**Model fitting**

*Model description*

To each dataset, we fit hierarchical models with different combinations of group (species)-varying coefficients. 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 general form the model is:

(1)

(2)

(3)

where is the th observation for species for rate *y*, is a group-varying intercept, is a predictor (e.g. mass, temperature or an interaction) and is its coefficient (, where is the number of predictors considered in the model). Species-level intercepts follow a normal distribution with hyperparameters (grand intercept) and (between-species standard deviation). For most models we also allow the coefficient(s)vary between species, such that is replaced by , where . Here, and correspond to the mean and standard deviation of the normal distribution of species-level coefficients. For each dataset, we evaluate multiple combinations of varying coefficients (from varying intercept to varying coefficients). Priors for parameters and hyperparameters are in Table X, and the structure of models and their random effects are shown in Table X-Y. Below we describe how the model in Eqns. 1-3 is applied to each data set with respect to response and predictor variables.

*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. On a linear scale, this more general scaling relationship is , where is a rate (growth, maximum consumption or metabolism), is mass and is temperature. After log-transformation it becomes: , where is the intercept, is the mass scaling exponent (on a linear scale) when () and is the interaction coefficient.

When applied to Eqns. 1-3, is the th observation for species of the natural log of the rate (growth, consumption or metabolism), and the predictors are (natural log of body mass), (Arrhenius temperature ( in unit ) (both mean-centred), and their interaction. 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 to a subset of these data containing only species with data points extending beyond such a peak temperature. For these data, in Eqn. 1 refers to the th observation of mass-specific consumption rates for species divided by the mean value for species (). We consider the following predictors (in Eqn. 2): mean-centred body mass (), standardized temperature (, where is the mid-point of the temperature in the environment of species ), as well as the square and cube of this temperature-variable. The rescaling is done to control for differences between species with respect to the experimental temperatures relative to the temperature that maximizes their consumption rate. We only consider the intercept to be species-varying.

*Mass-dependence of optimum growth temperature*

To evaluate how the optimum temperature (, in degrees Celsius) for individual growth depends on body mass, we fit Eqns. 1-3 with as the mean-centred optimum growth temperature within species (), to account for species being adapted to different thermal regimes. , the predictor variable for this model, is the natural log of the ratio between mass and body mass at maturation within species: . This rescaling is done because we are 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. We consider both the intercept and the effect of mass to potentially vary between species.

*Parameter estimation*

We fit the models in a Bayesian framework, using R version 4.0.2 (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 (5 and 500 g), which roughly correspond to the 25th and 75th percentile in the datasets, 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). Because maximum consumption reaches a peak over temperature, is based on the polynomial model (but without a mass-coefficient and an intercept, because the mass-coefficent is applied through the allometric function and is rescaled to become a multiplier). 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 of model parameters (type and 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), but note that when a model is fitted with a common rather than species-varying coefficient, e.g. instead of , we use the same prior 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 (common mass coefficient) |  |
|  | Parameter (common temperature coefficient) |  |
|  | Parameter (common quadratic temperature coefficient) |  |
|  | Parameter (common 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.) |  |