

1

IMPERIAL COLLEGE LONDON

2

CMEE MINIPROJECT

3

4

5

6

7

8

**Assessing the performance of
mechanistic and phenomenological
models on a large thermal
response dataset**

9

Author

10

Fernando Pedraza Pérez

11

CID

12

01451775

13

Word Count

14

3354

15

June 29, 2018

16 Introduction

17 Complexity pervades biological systems at all scales [1]. On the small-
18 est scale unicellular organisms undergo a vast amount of finely controlled
19 metabolic reactions to survive. While at macroscopic scales organisms gen-
20 erate complicated networks of interaction. Furthermore, the types of in-
21 teractions as well as internal processes that organisms undergo is largely
22 dependent on the environment where they are found and the phylum they
23 belong to. This inherent complexity of biology can seem overwhelming, and
24 the search for unifying principles can sometimes seem a daunting task [2, 3].

25 One of the tools used to look for unifying patterns and principles in
26 biological data is the use of mathematical models. Two general types of
27 models exist: phenomenological and mechanistic. The former aims to ex-
28 plain a mechanism’s behavior while the latter aims to explain the mechanism
29 itself [4]. Ideally both types of models should be used in synergy. However,
30 in practice, many times only phenomenological models are used while the
31 underlying mechanisms are overlooked. Other times, overcomplicated mod-
32 els are constructed, sometimes specifically tailored to a particular dataset,
33 and therefore sacrificing generality. Thus, as stated by Levins [5], in order
34 to maximize the explanatory power of models we must aim to find a model
35 (or sets of models) that: i) has a small number of parameters and these
36 parameters are easily measurable, ii) has soluble equations and iii) gives
37 biologically relevant estimates.

38 One of the fields in biology which has recently seen a push for the search
39 of unifying principles across scales is metabolic ecology [6, 7]. It is argued

40 that since all organisms rely on the transformation of energy (i.e. on their
41 metabolism) to survive, it follows that metabolism controls not only sur-
42 vival, growth and reproduction but also the consumption of resources in
43 their environments and thus shapes how species interact with one another
44 [6]. Furthermore, because metabolic rates are governed by temperature,
45 and these rates in turn affect ecological [8] and even evolutionary rates [9],
46 understanding how metabolic traits change as a function of temperature
47 can greatly increase our understanding of how ecological systems behave
48 [10, 11, 12].

49 Many studies have reported temperature dependence of metabolic, phys-
50 iological, ecological and evolutionary rates [8, 9, 13, 14, 15]. Consequently, a
51 large number of mechanistic models have been proposed to explain reported
52 tendencies [16]. One of the most used is the Schoolfield model (SI) [17] which
53 essentially aims to explain the temperature dependence of a given trait as
54 a function of the activity of an enzyme [18]. This model effectively pro-
55 vides a metabolic explanation to the observed variations in ecological rates
56 with temperature by equating the trait temperature dependence to that of
57 the temperature dependence of enzymatic kinetics. It is expected that an
58 enzyme's activity will peak at a given temperature and be reduced as the
59 temperature is decreased or increased from the that of the peak. Thus, SI
60 is a good non-linear mechanistic method of modeling thermal performance
61 curves (TPCs) of biological traits, which usually peak at a certain temper-
62 ature value and fall towards higher or lower temperatures.

63 Moreover, two variants of SI exist, which are designed to capture enzyme
64 activity at high (SII) and low (SIII) temperatures. These variants are useful

65 when dealing with TPCs where either extremely high or low temperatures
66 were recorded. If mechanistic models like SI (and its variants) systematically
67 provide better fits on TPC data across environments and scales when com-
68 pared to simple phenomenological models, we would have a good indicator
69 that we are close to understanding the mechanisms that shape trait temper-
70 ature dependence. Furthermore, this could provide additional evidence for
71 the validity of a unifying theory of metabolic ecology [6].

72 In this study the performance of phenomenological and mechanistic mod-
73 els to explain TPCs tendencies was assessed for a large database of metabolic
74 traits. A cubic (phenomenological) and all three Schoolfield (SI - SIII) were
75 fitted on all TPCs. Model performance was assessed across metabolic trait
76 type, species habitat and kingdom. In general, phenomenological mod-
77 els fared better their mechanistic counterparts. In most cases the high-
78 temperature variant of the Schoolfield equation (SII) was the best between
79 mechanistic models.

80 **Methods**

81 Metabolic trait data was obtained from the Biotraits data, a large com-
82 pendium of TPCs from a wide range of organisms [19]. The database con-
83 tained: i) the name of the measured metabolic trait, ii) the value of the
84 measured trait, iii) the temperature at which the trait was measured, and
85 iv) metadata on the species characteristics. A thermal performance curve
86 (TPC) was defined as a set of observations of a particular metabolic trait for
87 a given consumer species which had at least five observations and only pos-

itive trait values. A total of 1,936 TPCs were used in the analyses. Models were fit on each TPC to assess the effect of temperature on trait value. Two general classes of models were used: phenomenological and mechanistic.

Model Fitting

Phenomenological models

Metabolic trait values were regressed on temperature using a cubic model with the general structure:

$$M = \beta_0 + \beta_1 T + \beta_2 T^2 + \beta_3 T^3$$

where M is the metabolic trait value and T represents the recorded temperature in centigrades. Model fitting was performed using a Least-Squares method. For each fitted model, the Akaike Information Criterion (AIC) was calculated to perform subsequent model selection. Linear models and AIC were obtained using the “statsmodels” module in Python 2.7.

Mechanistic models

Three non-linear mechanistic models were used to model TPCs. The full Schoolfield equation (SI) is defined as follows:

$$SI) \quad B = \frac{B_0 e^{\frac{-E}{k}(\frac{1}{T} - \frac{1}{283.15})}}{1 + e^{\frac{E_l}{k}(\frac{1}{T_l} - \frac{1}{T})} + e^{\frac{E_h}{k}(\frac{1}{T_h} - \frac{1}{T})}}$$

where B is the trait value at a given temperature, B_0 is the reference trait value at 283.15 K and k is the Boltzmann constant. E is the enzyme’s activation energy, E_h is the enzyme’s high-temperature de-activation energy

and E_l is the enzyme's low-temperature de-activation energy. T_l and T_h correspond to the temperatures (low and high) at which 50% deactivation occurs [17].

Two variantes of the Schoolfield model were employed to capture the effect of either high (SII) or low (SIII) temperature deactivation.

$$SII) \quad B = \frac{B_0 e^{\frac{-E}{k}(\frac{1}{T} - \frac{1}{283.15})}}{1 + e^{\frac{E_h}{k}(\frac{1}{T_h} - \frac{1}{T})}}$$

$$SIII) \quad B = \frac{B_0 e^{\frac{-E}{k}(\frac{1}{T} - \frac{1}{283.15})}}{1 + e^{\frac{E_l}{k}(\frac{1}{T_l} - \frac{1}{T})}}$$

Schoolfield equations (SI - SIII) were used to model the effect of temperature (in K) on metabolic trait values. For each TPC, all three models were fitted. To do this, initial parameter values were first estimated from the data and subsequently model fitting was performed.

The procedure described below for estimating initial parameter values was performed for each individual TPC. B_0 was initialized as the trait value that corresponded to the closest recorded temperature to 283.15 K. For the activation energy (E), the highest trait value and its corresponding temperature were recorded, hereafter referred to as 'peak'. From this, the TPC was divided in two sections: one containing the temperatures (and their corresponding trait values) that were below the peak (hereafter referred to as left-hand of the curve) and another with values higher than the peak (referred to as right-side of the curve). For each subsection, temperature values were transformed to be their reciprocal multiplied by the Boltzman constant (K , i.e. from T to $1/KT$) and trait values were logged. Next, a linear regression was fit to model the effect of $1/KT$ on the logarithm of

131 the trait value for data on the left-hand of the curve. E was set to be the
 132 slope of the fitted linear model. E_h was estimated to be twice the value of
 133 E , while E_l was initialized as half the value of E . Finally, temperatures at
 134 which 50% deactivation occurred were estimated from linear models. For
 135 high temperature deactivation, a linear regression was fit to model the effect
 136 of $1/KT$ on the logarithm of the trait value for data on the right-hand of
 137 the curve. From the fitted model, T_h was estimated to be the temperature
 138 value at which the trait value was halved from the peak. T_l was estimated
 139 in the same way, using a linear model fit to the data on the left-hand of the
 140 curve. For cases in which linear models could not be fit, E was initialized
 141 as 0.65, as this has been reported to be the mean interspecific activation
 142 energy value [6] (consequently, $E_l = 0.325$ $E_h = 1.300$), T_h was estimated
 143 to be the highest recorded temperature value in the TPC, while T_l was the
 144 lowest.

145 The three Schoolfield equations (SI - SIII) were fitted using “lmfit” in
 146 Python 2.7. Model fitting was performed by finding the parameter values
 147 that yielded the lowest residuals. Briefly, for a given TPC, the algorithm
 148 calculates the estimated metabolic trait values that result from substitut-
 149 ing the initial parameter values and the recorded temperature values. The
 150 residuals (i.e. the difference between expected and observed metabolic trait
 151 values) are then computed. The algorithm modifies parameter values and
 152 recomputes the residuals with the updated parameter values. This process
 153 continues until the residuals are minimized. The algorithm was free to vary
 154 all parameter values except for E_h and E_l which were bounded to always be
 155 above and below E , respectively. K was not varied throughout the model

156 fitting. To simplify the fitting process, the logarithm of the trait values was
 157 used. For all cases in which the residuals were successfully minimized, the
 158 estimated parameter values and the AIC were recorded.

159 **Model Selection**

160 Fitted phenomenological and mechanistic models for a given TPC were com-
 161 pared using their respective AIC to determine which produced the best fit
 162 [20]. However, since the data used to fit the mechanistic models had been
 163 logged transformed, a direct comparison of AIC values would not be repre-
 164 sentative of the actual difference in fits [21]. Thus, AIC values were recalcu-
 165 lated for the mechanistic models by calculating the RSS for the non-logged
 166 data given the estimated parameter values. AICs were estimated from RSS
 167 by applying (where n is the number of data points and k is the number of
 168 parameters):

$$169 \quad AIC = n \frac{\log(2\pi)}{n} + n + 2 + n \log(rss) + 2k$$

170 Once AIC scores were comparable between model types, model selection
 171 was performed. A model was defined to be significantly different from an-
 172 other if their delta AICs was larger than 2. The best model was the one
 173 which had the smallest AIC score. If two or more models were not signifi-
 174 cantly different and their AIC scores were the lowest, they were deemed to
 175 be the best fit.

176 **Model Performance by Groups**

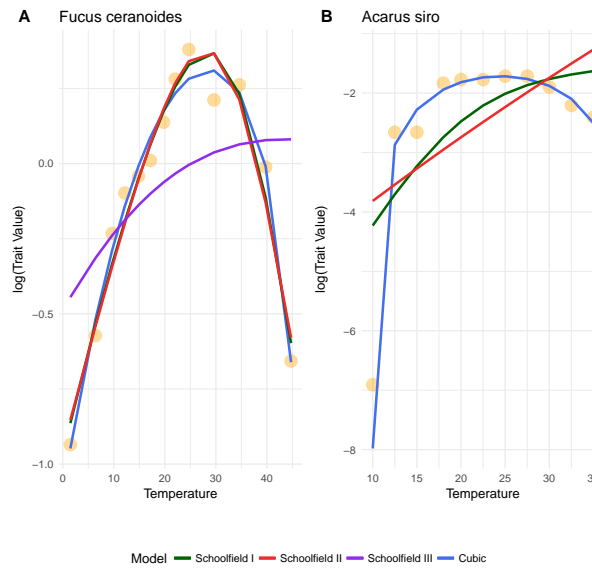
177 To determine if there were differences in the performance of models between
178 different habitats, kingdoms and trait types the relative performance for
179 each model was calculated. Thus, the overall number of times a model type
180 (e.g. Cubic, SI, SII and SIII) was determined to have the best fit was divided
181 by the total number of times the model was fitted. The relative performance
182 was computed for subsets of data based on habitat type, kingdom and type
183 of metabolic trait.

184 **Computing Languages**

185 R version 3.4.0 was used to organize the original dataset, build TPCs and
186 generate all plots. Data wrangling and plotting were performed using the
187 “tidyr”, “ggplot2” and “cowplot” packages. R was selected to perform these
188 tasks because the available tools to manipulate datasets as well as plot
189 results are vast and efficient. Python was used to fit both phenomenological
190 and mechanistic models. Python has an extensive set of modules designed
191 to perform model fitting, especially for minimization tasks, and thus, was
192 the preferred language for this part of the project. Bash was used to run all
193 R and Python scripts and to compile the L^AT_EX document. Bash scripting
194 is a valuable tool to string together a workflow by running sets of code from
195 different languages in sequence.

196 Results

197 A total of 1,936 thermal performance curves (TPCs) of metabolic traits were
 198 obtained after data-wrangling. Cubic phenomenological models were able
 199 to be fit on all TPCs. For mechanistic models: SII and SIII fit on virtually
 200 all TPCs (0.9917% and 0.9958% of fits, respectively) while SIII attained
 201 a fit for 80% of the TPCs. In most TPCs trends were captured by both
 202 phenomenological and mechanistic models (Figure 1A). However, in some
 203 cases only the Cubic model generated an appropriate fit (Figure 1B).

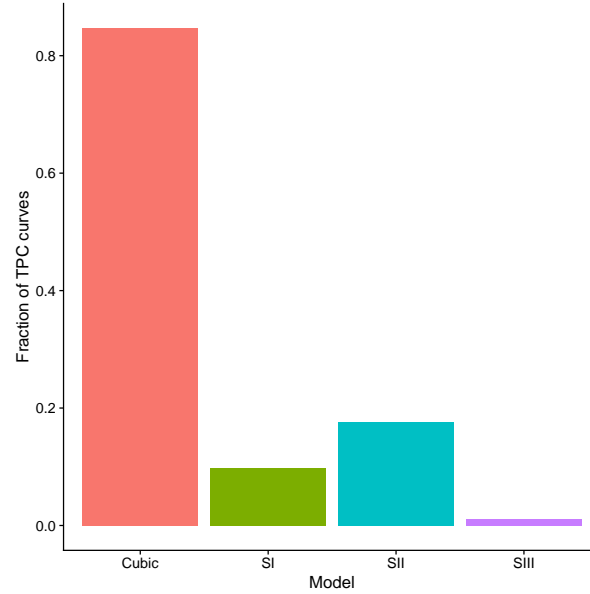


204

Figure 1: Two example TPCs. A) A curve where both SI and SII as well
 205 as the cubic model capture the general tendency of the data. B) Only the
 206 cubic model is able to fit the data adequately.

206 In general, the cubic models outperformed the mechanistic ones (Figure
 207 2). When comparing mechanistic models, SII (i.e. the high variation of the
 208 Schoolfield model) was the best performing. Surprisingly, the full model

209 fared better than the low-temperature variation (Figure 2).

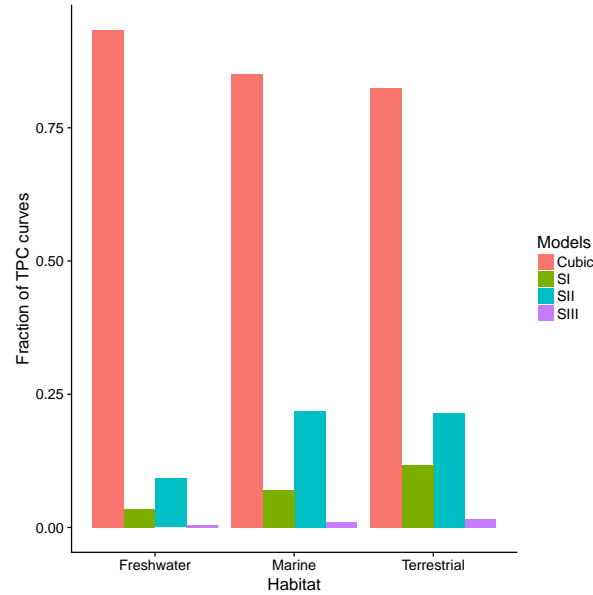


210

Figure 2: Overall model performance. The fraction of TPCs for which a model was the best performing is displayed for all fitted models. Models were compared using AICs, significant differences were detected when models had a delta AIC of 2 or more units.

211

212 When comparing how models performed within different consumer habi-
213 tats, the same general trend is observed (Figure 3). The cubic model con-
214 sistently outperformed the other mechanistic models. SII consistently per-
215 formed best for the mechanistic models across habitats.

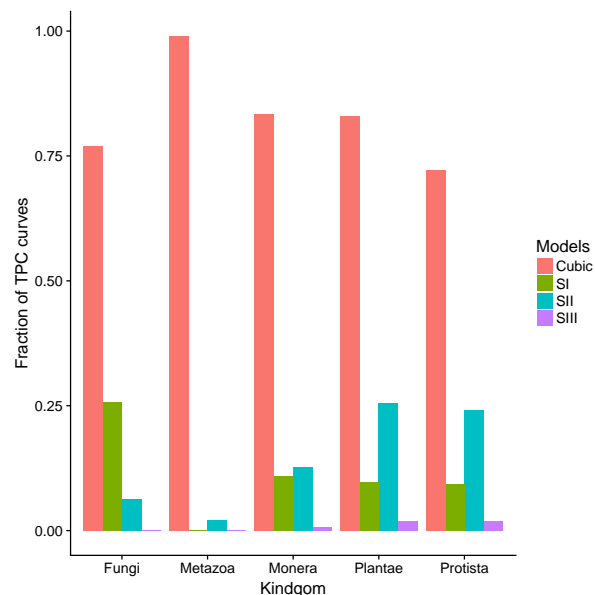


216

Figure 3: Model performance across habitats. The fraction of TPCs for which a model was the best performing is displayed for freshwater, marine and terrestrial habitats. Models were compared using AICs, significant differences were detected when models had a delta AIC of two or more units.

217

218 Cubic models were found to be the best performing model across all
 219 kingdoms (Figure 4). Nevertheless, differences in the performance of the
 220 mechanistic models were observed. For the Metazoa kingdom, virtually no
 221 mechanistic models outperformed the Cubic ones. Yet, for Monera, Plantae
 222 and Protista mechanistic models fared much better. In addition, SI was the
 223 best performing mechanistic model for Fungi, reverting previously observed
 224 trends (Figure 4).

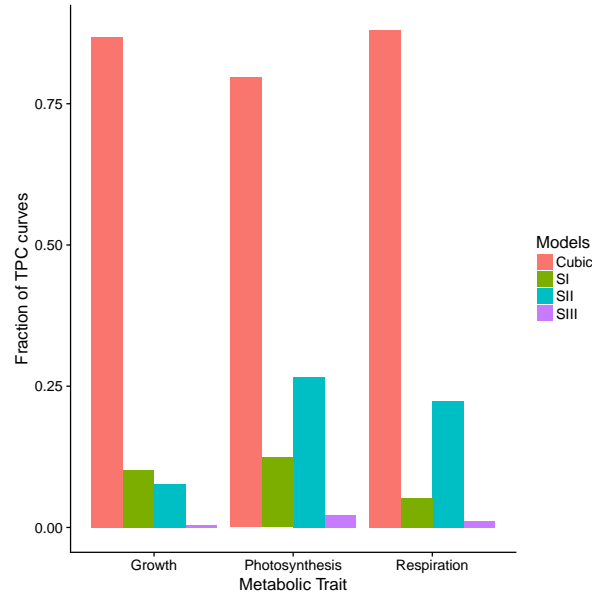


225

Figure 4: Model performance across kingdoms. The fraction of TPCs for which a model was the best performing is displayed for the five kingdoms. The Monera kingdom was comprised of both Archea and Bacteria. The Protista kingdom includes Chromista, Protista and Protozoa organisms. Models were compared using AICs, significant differences were detected when models had a delta AIC of two or more units.

226

227 Cubic models yielded the best fits regardless of the type of metabolic
 228 trait evaluated (Figure 5). In turn, deterministic models performed best
 229 when estimating metabolic trait related to photosynthesis. The lowest per-
 230 formances were recorded for growth related metabolic traits.



231

Figure 5: Model performance across types of metabolic traits. The fraction of TPCs for which a model was the best performing is displayed for growth, photosynthetic and respiration traits. Growth traits include: individual growth rate, individual mass growth rate, population growth rate, radial growth rate and specific growth rate. Photosynthetic traits include: rate of photosynthesis, gross and net photosynthesis. Respiration traits include: mass-specific respiration rate and respiration rate. Models were compared using AICs, significant differences were detected when models had a delta AIC of two or more units.

232

233 Discussion

234 In general both mechanistic and phenomenological models had a high rate of
 235 convergence and seemed to capture the trends of the TPCs. However, when
 236 performing AIC-based model selection cubic models were consistently the
 237 best-fitting regardless of the type of metabolic trait measured, the kingdom
 238 or habitat of the species to which the TPC corresponded. These results are

239 in sharp contrast to previous findings where Schoolfield models have gener-
240 ated adequate fits. These discrepancies could be due to the sheer diversity
241 of metabolic traits analyzed and the difficulty of estimating adequate initial
242 parameter values, inadequate implementations of fitting algorithms or sim-
243 ply because the mechanistic models failed to adequately explain tendencies.

244 **Model Performance**

245 Model convergence was very high in the utilized TPC dataset. Strikingly,
246 nearly all SII and SIII models were able to be fitted to the data. This is
247 indicative that the general structure of the underlying equations do in fact
248 reflect the normal behavior of TPCs. This is why Schoolfield-like models
249 have been widely used to model physiological, ecological and evolutionary
250 traits [8, 9, 13, 14, 15]. As was expected, SI had a lower conversion rate
251 (80%) possibly due to the difference in the number of estimated parameters
252 when compared to SII, SIII and the cubic models. Thus, for the fitted
253 models it would seem that for each additional estimated parameter we lose
254 10% of the convergence rate.

255 In terms of model performance, cubic models were vastly superior to
256 their mechanistic counterparts. This is possibly due to the fact that phe-
257 nomenological models do not have a 'constrained' form and thus can more
258 freely adapt to TPC patterns. However, when looking for underlying prin-
259 ciples that generate observed patterns, the fact that mechanistic models
260 systematically perform best is discouraging.

261 When comparing performance across mechanistic models, SII generally
262 comes on top. This could be indicative of the fact that most TPCs used had

high temperature values recorded or because the estimated initial values for E_h and T_h were better than those of E_l and T_l . Moreover, low temperature deactivation of TPCs has been reported to be hard to detect [22]. This could explain the large differences in performance between SII and SIII. SI had a performance which was comparable to SII in some cases (Figure 2 and Figure 4: Monera) and greater than SII in others (Figure 4: Fungi and Figure 5: Growth). Schoolfield models have been previously reported to model growth rates in both fungi and bacteria better than other model types [23, 24], which could explain the improvement in performance for both the Fungi kingdom and when modeling growth rates.

Initial Parameter Estimation and Model Fitting

Estimation of initial parameters was performed in the same way for all analyzed TPCs. Though this makes approximations a quick process, it could be an inadequate approach for certain datasets. In order to find suitable initial parameter values, a set of assumptions are made about the TPC in question. Namely that the data describe a sigmoid shape with a clearly defined maximum trait value and low trait value at high and low temperatures. However, this was not the case for all TPCs used. In some cases, a maximum trait value was observed at more than one temperature value. When this was occurred, the lowest temperature at which the trait was maximized was defined to be the peak of the curve. However, it could be the case that this was a measuring error and thus the peak trait value was found elsewhere on the curve. Other times, an unrealistic temperature or trait values were found to have been recorded. Evidently this generated

287 over or underestimated initial parameter values. These issues inherently
288 arise when dealing with large and diverse datasets, however in order to
289 maximize the efficiency of mechanistic models to predict TPCs we must be
290 certain that our estimates of initial values are as close to reality as possible.
291 Perhaps comparing the performance of different ways of estimating initial
292 parameter values, like those described by Shi [25], will shed some light on
293 the arduous task that is estimating parameter values from TPCs and make
294 our methods more robust.

295 Model fitting of mechanistic equations was highly successful (99% for SII
296 and SIII, 80% for SI) despite the diversity of measured traits and potentially
297 erroneous estimations of initial parameter values. Nevertheless, for a model
298 to be useful it should also provide meaningful and realistic values of its
299 parameter estimates [5]. The mode of the fitted E values from all three
300 mechanistic models were consistently higher ($SI = 1.32$, $SII = 1.63$ and
301 $SIII = 5.62$) than the reported mean activation of 0.65 across species [6].
302 Moreover, some models estimated activation energy values of up to 900
303 (kJ/mol). Clearly these estimates are meaningless. These issues could be
304 resolved by setting tougher restrictions on how the model fitting algorithm
305 modifies parameter values. However, if it were the case that biologically
306 meaningless parameter values are systematically produced by a model then
307 the model would have to be reevaluated. A possible solution would be
308 to make the model more parsimonious, as this has been found to be an
309 adequate approach for reducing model over fitting and increasing predictive
310 power [26].

311 **Concluding Remarks**

312 The reported results are in sharp contrast with previous reports on the
313 accuracy of Schoolfield models to predict TPCs [27, 28]. These unexpected
314 findings are likely due to the diversity of trait data used and the one-size-
315 fits-all method of estimating initial parameter values. This in turn likely
316 generated dubious parameter estimates after fitting, which hindered model
317 performance when compared to simple phenomenological models. Though
318 these results may not shed light into the matter of phenomenological vs
319 mechanistic model performance in TPCs, they do highlight the importance
320 of having robust parameter estimation procedures. Schoolfield models are
321 far from perfect [18] and an effort should be made to evaluate how close we
322 are to understanding the mechanistic underpinnings of TPCs.

323 References

- 324 [1] S. A. Levin, “The problem of pattern and scale in ecology: The robert
325 h. macarthur award lecture,” *Ecology*, vol. 73, no. 6, pp. 1943–1967,
326 1992.
- 327 [2] R. Margalef, “On certain unifying principles in ecology,” *The American*
328 *Naturalist*, vol. 97, no. 897, pp. 357–374, 1963.
- 329 [3] M. Elgin, “There may be strict empirical laws in biology, after all,”
330 *Biology and Philosophy*, vol. 21, pp. 119–134, Jan 2006.
- 331 [4] C. F. Craver, “When mechanistic models explain,” *Synthese*, vol. 153,
332 pp. 355–376, Dec 2006.
- 333 [5] R. Levins, “The strategy of model building in population biology,”
334 *American Scientist*, vol. 54, no. 4, pp. 421–431, 1966.
- 335 [6] J. H. Brown, J. F. Gillooly, A. P. Allen, V. M. Savage, and G. B.
336 West, “Toward a metabolic theory of ecology,” *Ecology*, vol. 85, no. 7,
337 pp. 1771–1789, 2004.
- 338 [7] M. M. Humphries and K. S. McCann, “Metabolic ecology,” *Journal of*
339 *Animal Ecology*, vol. 83, no. 1, pp. 7–19, 2014.
- 340 [8] A. I. Dell, S. Pawar, and V. M. Savage, “Systematic variation in
341 the temperature dependence of physiological and ecological traits,”
342 *Proceedings of the National Academy of Sciences*, vol. 108, no. 26,
343 pp. 10591–10596, 2011.

- 344 [9] J. F. Gillooly, A. P. Allen, G. B. West, and J. H. Brown, “The rate of
345 dna evolution: Effects of body size and temperature on the molecular
346 clock,” *Proceedings of the National Academy of Sciences*, vol. 102, no. 1,
347 pp. 140–145, 2005.
- 348 [10] Hans O. Pörtner, Albert F. Bennett, Francisco Bozinovic, Andrew Clarke,
349 Marco A. Lardies, Magnus Lucassen, Bernd Pelster, Fritz Schiemer, and
350 Jonathon H. Stillman, “Tradeoffs in thermal adaptation: The need for
351 a molecular to ecological integration,” *Physiological and Biochemical
352 Zoology*, vol. 79, no. 2, pp. 295–313, 2006. PMID: 16555189.
- 353 [11] H. O. Pörtner and R. Knust, “Climate change affects marine fishes
354 through the oxygen limitation of thermal tolerance,” *Science*, vol. 315,
355 no. 5808, pp. 95–97, 2007.
- 356 [12] A. P. Allen, J. H. Brown, and J. F. Gillooly, “Global biodiversity, bio-
357 chemical kinetics, and the energetic-equivalence rule,” *Science*, vol. 297,
358 no. 5586, pp. 1545–1548, 2002.
- 359 [13] J. Rgnire, J. Powell, B. Bentz, and V. Nealis, “Effects of temperature
360 on development, survival and reproduction of insects: Experimental de-
361 sign, data analysis and modeling,” *Journal of Insect Physiology*, vol. 58,
362 no. 5, pp. 634 – 647, 2012.
- 363 [14] J. F. Gillooly, J. H. Brown, G. B. West, V. M. Savage, and E. L.
364 Charnov, “Effects of size and temperature on metabolic rate,” *Science*,
365 vol. 293, no. 5538, pp. 2248–2251, 2001.

- [15] VanM.Savage, J. F.Gillooly, JamesH.Brown, G. B.West, and E. L. Charnov, “Effects of body size and temperature on population growth.,” *The American Naturalist*, vol. 163, no. 3, pp. 429–441, 2004. PMID: 15026978.
- [16] J. P. DeLong, J. P. Gibert, T. M. Luhring, G. Bachman, B. Reed, A. Neyer, and K. L. Montooth, “The combined effects of reactant kinetics and enzyme stability explain the temperature dependence of metabolic rates,” *Ecology and Evolution*, vol. 7, no. 11, pp. 3940–3950, 2017.
- [17] R. Schoolfield, P. Sharpe, and C. Magnuson, “Non-linear regression of biological temperature-dependent rate models based on absolute reaction-rate theory,” *Journal of Theoretical Biology*, vol. 88, no. 4, pp. 719 – 731, 1981.
- [18] D. G. Kontopoulos, B. Garca-Carreras, S. Sal, T. P. Smith, and S. Pawar, “Use and misuse of temperature normalisation in meta-analyses of thermal responses of biological traits,” *PeerJ*, vol. 6, p. e4363, Feb. 2018.
- [19] A. I. Dell, S. Pawar, and V. M. Savage, “The thermal dependence of biological traits,” *Ecology*, vol. 94, no. 5, pp. 1205–1206, 2013.
- [20] J. B. Johnson and K. S. Omland, “Model selection in ecology and evolution,” *Trends in Ecology and Evolution*, vol. 19, no. 2, pp. 101 – 108, 2004.

- 388 [21] H. Akaike, “On the likelihood of a time series model,” *Journal of the*
389 *Royal Statistical Society. Series D (The Statistician)*, vol. 27, no. 3/4,
390 pp. 217–235, 1978.
- 391 [22] S. Pawar, A. I. Dell, V. M. Savage, and J. L. Knies, “Real versus artifi-
392 cial variation in the thermal sensitivity of biological traits,” *The Amer-*
393 *ican Naturalist*, vol. 187, no. 2, pp. E41–E52, 2016. PMID: 26731029.
- 394 [23] A. M. Gibson and A. D. Hocking, “Advances in the predictive modelling
395 of fungal growth in food,” *Trends in Food Science and Technology*,
396 vol. 8, no. 11, pp. 353 – 358, 1997.
- 397 [24] C. Adair, D. Kilsby, and P. Whittall, “Comparison of the schoolfield
398 (non-linear arrhenius) model and the square root model for predicting
399 bacterial growth in foods,” *Food Microbiology*, vol. 6, no. 1, pp. 7 – 18,
400 1989.
- 401 [25] P. Shi, T. Ikemoto, C. Egami, Y. Sun, and F. Ge, “A modified pro-
402 gram for estimating the parameters of the ssi model,” *Environmental*
403 *Entomology*, vol. 40, no. 2, pp. 462 – 469, 2011.
- 404 [26] G. Cox, J. Gibbons, A. Wood, J. Craigon, S. Ramsden, and N. Crout,
405 “Towards the systematic simplification of mechanistic models,” *Ecolog-*
406 *ical Modelling*, vol. 198, no. 1, pp. 240 – 246, 2006.
- 407 [27] D. Padfield, G. Yvon-Durocher, A. Buckling, S. Jennings, and G. Yvon-
408 Durocher, “Rapid evolution of metabolic traits explains thermal adap-
409 tation in phytoplankton,” *Ecology Letters*, vol. 19, no. 2, pp. 133–142,
410 2016.

411 [28] D. R. Barneche, M. Kulbicki, S. R. Floeter, A. M. Friedlander, J. Maina,
412 and A. P. Allen, “Scaling metabolism from individuals to reef-fish
413 communities at broad spatial scales,” *Ecology Letters*, vol. 17, no. 9,
414 pp. 1067–1076, 2014.