Eq. 7) to a subset of these data containing only species with data points extending beyond such a peak temperature. The models were fit with a random intercept ( to account for variation across species. The models of are:

|  |  |  |
| --- | --- | --- |
|  |  | (6) |
|  |  | (7) |
|  |  | (8) |

where in Eq. 6 refers to the th observation of mass-specific consumption rates for species divided by the mean value for species (), is the standard deviation and are coefficients. (species-level intercepts) follow a normal distribution with hyperparameters (global mean) and (between-species standard deviation). in Eq. 7 is mean-centred body mass () and is the mid-point of the temperature in the environment of species subtracted from the temperature used in the experiment (). This rescaling is done to control for differences between species with respect to the experimental temperatures relative to the temperature that maximizes their consumption rate.

*Mass-dependence of optimum growth temperature*

To evaluate how the optimum temperature (, in degrees Celsius) for individual growth depends on body mass, we fit the following hierarchical model to account for variation between species in both the intercept and slope:

|  |  |  |
| --- | --- | --- |
|  |  | (9) |
|  |  | (10) |
|  |  | (11) |

Here is mean-centred optimum growth temperature within species (), to account for species being adapted to different thermal regimes, is the standard deviation and are coefficients. Species-level coefficients, , (where ) follow a normal distribution with hyperparameters (global mean) and (between-species standard deviation). is the natural log of the ratio between mass and body mass at maturation within species: , as we were interested in examining relationships within species while accounting for variation in relative body masses between experiments, and because we do not expect an interspecific relationship between optimum growth temperature and body mass. Subscript in Eq. 11 refers to regression parameters (0 for intercept and 1 for slope). We also fit the model with only a random intercept.

*Parameter estimation*

We fit the models in a Bayesian framework, using R version 3.5.0 (R Core Team 2018) and JAGS (Plummer 2003) through the R-package ‘*rjags*’ (Plummer 2019). We used a mix of flat, weakly informative and non-informative priors to facilitate convergence (Table 1). Weakly informative priors were given mean values around average prediction from the MTE (Brown *et al.* 2004), with large variances to make them less informative. We used 3 Markov chains with 5000 iterations for adaptation, followed by 15000 iterations burn-in and 15000 iterations sampling where every 5th iteration saved. Model convergence was assessed by visually inspecting trace plots and potential scale reduction factors () (Gelman *et al.* 2003) (Appendix S1). compares chain variance with the pooled variance, and values <1.1 suggest all three chains converged to a common distribution. We relied heavily on the R packages within ‘*tidyverse’* (Wickham 2017) for data processing, as well as ‘*ggmcmc*’ (Fernández-i-Marín 2016), ‘*mcmcviz*’ (Youngflesh 2018) and ‘*bayesplot*’ (Gabry *et al.* 2019) for visualization.

*Model comparison*

We compared the parsimony of models with different hierarchical structures, and with or without mass-temperature interactions, using the Watanabe-Akaike information criterion (WAIC) (Watanabe 2013; Vehtari *et al.* 2017), which is based on the posterior predictive distribution. We report WAIC for each model descried above (Table 2), and examine models with WAIC values < 2, where WAIC is each models difference to the lowest WAIC across models, in line with other studies (Olmos *et al.* 2019).

*Net energy gain*

The effect of temperature and mass dependence of maximum consumption and metabolism (proportional to biomass gain and losses, respectively) (Ursin 1967; Kitchell *et al.* 1977; Essington *et al.* 2001) on growth is illustrated by visualizing the net energy gain. The model for the net energy gain (growth) can be viewed as a Pütter-type model, which is the result of two antagonistic allometric processes: , where is body mass and is temperature. We convert metabolism from oxygen consumption to by assuming 1 = 295 (based on an oxycaloric coefficient of 14.2 ) (Hepher 1988), 1 = 4184 and an energy content of 5600 (Rijnsdorp & Ibelings 1989). Consumption and metabolic rate are calculated for two sizes (10 and 100 g), using the global allometric relationships found in the log-log models fit to sub-peak temperatures. These allometric functions are further scaled with the temperature correction factor , (subscript for consumption and for metabolism). For maximum consumption, is based on Eq. 7 (but without a mass-coefficient and an intercept as it is rescaled to become a multiplier), as it reaches a peak over temperature. It can be written as: , where is temperature in and is a constant that scales the term to 1 at the mean temperature in the data (19). is defined as where , is in unit K and is a constant that scales the term to 1 at the mean temperature in the data (19). Note that when estimating these parameters, temperature is centred to the median temperature in the environment for species in the polynomial, whereas for the log-log model it is centred to the overall mean in the data.

**Table 1** Description the parameters in the full models (parameter type, as well as its interpretation in brackets), and their prior distributions. refers to a normal distribution (mean and standard deviation s.d.) and to a uniform distribution (interval). For simplicity, only the parameters of the full model are shown here (i.e. with most coefficients varying by species). When a model is fitted with a common rather than species-varying coefficient, e.g. instead of , the same prior is used for as for .

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Parameter | Description | Prior distribution |
| Log-linear regressions  for growth, consumption and metabolism (Eqns. 3-5) |  | Hyperparameter (average intercept across species) |  |
|  | Hyperparameter (average mass coefficient across species) |  |
|  | Hyperparameter (average temperature coefficient across species) |  |
|  | Hyperparameter (average interaction coefficient across species) |  |
|  | Hyperparameter (s.d. of species-intercepts) |  |
|  | Hyperparameter (s.d. of species mass coefficients) |  |
|  | Hyperparameter (s.d. of species temperature coefficients) |  |
|  | Hyperparameter (s.d. of species interaction coefficients) |  |
|  | Parameter (s.d.) |  |
| Polynomial models  for consumption (Eqns. 6-8) |  | Hyperparameter (average intercept across species) |  |
|  | Parameter (global mass coefficient) |  |
|  | Parameter (global temperature coefficient) |  |
|  | Parameter (global quadratic temperature coefficient) |  |
|  | Parameter (global cubic temperature coefficient) |  |
|  | Hyperparameter (s.d. of species-intercepts) |  |
|  | Parameter (s.d.) |  |
| Linear  models  (Eqns. 9-11) |  | Hyperparameter (average intercept across species) |  |
|  | Hyperparameter (average mass coefficient across species) |  |
|  | Hyperparameter (s.d. of species-intercepts) |  |
|  | Hyperparameter (s.d. of species mass coefficients) |  |
|  | Parameter (s.d.) |  |