*Intraspecific scaling of individual growth, consumption and metabolism with temperature and body mass across fishes*

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**Abstract**

1. Warming of aquatic communities is generally predicted to increase individual growth rates and reduce asymptotic body sizes of ectotherms. However, we lack a comprehensive overview of average intraspecific scaling of growth with body mass and temperature from controlled experiments, and mechanistic growth models are usually not informed by empirical scaling relationships of key processes such as metabolism and consumption. This limits our ability to link experimental data to observed patterns of growth, as well as developing models of growth as well as food web dynamics.
2. To estimate the effect of body size and temperature on growth, and to examine the link between growth rate and rates of metabolism and consumption, we collated experimental data through a systematic literature review. We used only studies with both body mass and temperature treatments, and fit hierarchical models to evaluate how these rates scale jointly with mass and temperature within species while accounting for variation between species.
3. We find clear negative relationships between optimum growth temperature and with body mass within species. In addition, we find negative effects of temperature on the mass-scaling exponent of metabolism at sub-optimum temperatures, but not for consumption or growth. In general activation energies of growth, metabolism and consumption at sub-optimum temperatures conform to theoretical predictions and interspecific estimates, while mass scaling exponents deviate from the commonly predicted ¾.
4. Thus, small individuals within a species will likely be able to increase their growth rates with initial warming and larger individuals will be the first to experience negative effects of warming on growth.

**Introduction**

Individual body growth is a fundamental process powered by metabolism, and thus depends on body size and temperature. It affects individuals’ fitness and life history traits such as maturation size, population growth rates (Savage *et al.* 2004) and ultimately energy transfer across trophic levels (Andersen *et al.* 2009; Barneche & Allen 2018). Therefore, understanding how it scales with body size and temperature is important for predicting the impacts of global warming on the structure and functioning of ecosystems.

Global warming is predicted to lead to declines in the body size of organisms (Daufresne *et al.* 2009; Gardner *et al.* 2011). The temperature size-rule predicts that warmer rearing temperatures lead to faster developmental times (and larger initial size-at-age or size-at-life-stage), but smaller adult body sizes (Atkinson 1994). This relationship is found in numerous experimental studies (Atkinson 1994), as well as latitudinal gradient studies of insects (Horne *et al.* 2015), and is stronger in aquatic than terrestrial environments (Forster *et al.* 2012; Horne *et al.* 2015). The underlying mechanisms are not well understood, but are likely results of interplay between ecology and physiology (Ohlberger 2013; Audzijonyte *et al.* 2018; Neubauer & Andersen 2019). Empirical evidence of climate signals in time series of individual growth rate is accumulating. For instance, reconstructed growth histories of individual fish through ageing based on bony structures (otoliths) often show positive correlations between growth rates and increasing temperatures (Thresher *et al.* 2007; Neuheimer *et al.* 2011; Baudron *et al.* 2014; Huss *et al.* 2019). This increased growth rate can also be predicted from numerous experimental studies showing growth increases with temperature until a peak is reached, after which additional warming is deleterious (Brett *et al.* 1969; Elliott & Hurley 1995; Jobling 1997; Morita *et al.* 2010a; García García *et al.* 2011). Less clear, however, is the negative effect of warming on the growth of large fish within populations. Some studies have found negative correlations between maximum or asymptotic body size and temperatures in commercially exploited fish species (Baudron *et al.* 2014; van Rijn *et al.* 2017), whereas others, including large scale experiments, controlled experiments and latitudinal studies, have failed to find this relationship between maximum size (Barneche *et al.* 2019; Huss *et al.* 2019; van Denderen *et al.* 2019). Predictions about declines in asymptotic body mass have also been made from theoretical growth models (Pauly & Cheung 2018b). However, the physiological basis of these models has been questioned for multiple reasons, both for the mechanism leading to asymptotic growth (resource limitation) (Marshall & White 2019a) as well as the mechanism causing the asymptote to decline with warming (Lefevre *et al.* 2017). As empirical findings vary and theoretical predictions are questioned, it remains unclear to which extent the growth of large fish within populations is limited by warming.

The specific somatic growth rate of an individual can be represented as the difference between energy acquisition and expenditure (von Bertalanffy 1938; Kitchell *et al.* 1977; Jobling 1997). Around the maturation size, the remaining excess energy is partitioned between somatic growth and gonads. Energy acquisition, or assimilation, is typically the amount of energy available in consumed food and expenditure is defined as fasting, activity and feeding metabolism. Metabolic processes are in turn usually assumed to be related to resting metabolism, often measured as the oxygen consumption of unfed fish at rest (Jobling 1997). These components of the biomass dynamics of growth are found in simple mechanistic Pütter-type growth models, such as the von Bertalanffy Growth Model (VBGM), or the Ontogenetic Growth Model (OGM) (Pütter 1920; von Bertalanffy 1938; Ursin 1967; West *et al.* 2001), as well as more complex dynamic energy budget models (Kooijman 1993; Kearney 2019) including multispecies dynamics models such as physiologically structured population models (PSPMs) (Roos & Persson 2001) and size-spectrum models (Hartvig *et al.* 2011; Maury & Poggiale 2013; Blanchard *et al.* 2017). In order to understand growth dynamics in changing environments and to evaluate the physiological basis of growth models of varying complexity, it is therefore important to understand how metabolism and consumption rates in general scale with body size and temperature.

Assessing these dependencies should ideally be done at the intraspecific level, rather than interspecific, to better represent the individual-level processes, as scaling within and between species can differ. However, the average scaling of individual growth, metabolism and consumption with body mass and temperature is often inferred from interspecific data even when applied to represent processes in individuals. In addition, the temperature- and mass dependence of metabolism and other related rates are also often assumed to follow Arrhenius fractal supply model (AFS) in the metabolic theory of ecology (Gillooly *et al.* 2001; Brown *et al.* 2004; Downs *et al.* 2008). The AFS assumes that metabolically-driven rates () (individual growth, metabolism and consumption), to scale as: , where is the activation energy, is Boltzmann’s constant and is temperature in Kelvin. Importantly, the model assumes mass-scaling of ¾ when estimating temperature effects, as well as independent effects of mass and temperature (Downs *et al.* 2008). There is, however, numerous examples of deviations from this mass-scaling exponent (Clarke & Johnston 1999; Bokma 2004; Jerde *et al.* 2019), and cases when body mass and temperature can have interactive effects (Xie & Sun 1990; García García *et al.* 2011; Ohlberger *et al.* 2012; Lindmark *et al.* 2018) (but see (Jerde *et al.* 2019)). Moreover, while the AFS tends to provide good statistical fits to interspecific data (Clarke 2004), and could also fit intraspecific data depending on the temperature range (Brown *et al.* 2004; Clarke 2004) (but see (Englund *et al.* 2011)), within-species thermal response curves are generally unimodal (Dell *et al.* 2011; Englund *et al.* 2011; Rall *et al.* 2012). These assumption-violations, and model oversimplifications, are likely to affect the estimates of temperature-dependencies (Downs *et al.* 2008). Instead of mass-correcting according to the AFS (Brown *et al.* 2004), it could be more appropriate to fit multivariate models where coefficients are estimated jointly (Downs *et al.* 2008), as well as fit non-linear models that can capture the de-activation of biological rates at higher temperatures (Dell *et al.* 2011; Englund *et al.* 2011).

Overall, average intraspecific scaling of rates with mass and temperature is less understood than interspecific scaling relationships. Contributing factors could be the logistical challenges of replicating experiments for ranges of body masses and temperature (Jerde *et al.* 2019) and a lack of comprehensive data (Dell *et al.* 2011). This appears to be especially true for consumption and growth rates (Englund *et al.* 2011; Barrios‐O’Neill *et al.* 2019). Scaling parameters are therefore often based on single experiments, which makes generalization across species difficult. However, it is important to understand both general tendencies and variability of intraspecific body mass and temperature-scaling relationships, given the importance of intraspecific trait variation as a driver of ecological dynamics (Bolnick *et al.* 2011; Miller & Rudolf 2011; Persson & De Roos 2013). Therefore, overcoming the knowledge gap about intraspecific scaling is important for advancing trait-based approaches to ecology.

In this study, we performed a systematic literature review by searching the Web of Science Core Collection to compile a dataset on individual growth rates, consumption- and metabolic rates of fish from experiments in which the effect of fish body mass is replicated across multiple temperatures within species. We fit hierarchical Bayesian models to account for variation between species and to acquire general intraspecific predictions on how the rates depend on temperature and body mass, based on partial pooling of data across species to minimize the influence of extreme observations for general scaling relationships. For maximum consumption rates, we also fit quadratic models to a subset of the data to characterize the unimodal temperature dependence. We find that the temperature-dependence of growth, consumption and metabolism in general is close to average intraspecific predictions (activation energies approximately 0.6 ), whereas mass-exponents deviate from the predicted ¾.

**Methods**

**Data acquisition**

We searched the literature for experimental studies measuring the temperature and mass dependence of individual growth rate, maximum consumption rate (feeding rate at unlimited food supply, *ad libitum*) and resting, routine and standard (see ‘*model fitting’*) oxygen consumption rate as a proxy for metabolic rate (Nelson 2016). We used three different searches on the Web of Science Core Collection. For growth rate, we used the following topic terms: (growth) AND (mass OR weight OR size) AND (temperature\*) AND (optimum), as well as: (growth) AND (mass OR weight OR size) AND (temperature\*) AND (optim\*). For metabolic rate we used: (metabolism OR "oxygen-consumption" OR "oxygen consumption") AND (mass OR weight OR size) AND (temperature\*). For maximum consumption we used: (consumption or feeding$rate or food$intake or bio$energ\* or ingestion or food-intake) AND (mass or weight or size) AND (temperature\*), as well as: (feeding-rate or bio-energ\*) AND (mass or weight or size) AND (temperature\*). We also applied additional filters on subject: ‘marine freshwater biology’, ‘fisheries’, ‘ecology’, ‘zoology’, ‘biology’, ‘physiology’. For growth rates, we in addition included ‘limnology’ and for maximum consumption we included ‘limnology’ and ‘evolutionary biology’. The wider searches for growth and consumption is due to less studies being found in the searches. For more detailed information about the search protocol, we refer to Appendix S1.

We selected studies with a factorial body mass-temperature setup in order to estimate how these rates depend on body size and temperature within species. While this reduces the number of data points available in the literature (as most experimental studies only use size or temperature treatments), it allows us to fit multivariate models and estimate the effects of mass and temperature jointly, and to evaluate the probability of interactive mass- and temperature effects within species. We excluded larval studies as they represent a small fraction of the ontogeny of most fish. Studies were included if (i) a unique experimental temperature was recorded for each trial (), (ii) fish were provided food at *ad libitum* for consumption and growth data, fish were unfed for measurements of resting, standard or routine metabolic rate , (iii) fish exhibited normal behavior. We used only one study per species to ensure that all data within a given species are comparable as measurements of these rates can vary between studies due to e.g. measurement bias or differences in experimental protocols (Armstrong & Hawkins 2008; Jerde *et al.* 2019). In cases where we found more than one study for a species, we selected the study we found most suitable, based on how well it fit with our pre-defined criteria (Appendix S1). A more detailed description of the search protocol, criteria to select data, data acquisition procedure, quality control, collation of additional information and standardizing rates to common units can be found in Appendix S1.

We compiled four datasets: growth-, metabolic-, and maximum consumption rate, and the optimum growth rate temperature for each combination of body mass group and species. We compiled in total 154, 2790 and 626 data points from published articles on growth rates (i.e. from studies including optimum temperatures for different body sizes within species), metabolic rate and maximum consumption rate, from 13, 35 and 18 species, respectively, representing a diverse range of taxonomic groups, habitats and lifestyles (Appendix S1). Data were extracted from published tables or figures using Web Plot Digitizer (Rohatgi 2012).

Between experiments, individuals differed in their body masses, both in absolute values and relative to their maximum body size. Experimental temperatures also varied in relation to the species normal temperature-range between studies (Fig S2, S6-S7). For the analysis of optimum growth temperature, we therefore rescaled body mass and temperature to relative variables, by species. Relative body mass is defined as mass relative to maximum mass (based on literature estimates taken from FishBase (Froese & Pauly 2016) between 2019-06-01 and 2019-12-01), as we were interested in examining relationships within species while accounting for variation in relative body masses between experiments. Relative temperature was acquired by normalizing to mean optimum growth temperature within species (of different size-classes), to control for species having different thermal optima. The optimum growth and consumption temperatures were also evaluated in relation to the mid-point of the ranges of environmental temperatures experience by the species (also taken from FishBase), which was subtracted from the experimental temperature. In the growth data, this information was not available on Fishbase for marbled sole (*Pseudopleuronectes yokohamae*), hence 13.5 (mid-point of 3 and 24) was used (Joh *et al.* 2013; Mitamura *et al.* 2020). In the consumption data, this information was not available from FishBase for Orange-spotted grouper (*Epinephelus coioides*) and Japanese flounder (*Paralichthys olivaceus*), and instead the midpoint was taken from the minimum and maximum of the preferred temperature based on distributional maps (FishBase).

**Model fitting**

*Mass-dependence of optimum growth temperature*

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

|  |  |  |
| --- | --- | --- |
|  |  | (1) |
|  |  | (2) |
|  |  | (3) |

Here is the *i*th observation of the rescaled optimum growth temperature (rescaled by species : ). is the natural log of the ratio between either geometric mean body mass or size class, as defined in the original study, in the growth trial and the maximum body mass within species: . Subscript in Eq. 3 refers to parameter (0 for intercept and 1 for slope). We also fit a model with a global mass-coefficient (i.e. not varying by species). Body mass and temperature are in addition mean-centered, such that 0 corresponds to the mean of all across all data points

*Mass- and temperature scaling of growth, metabolism and consumption below optimum temperatures*

Below optimum temperatures (i.e., a subset of the data sets including only data points below the temperature at which the rate was maximized, by size group), we assumed individual growth, metabolic rate and maximum consumption rate to scale as a generalized version of the Arrhenius fractal supply model (Gillooly *et al.* 2001; Brown *et al.* 2004). Note that the term optimum is misleading for metabolic rate data, but since do not have data points beyond the temperature where metabolism is maximized, optimum or temperature at max rate value only refers to to consumption or growth data. Mass and temperature dependence was not assumed a priori but estimated jointly to evaluate the effects of temperature and body mass simultaneously. This approach is more appropriate if the mass-scaling exponent is not exactly 3/4 (Downs *et al.* 2008), as suggested by empirical data (Sibly *et al.* 2015; Jerde *et al.* 2019). It also allows estimation of size\*temperature interactions. We thus assumed the natural log of rate (growth, metabolism or maximum consumption) scales with mass and temperature as:

|  |  |  |
| --- | --- | --- |
|  | , | (4) |

which on normal scale becomes:

|  |  |  |
| --- | --- | --- |
|  | *,* | (5) |

where is the intercept, is the mass-scaling exponent when , is the interaction coefficient, is the activation energy, and is Boltzmann’s constant in (). We fit hierarchical models with different combinations of group (species)-varying coefficients. The full model with uncorrelated species-varying intercepts, mass-, temperature- and interaction-coefficients, can be written as:

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

where is the th observation of the natural log of the rate (growth, metabolism or consumption), and indexes regression coefficient (. In Eq. 7, is the mean-centered natural log of body mass (), and mean-centered Arrhenius temperature ( in unit Kelvin). For metabolism and maximum consumption rates, is mass in , whereas for growth rates, is either the geometric mean of the initial and final mass of the growth experiment, or the size-class, as defined by the authors. Growth rates were expressed as unit , consumption rates as unit and metabolic rates as unit (Appendix S1). 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 55% of the data used and standard metabolism 45%. We accounted for potential differences between these metabolic rate measurements by using a random species effect and a single experiment/dataset per species.

*Mass- and temperature scaling of growth and consumption including beyond optimum temperatures*

Growth and consumption are unimodal over a large enough thermal range, and we refer to the temperature where these rates are maximized as optimum temperature (Dell *et al.* 2011; Englund *et al.* 2011). To evaluate the intraspecific unimodal scaling of these rates, we fit quadratic models to a subset of these data containing only species with data points extending beyond the temperature at which the rate is maximized. The models were fit by species and then aggregated, i.e. without any hierarchical structure accounting for species variation. This was due to the difficulty of standardizing optimum-data to a common scale, as species have different consumptions rates at optimum temperature, different widths of the thermal performance curves and different optimum temperatures. By fitting models by species, we thus avoid the risk of removing true effects in data, at the cost of losing the benefits of the hierarchical model for inferring general intraspecific scaling. The model of is for the full data set defined as:

|  |  |  |
| --- | --- | --- |
|  |  | (9) |
|  | , | (10) |

where in Eq. 9 refers to consumption rates divided by the mean value by species (), in Eq. 10 is mean-centered natural log of body mass in unit and is mean-centered rescaled temperature by species, where the rescaledtemperature is defined as .

For illustrations of model fits, we predict over the temperature range of the data for species while keeping body mass at 0 (corresponding to the species-specific mean body mass in ). The species predictions and data are plotted together in Fig. S21 to illustrate the spread in optimum temperature measured as distance to environmental median. Due to general data limitation we did not fit an interaction term that alters the optimum temperature by mass, however this has been identified in data-rich single-species experiments (García García *et al.* 2011).

*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 depending on how well known the parameter is, based on previous literature (<https://github.com/stan-dev/stan/wiki/Prior-Choice-Recommendations>) (Table 1). We used 3 Markov chains with 10000 iterations each, following 10000 iterations for burn-in and 5000 for adaptation. Model convergence was assessed by visually inspecting trace plots and (Appendix S1). compares chain variance with the pooled variance, and values <1.1 ensures all three chains converged to a common distribution (Gelman & Rubin 1992). We relied heavily on the R packages within the *tidyverse’* (Wickham 2017) for data processing, as well as ‘*ggmcmc*’ (Fernández-i-Marín 2016) and ‘*bayesplot*’ (Gabry *et al.* 2019) for visualization. All data and R code (data manipulation, analyses and figures) can be downloaded from a GitHub repository (<https://github.com/maxlindmark/scaling>) and will be archived on Zenodo upon publication.

*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 evaluate models within with WAIC values < 2, where WAIC is each models difference to the lowest WAIC across models, in line with common convention (Olmos *et al.* 2019).

**Table 1** Description of model parameters and their prior distributions. refers to a normal distribution and to a uniform distribution.

|  |  |  |  |
| --- | --- | --- | --- |
| Model | Parameter | Description | Prior distribution |
| Linear  model  (Eqns. 1-3) |  | Hyperparameter (intercept) |  |
|  | Hyperparameter (mass coefficient) |  |
|  | Hyperparameter (intercept variance) |  |
|  | Hyperparameter (mass coefficient variance) |  |
|  | Variance |  |
| Log-linear regressions  for growth, consumption and metabolism (Eqns. 6-8) |  | Hyperparameter (intercept) |  |
|  | Hyperparameter (mass exponent) |  |
|  | Hyperparameter (activation energy) |  |
|  | Hyperparameter (interaction) |  |
|  | Hyperparameter (intercept variance) |  |
|  | Hyperparameter (mass exponent variance) |  |
|  | Hyperparameter (activation energy variance) |  |
|  | Hyperparameter (interaction variance) |  |
|  | Variance |  |
| Quadratic model  for consumption and growth  (Eqns. 9-10) |  | Intercept |  |
|  | Mass coefficient |  |
|  | Temperature coefficient |  |
|  | Quadratic temperature coefficient |  |
|  | Variance |  |

**Results**

The optimum temperature for growth declines with body size by -0.3 per unit increase in the natural log of relative body mass (Fig. 1). This decline in optimum temperature is very clear, because 99% of the posterior density of the slope estimate () is below 0. The two models, with and without species-varying slopes, were indistinguishable in terms of WAIC (WAIC = 1.3), and we therefore present the results for the global slope model for parsimony. The general relationship is given by the model: , where is relative mass.

We find that the average intraspecific mass- and temperature dependence of specific growth at below optimum temperatures across species can be described by the equation: . This model (M1, Table 2) contains a body mass-temperature interaction. However, the estimated interaction coefficient is small (-0.02 [-0.1, 0.06], where brackets indicate 95% Bayesian credible intervals) and uncertain, as about 72% of the posterior density is above 0 (Fig. 2), and only leads to marginal better fits to data (WAIC around 2.4 compared to model without interaction, Table 2). We estimate the mass-scaling exponent of growth, i.e. the mass-coefficient on log-log scale, to be -0.3 [-0.43, -0.17]. The activation energy, , of growth is estimated to be -0.76 [-0.99, -0.54]. This is lower, i.e. more temperature-sensitive, than what is typically found for metabolic rate (Downs *et al.* 2008) and for growth based on field data (Sibly *et al.* 2015). We also find that 86% of the posterior density of the temperature-effect is below -0.65. To illustrate this in terms of specific growth, an increase in temperature from 15 (overall mean in data) to 25 leads to an increase in predicted natural log of growth by a factor of 2.9 for a fish of mean mass (~190).

We find that the global intraspecific scaling of whole-organism metabolic rate can be described by the equation , and consumption rate at temperatures below optimum as (see Fig. 3 for a general intraspecific prediction for a given mass and two temperatures). In the models of consumption, all coefficients vary by species (M5) whereas for metabolism, all but the interaction coefficient vary by species (M2) (Table 2).

Some notable differences exist in the mass- and temperature-dependences of these two rates. First, metabolic rate scales with a slightly larger mass-scaling exponent (0.77 [0.7, 0.83]) than maximum consumption (0.64 [0.56, 0.73), inferred from largely non-overlapping Bayesian 95% credible intervals (indicated in square brackets) (Fig. 4). This difference implies that metabolic processes increase faster with body mass than maximum consumption rates. We also find it probable that both mass-scaling exponent of maximum consumption differ from the predicted 0.75 from the metabolic theory of ecology, because 99.5% of the posterior distribution is below 0.75. The mass-exponent for metabolism is closer to 0.75, with 70% of the posterior distribution above 0.75. Activation energies of metabolism and maximum consumption rate are both similar (-0.61 [-0.67, -0.56] and -0.66 [-0.83, -0.49], respectively) and largely fall within the prediction from the MTE (0.6-0.7 eV) (Brown *et al.* 2004)).

We find strong statistical support for a negative global interaction between the effect of body mass and temperature on metabolic rate (99.9% of the posterior distribution of is above 0, Fig, 5), yet the effect size is relatively small. We estimate it to be 0.017 [0.0067, 0.03] on an Arrhenius temperature scale, which corresponds to a decline in the mass scaling exponent of metabolic rate by ~0.0023 . For maximum consumption, the model with a global interaction, , term has a WAIC of 2, meaning that WAIC offers little support for one of these models over the other. For illustration of model predictions we therefore chose model M5 because it is simpler and the estimate of is uncertain (82% of posterior is < 0) and small (posterior median of -0.018 on Arrhenius temperature scale). For metabolism, the model with a species-varying interaction term has a WAIC of 1.2, suggesting it is comparable to the global-interaction only model. We chose the latter to illustrate predictions for the simpler model structure.

Over a larger temperature range, biological rates tend to be unimodal. We identified such tendencies in nine species in the consumption data set, and fit quadratic models to the consumption rate in those species (Fig. 6). The unimodal temperature-dependence implies that even if maximum consumption rates increase faster than metabolic rates with temperature at sub-optimum temperatures (due to larger activation energy), eventually consumption rates decline relative to metabolism with further warming. In other words, the effect of temperature on the mismatch between metabolic costs and feeding gains depends on the current temperature relative to optimum temperature. However, when standardizing the temperature data to a common unit, here relative to median temperature in the environment (i.e. ) in unit , we find large variations in the relative temperature at which consumption is maximized (“optimum”) (Fig. 6). These temperatures range from -2.3 to +17. Across species, the mean in intraspecific is 6 in the same unit (with a standard deviation of 6).

**Table 2**. Model comparison for the log-linear regressions of how consumption, metabolism and growth depend on mass and temperature (below optimum temperatures). M1 is the full model and is described in text (Eqns. 3-5). The column m\*t indicates whether the model for the rate includes an interactive effect of mass and temperature. The WAIC columns shows WAIC and absolute WAIC in brackets, rounded to the nearest decimal, where WAIC is the difference between each models’ WAIC and the lowest WAIC across models. Bold indicates models with WAIC < 2.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Model | m\*t | Species-varying parameter(s) | WAIC  metabolism | WAIC consumption | WAIC growth |
| M1 | Yes |  | **1.2 (291.3)** | 3.5 (530.3) | **0 (43)** |
| M2 |  | **0 (290)** | **2 (528.7)** | 2.7 (45.6) |
| M3a |  | 297.8 (587.9) | 132.5 (659.2) | 27.4 (70.4) |
| M3b |  | 844.5 (1134.6) | 48 (574.7) | 48.2 (91.2) |
| M4 |  | 1063.6 (1353.7) | 157.4 (684.1) | 59.2 (102.2) |
| M5 | No |  | 6.4 (296.5) | **0 (526.7)** | 2.4 (45.3) |
| M6 |  | 1167.6 (1457.6) | 185.5 (712.2) | 56.8 (99.8) |
| M7 |  | 2363.7 (2653.9) | 681.9 (1208.7) | 191.1 (234.1) |
| M8 |  | 4200 (4491) | 672 (1198.8) | 138.3 (181.2) |

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**Fig. 1**. *Optimum temperature for growth (rescaled to optimum temperature within species) as a function of mean centered natural log of rescaled body mass (mass/maximum mass within species). Probability bands represent 80% and 95% credible intervals and solid line represent the median prediction from the average across-species effect ( and ). Colors indicate species (n=13) (see Appendix S1) and point size corresponds to mass in unit .*

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**Fig. 2**. *Effects of temperature and body mass on body growth. Panel A) shows growth rate [% day-1] as a function of mean centered body mass, both on natural log scale. Lines are global predictions from model M1 for an average species at temperatures 15 (blue line and ribbon), which is close to the mean temperature (14.3) in data and 25 (red line and ribbon). Note the model is fitted using mean-centered Arrhenius temperature (1/kT), and then converted for easier interpretation. Shaded areas correspond to 80% and 95% credible interval and the solid line is the median prediction from the average across-species prediction. Point colors indicate species (n=13, legend not shown). The slope corresponds to the mass-scaling exponent. Posterior distributions of the average mass-scaling exponent, , (B) activation energy,, (C) and mass-temperature interaction, , (D) are shown in the bottom row. Dashed white line shows the posterior median.*

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***Fig 3****. Natural log of metabolic rate (A) and maximum consumption rates (B) vs. natural log of mass [g]. Lines are global predictions for an average species at temperatures 15 (blue line and ribbon) and 25 (red line and ribbon). The average temperatures in the data are 19 and 18 for metabolism and maximum consumption, respectively. Note the model is fitted using mean-centered Arrhenius temperature (1/kT), and then converted for easier interpretation. Shaded areas correspond to 80% and 95% credible interval. Point colors correspond to species (n=18 and n=35 for consumption and metabolism, respectively).*

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***Fig. 4****. Posterior medians of the global activation energies and mass-exponent of metabolism (model M2) and maximum consumption (model M5) from the hierarchical model fitted to below temperature optimum data (white triangles and circles, respectively), and their 80% and 95% credible interval (vertical short and long lines, respectivelly). Vertical dashed lines correspond to the median prediction for an unknown species (i.e. and in Eqs. 6-8 for the mass and temperature coefficient, respectively). Shaded vertical areas correspond to posterior median standard deviations of the posterior median.*

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***Fig. 5.*** *Rescaled maximum consumption rates (consumption divided by mean consumption within species) as a function of rescaled temperature (), where colors indicate species. The data is a subset of the maximum consumption data containing only species with observations at temperatures higher than where the rate is maximized (“optimum”). Lines are predictions from the quadratic model where the mean-centered body mass is held at 0 (corresponding to mean mass within species), and open circles are data. The shaded areas show 80% credible interval for the median prediction. Arrows depict the optimum temperature for each species and the vertical dashed and dotted lines correspond to the across-species mean optimum temperature 1 standard deviation.*

A close up of a map

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***Fig. 6.*** *Illustration of the thermal response (mean-centered) of maximum consumption (green), metabolism (purple) and their difference (orange) for two body sizes (small = solid, large = dashed). The body masses on normal scale correspond approximately to 200 g and 400 g, respectively. The consumption-curve is based on the quadratic model for C.argus (Appendix S1, Fig SX), and metabolism is calculated from the global model (see ‘Results’), and both rates are expressed as relative to their maximum. Arrows indicate the temperature where the difference in net energy acquisition is maximized for the two body sizes.*

***A screenshot of a cell phone

Description automatically generated***

***Fig. 7.*** *Environmental temperature versus experimental and optimum growth temperature. Vertical green lines show the minimum and maximum environmental temperature based on either temperature in distribution range (triangles) or modelled distribution maps (circles), both taken from FishBase, and green points show the midpoint. Gray points below each line indicates experimental temperatures and orange points show the optimum temperatures for all size-classes per species, where the circle size is proportional to number of observations at that temperature. The average distance between environmental mid-point temperature and mean optimum temperature (per species) is 6.52.6 s.d.*

**Discussion**

Individual growth, consumption and metabolic rate represent fundamental processes in ecology, and their scaling with body mass and temperature is used to predict the effects of warming on individual growth, population and community dynamics using mechanistic models (Vasseur & McCann 2005; Rall *et al.* 2010; Cheung *et al.* 2013). Relationships of how biological rates scale with temperature and/or mass are commonly inferred from either meta-analysis of single-species studies (Glazier 2005) or interspecific relationships. However, the former can result in large variation in intraspecific scaling parameters, and the latter relies on the assumption that rates scale identically within and between species, which is often not the case (Glazier 2005; Rall *et al.* 2012; Jerde *et al.* 2019). As growth, consumption and metabolic rate represent individual-level processes, it is important to understand how these rates depend on temperature and mass at the intraspecific level. We find that the optimum temperature for growth declines with body size. At temperatures below optimum, we generally find that activation energies metabolism, consumption and growth are close to predictions from the metabolic theory of ecology (MTE), which predicted mass-corrected rates to scale with temperature with an activation energy of ~0.6 . However, the mass-scaling exponent of metabolism is greater than the predicted 3/4, which is often found in fish, e.g. (Clarke & Johnston 1999; Jerde *et al.* 2019). By contrast, the mass-exponent of maximum consumption is smaller than predicted by the MTE. This has implications for mechanistic models of individual growth, as well as population and food web dynamics.

That optimum growth temperatures decline with body size has been reported in some studies, including but not limited to fish (Panov & McQueen 1998; Steinarsson & Imsland 2003; Björnsson *et al.* 2007; Handeland *et al.* 2008), but was not found for e.g. brown trout (*Salmo trutta*) (Elliott & Hurley 1995). Here, we find strong support that the optimum growth temperature for an average fish decline as they in mass over ontogeny. The effect size also appears relatively large considering the small range of body sizes used in the experiments (a decline in by 0.3 per unit increase in the natural log of relative mass, ). Because 73% of individuals in the experiments assembled for this study are < 1% of their maximum, the individuals in the experiments likely invest little energy in reproduction. This suggests that reduced growth performance of large fish with increased temperatures cannot only be explained by earlier maturation.

Translating effects of experimentally derived optimum growth temperatures to natural systems is challenging because experimental conditions such as unlimited food supply, lack of predation, and constant temperatures do not reflect natural condition, yet these variable affect growth rates and optimum temperatures for growth (Brett *et al.* 1969). Nevertheless, the finding that large fish would be the first in a population to experience negative effects of warming suggests there might be purely physiological constraints to body growth of large fish. However, this also depends on if larger individuals within a species live closer to their thermal optimum for growth, which they may not do given that ontogenetic habitat shifts are common and could (partly) compensate for such negative effects of warmingss (see e.g. Heincke’s law (Heincke 1913; Werner & Hall 1988; Audzijonyte & Pecl 2018)). That said, there is already empirical evidence of the largest individuals being the first to suffer negative impacts of warming from e.g. heatwaves (Pörtner & Knust 2007). It is also commonly assumed that species occupy thermal habitats below their optimum for growth, as sub-optimum temperatures are in fact optimal in temperatures fluctuate (Bernhardt et al 2019). However, warming can have negative (or lack of positive) effects on populations living at the edge of their physiological tolerance in terms of growth (Neuheimer *et al.* 2011; Huss *et al.* 2019) or even survival (Pörtner & Knust 2007). This suggests that assuming that species occupy thermal habitats where warming can lead to increased growth rate (i.e. the exponentially increasing part of a thermal response curves) is a simplification that may not always be warranted in a climate change context.

Interestingly, a decline in optimum growth temperature with mass is also predicted by the von Bertalanffy growth model (VBGM) , where is body mass and is temperature), under two conditions: (which also is a necessity for asymptotic growth) and that growth has an optimum over temperature, as shown by (Morita *et al.* 2010b). While this is one of the most commonly applied growth models, the first condition has been debated recently. in the classic VBGM is assumed to be proportional to body mass. This originates from the argument that maintenance should be proportional to mass, as spontaneous denaturation occurs in every cell (von Bertalanffy 1957; Pauly & Cheung 2018a) (and likely also from mathematical convenience and a lack of empirical data (Ursin 1967)). From a physiological perspective, it is more common to assume maintenance costs are proportional to standard metabolic rate (oxygen consumption of a resting and fasting organism) (Ursin 1967; Jobling 1997; Lefevre *et al.* 2017). In this case, supply and demand models of growth, such as the VBGM or the similar OGM (West *et al.* 2001), either fail to represent the physiological processes they aim to capture or fail to exhibit asymptotic growth. This is especially true if assuming a ‘universal’ mass scaling exponents of 3/4 for both assimilation and standard metabolic rate. This dichotomy can be resolved by considering the overlooked energetic investment into reproduction (and its hyper-allometric mass-scaling, i.e. exponent larger than 1) (Marshall & White 2019b), or by applying more complex energy pathways in dynamic energy budget models (Kearney 2019). This recent debate about scaling coefficients in growth models call for an investigation of the intraspecific scaling of metabolic rate in relation to assimilation or consumption. Our finding that the mass-scaling exponent of metabolism is larger than that for maximum consumption implies that “costs” for maintenance increase faster with body mass than energy assimilation – assuming no other processes such as assimilation efficiency scale in ways to counteract this. In natural systems, however, realized consumption is mediated by predator-prey encounter rates and search rates, whereas maximum consumption rates largely correspond to the physiology of digestion (Ursin 1967). Regardless, changes in the maximum feeding capacity could result in reduced growth efficiency over ontogeny and bioenergetics models may need to account for this difference in the mass-scaling of metabolism and consumption, which is in contrast to universal mass-scaling predictions.

In addition to resolving the scaling of net energy gain (e.g. difference between energy assimilation and costs) with body mass, it is important to understand how this balance is affected by temperature. The match, or mismatch, between the temperature dependence of feeding vs. metabolic rates is a central question in experiments, meta-analyses and food web models (Vasseur & McCann 2005; Lemoine & Burkepile 2012; Fussmann *et al.* 2014; Lindmark *et al.* 2019). We find that when using strictly sub-optimum temperatures, the general (average intraspecific) predictions about the activation energy of metabolism and consumption vary, but the 95% credible intervals largely overlap, meaning there is no clear loss or gain of energetic efficiency with warming. This result fits well with the finding that growth rates increase with temperature, which would be difficult to explain from a bioenergetics perspective if warming always reduced net energy gains.

We also find the general temperature scaling of metabolic and maximum consumption to be less uncertain than what has been reported previously (e.g. in (Downs *et al.* 2008; Englund *et al.* 2011)). A likely contributing factor is our use of hierarchal models and partial pooling to estimate higher level (across species) scaling from species-data as opposed to either aggregating all data (complete pooling) or summarizing single-species estimates (no pooling).

In contrast to the MTE, we also find that body mass can affect the temperature scaling on physiological rates, which previously has been reported only for single species studies (Beamish 1964; Xie & Sun 1990; Ohlberger *et al.* 2012; Fossen *et al.* 2019) and between species (Killen *et al.* 2010). This was however not found in a recent study on the intraspecific mass-scaling exponent of metabolic rate in fishes (Jerde *et al.* 2019), which could be due to different data collection protocols (where we valued temperature replication over mass-replication), differences the body size or temperature-ranges, or that we specifically searched for studies with temperature replicates within species. The effect size of the interaction is, however, relatively small. We do not find strong evidence for a global average of declThe ecological implications could therefore also be small, although larger estimates have been reported in single species studies (Ohlberger *et al.* 2012). It could also be that the overall effect is masked by variation between species, as studies have found both positive and negative interaction terms (Ohlberger *et al.* 2012; Messmer *et al.* 2016; Lindmark *et al.* 2018).

While we find no clear evidence of mismatch between metabolic demands and maximum consumption induced by temperature at sub-optimum temperatures, we do find clear mismatches at higher temperatures. These are due to consumption rates being unimodally related to temperature, whereas metabolic rates increase exponentially over essentially all temperatures. To what degree this is due to metabolic mismatch caused by the unimodal temperature-dependence of consumption vs the exponential one of metabolism (as is often argued from a conceptual point of view (Jobling 1997)) remains uncertain. This is perhaps best evaluated on a species level, given the large variation among species in their optimum temperature relative to their preferred temperature (Fig. 6).

Because we evaluated the joint effect of body mass and temperature on rates of body growth, metabolism and consumption, the number of studies included in our analysis constitutes a small fraction of the available data on experiments testing only a single temperature or body size (Appendix S1). It also resulted in that the size replicates within each temperature treatment or vice versa are relatively small. The relatively small amount of data is especially evident for the consumption experiments, which show larger variation both within and between species, compared to metabolism. This is likely due to the more manual estimations in feeding experiments (e.g. weighing added food and subtracting uneaten food) compared to oxygen depletion rates (metabolism) measured in respirometry, or growth trials. Therefore, the data collated here contains uncertainty from many sources, including differences in experimental protocols. Thus, our selection criteria leads to using a small fraction of all available data, which limits the hierarchical model structures we can consider (Jerde *et al.* 2019). However, as it is important to jointly estimate the effects of mass- and temperature when scaling coefficients differ from general predictions (Downs *et al.* 2008), we argue that our approach also has merit. One approach for overcoming difficulties with these relatively small data sets is using hierarchical models (e.g. in a Bayesian framework with literature-informed priors), which can aid estimation of general scaling relationships.

Understanding the scaling of rates such as growth, metabolism and consumption is fundamental for linking individual processes to population- and food web dynamics. We argue that one contributing factor to the mismatch between mechanistic models, general scaling theory and data is due to lack of synthesis of data at the intraspecific level. Systematic data-analysis of existing experimental data combined with models that account for uncertainty at the species-level constitutes an approach that can guide process-based predictions of climate change impacts from individuals and food webs.

**Author contributions**

ML conceived the study; ML, JO, AG designed research; ML performed research; ML analyzed data; ML, JO, AG wrote the paper and contributed to revisions of the manuscript.

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