**Appendix S1**

**Supporting Information for**

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

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Contents

[Literature search, selection process and criteria 3](#_Toc31714043)

[*Growth rates & optimum temperature for growth over body mass* 3](#_Toc31714044)

[*Metabolic rate* 4](#_Toc31714045)

[*Maximum consumption rate* 5](#_Toc31714046)

[Data exploration 6](#_Toc31714047)

[*Growth rate* 6](#_Toc31714048)

[*Metabolic & maximum consumption rate* 8](#_Toc31714049)

[Supplementary analysis 11](#_Toc31714050)

[Model validation 13](#_Toc31714051)

[*Optimum growth temperature* 13](#_Toc31714052)

[*Growth rate* 16](#_Toc31714053)

[*Metabolic rate* 19](#_Toc31714054)

[*Maximum consumption rate* 22](#_Toc31714055)

[References 25](#_Toc31714056)

# Literature search, selection process and criteria

Prior to starting the actual literature review, we conducted several test-searches with alternative search-strings on Web of Science Core Collection, basic search. This was done in order to find a manageable number of articles to review and to have a reasonable ratio article titles that passed the first screening, given our pre-defined criteria for when to choose a study. As we suspected that relatively few studies would have considered both size- and temperature treatments, our goal was to get an as extensive as possible list of studies. Therefore, we also evaluated articles cited by articles in the literature list, and from published review-type articles and reviews of applications of bioenergetics models such as the Wisconsin model (Deslauriers *et al.* 2017).

The search terms and subject categories are presented in the main text. We filtered out articles at three levels of the search: title, abstract and full article. Appendix SX contains lists of article titles at each of these steps in the filtering process. We also used studies that did not appear in the literature search but that we found by following cited literature when reading the full article. The source of the article (literature or cited literature) is indicated in the data sets. We removed studies from the lists if the titles made it clear the articles did not fulfill all of the following conditions: (1) experimental study, (2) fish as study organism in life stages older than larval (3) replicates across both size and temperature. In addition to these general criteria, we also had criteria specific for each rate (see below). When several studies were found for the same species, we did not include both but instead chose the study with the largest size and temperature range (in that order), as there can be large differences in absolute values of some physiological parameters between studies. While this reduces the number of data points, it avoids additional observation error due to different experimental setups and experimenters. All data were extracted from tables, or figures using Web Plot Digitizer (Rohatgi 2012) version 4.1.

## *Growth rates & optimum temperature for growth over body mass*

Growth rates were taken from data found in the literature search for optimum growth temperatures. The two searches for growth rates described in the main text resulted in 3313 articles (search date: 2019.03.22), and 3747 articles (search date: 2019.08.05), respectively. After applying additional filters by subject category, we acquired 566 and 893 studies, respectively (of which some are duplicates due to similar search-strings). We removed studies at the abstract and whole-article stage where the original reference could not be identified and evaluated, we could not extract actual growth rates, if there was not a controlled temperature for each growth trial or if there were not multiple defined size-classes. In addition, we ensured that no other treatment (e.g. food limitation) confounded the response variable and thus only used data from experiments with food supply corresponding to satiation. It is important to control for feeding rations as it affects the temperature optimum for growth (Brett *et al.* 1969). This was achieved in different ways in the different experimental studies, but normally involved excess feeding rations once or several times per day. The key description we looked for in the study was that food should not be limiting or “reduced” rations. In the case growth was length-based, we converted them to mass using weight-length-relationships from FishBase (Froese *et al.* 2014; Froese & Pauly 2016). We compiled two separate data sets: raw growth rates (growth\_data.xlsx) and temperature at optimum growth (growth\_data\_Topt.xlsx). In the latter, we defined optimum temperature for growth as either the fitted optimum temperature by size-class (in the original study). If the optimum-by-size was not estimated in the original study, we used the temperature where growth rate was maximized. All growth rates were expressed in unit .

## *Metabolic rate*

The search for metabolic rate experiments resulted in 8405 articles (search date: 2019.06.06), which was reduced to 3458 after applying filters for subject categories. Articles where filtered out at the abstract and whole-article stage if the original reference could not be identified and evaluated, if units were normalized using a priori defined scaling relationships (i.e. mass or temperature corrected rather than raw values), if it was not standard/routine/resting metabolic rate (i.e. oxygen consumption of an unfed fish at no or little spontaneous activity) or there was no acclimation. Metabolic rates were converted to the most common unit (as that is how it is typically measured) using standard conversions. These data where compiled in the file metabolism\_data.xlsx.

## *Maximum consumption rate*

The two searches for maximum consumption rates described in the main text resulted in 15259 articles (search date: 2018.12.18), with 3449 remaining after filtering by subject categories. The second search (search date: 2019.03.13) resulted in 431 additional titles after filtering by subject categories (of which some where duplicated from the first search). Articles where filtered out at the abstract and whole-article stage if the original reference could not be identified and evaluated, if units were normalized using a priori defined scaling relationships (i.e. mass or temperature corrected rather than raw values), there was no acclimation, or if it was not maximum consumption rate. As with the growth data, definitions of ad-libitum may differ between studies – the key for our purpose is that rations should lead to satiation and not be limiting. Consumption rates were converted to the unit . These data where compiled in the file consumption\_data.xlsx.

# Data exploration

## *Growth rate*

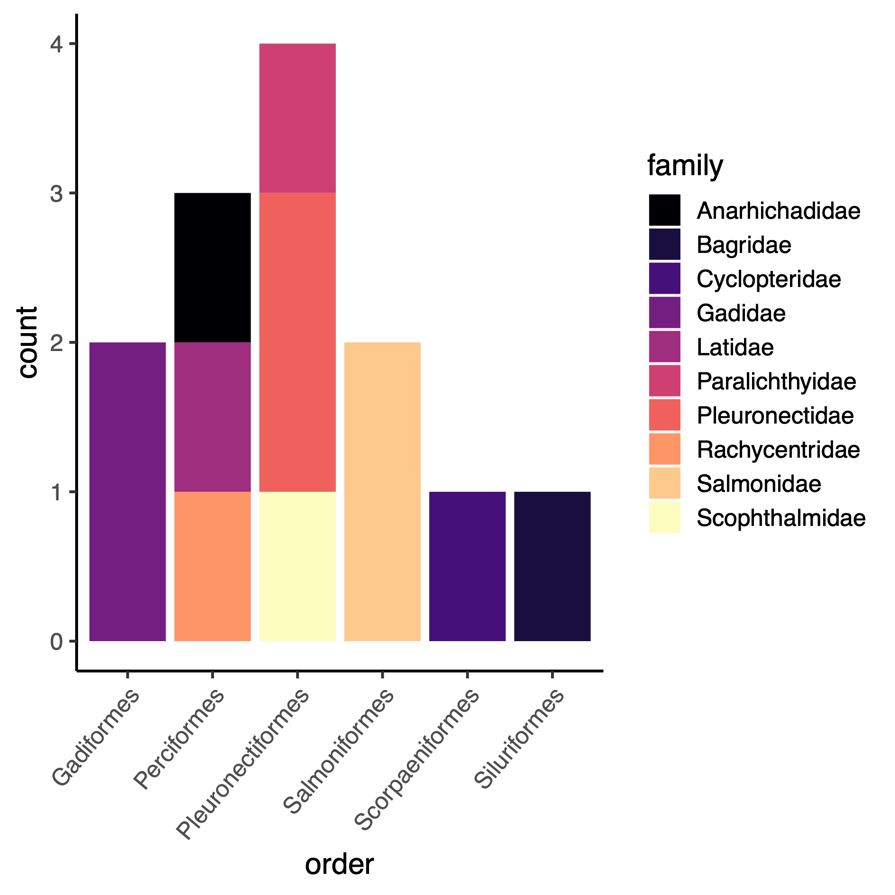


Fig. S1. Taxonomic representation in growth data set.

A picture containing screenshot

Description automatically generated

Fig. S2. Biogeography of species in growth data set.

A close up of a logo

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Fig. S3. Distribution of relative body masses in metabolism and consumption data set. Colors indicate species (legend not shown).

A close up of a piece of paper

Description automatically generated

Fig. S4. Log10 of maximum published weight of species in the growth data set.

## *Metabolic & maximum consumption rate*

A pencil and paper

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Fig. S5. Taxonomic representation in metabolism and consumption data set.

A picture containing screenshot

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Fig. S6. Biogeography of species in metabolism and consumption data set.

A screenshot of a social media post

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Fig. S7. Distribution of relative body masses in metabolism and consumption data set. Colors indicate species (legend not shown).

A close up of a map

Description automatically generated

Fig. S8. Log10 of maximum published weight of species in metabolism and consumption data set

# Supplementary analysis

A close up of a map

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Fig. S9. Posterior distributions of the average intraspecific mass-scaling exponents and activation energies (, and for metabolism also the non-species varying interaction coefficient () for metabolic rate (top row) and maximum consumption rate (bottom row). Numbers in the top left corner corresponds to the posterior median. Note that the final model for maximum consumption rate did not include a mass-temperature interaction term. The scale is the same within parameters across rates for comparison (and note that the mass-temperature interaction is estimated and presented on an Arrhenius temperature scale, 1/kT).

A close up of a map

Description automatically generated

Fig. S10. Predictions (line), 80% credible interval (band) and data (points) from polynomial models of maximum consumption rate versus rescaled temperature (), fitted separately to each species.

# Model validation

## *Optimum growth temperature*

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Fig. S11. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the highest-level parameters for model.

A picture containing sky

Description automatically generated

Fig. S12. Potential scale reduction factor () for the model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution.

A screenshot of a cell phone

Description automatically generated

Fig. S13. Model fit (mean and coefficient of variation) for -model. Vertical line corresponds to mean in data and histogram depicts each posterior mean. Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), and each simulated data is assigned a 0 or 1 if it is below or above the mean data point. The number in the plot corresponds to the mean of the vector of 0’s and 1’s.

## *Growth rate*

A close up of text on a black background

Description automatically generated

Fig. S14. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the highest-level parameters for the growth rate model at temperatures below optimum temperatures.

A close up of a logo

Description automatically generated

Fig. S15. Potential scale reduction factor () for the growth rate model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution.

A picture containing text

Description automatically generated

Fig. S16. Model fit (A=mean and B= coefficient of variation) for model of growth at temperatures below temperature optima. Vertical line corresponds to mean in data and histogram depicts each posterior mean. Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), and each simulated data is assigned a 0 or 1 if it is below or above the mean data point. The number in the plot corresponds to the mean of the vector of 0’s and 1’s.

## *Metabolic rate*

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Description automatically generated

Fig. S17. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the highest level parameters for the model of metabolic rate at temperatures below optimum temperatures.

A close up of a device

Description automatically generated

Fig. S18. Potential scale reduction factor () for the metabolism model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution.

A picture containing tree, text

Description automatically generated

Fig. S19. Model fit (A=mean and B=coefficient of variation) for metabolism model. Vertical line corresponds to mean in data and histogram depicts each posterior mean. Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), and each simulated data is assigned a 0 or 1 if it is below or above the mean data point. The number in the plot corresponds to the mean of the vector of 0’s and 1’s.

## *Maximum consumption rate*

A close up of text on a black background

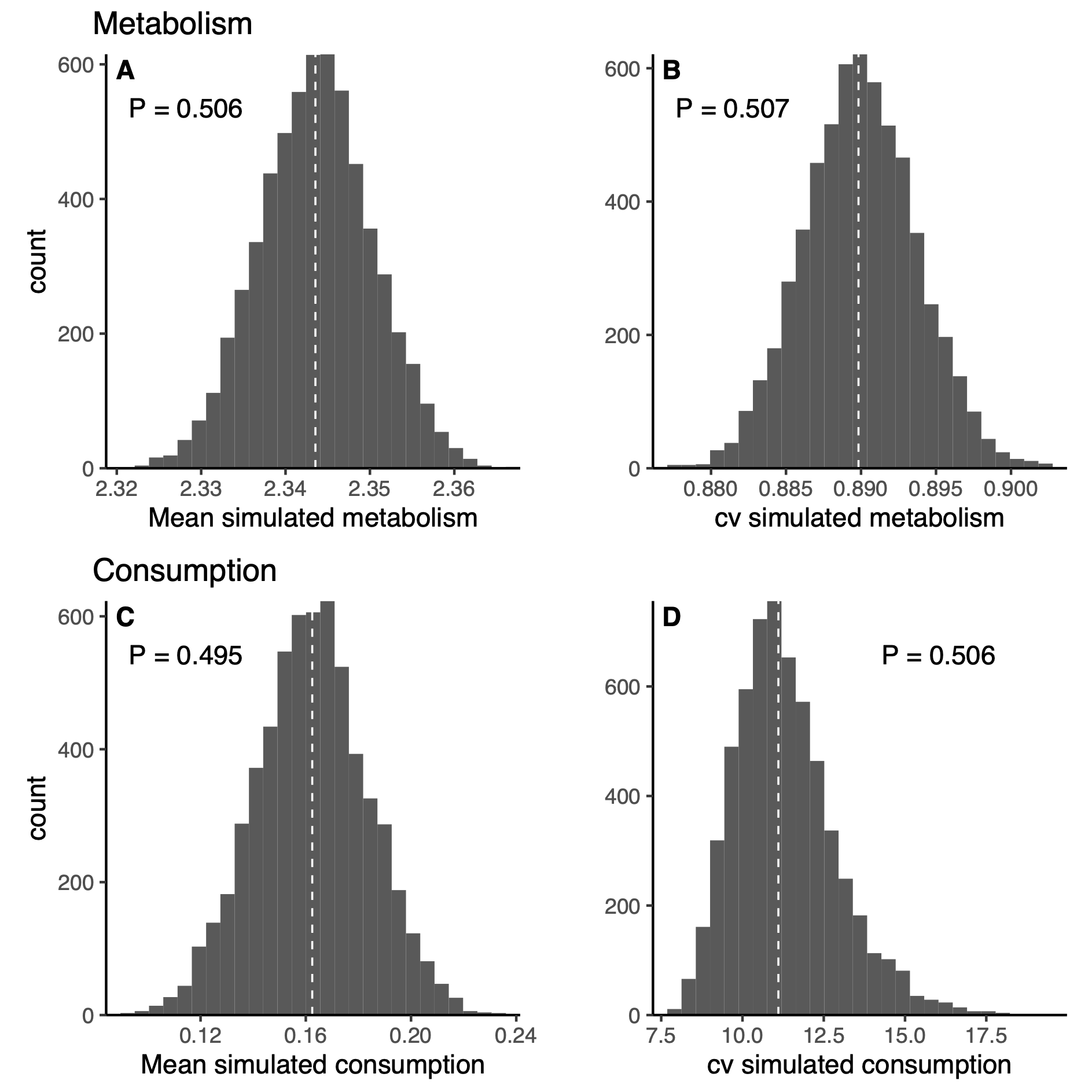
Description automatically generated

Fig. S20. Posterior densities and trace plots for evaluation of chain convergence (by chain, indicated by color), for the highest-level parameters for the model of log-linear (below optimum data) maximum consumption rate at temperatures below temperature optima.

A close up of a logo

Description automatically generated

Fig. S21. Potential scale reduction factor () for the maximum consumption model. This factor is based on the comparison of between and within-chain variation for the same parameter. A value close to one implies chains converged to the same distribution.



**A**

**B**

Fig. S22. Model fit (A=mean and B=coefficient of variation) for log-linear (below optimum data) consumption rate model. Vertical line corresponds to mean in data and histogram depicts each posterior mean. Fit is evaluated by simulating data from the likelihood (at each iteration of the MCMC chain), and each simulated data is assigned a 0 or 1 if it is below or above the mean data point. The number in the plot corresponds to the mean of the vector of 0’s and 1’s.

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