The universality and the future prospects of physiological energetics
Reply to comments on “Physics of metabolic organization”

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Abstract

In response to the comments on review “Physics of metabolic organization”, we discuss the universality and the future prospects of physiological energetics. The topics range from the role of entropy in modeling living organisms to the apparent ubiquity of the von Bertalanffy curve, and the potential applications of the theory in yet unexplored domains. Tradeoffs in outreach to non-specialists are also briefly considered.

Keywords: entropy, DEB theory, homeostasis, von Bertalanffy curve, metabolic acceleration

We would like to begin this reply by expressing our sincere gratitude to all the commentators for providing insightful and challenging comments. We are painfully aware that replies to many of the topics brought forward by the commentators could easily match the size of the original review [1], but do our best to provide concise and informative answers and notes. The fact that there is so much to discuss goes a long way in showing how much physics can inform biology—and vice-versa—in a quest to understand the links between metabolic processes and levels of biological organization ranging from molecules to individuals to ecosystems [2]. Commentators generally expressed their views on (i) the universality of physical principles on which to build full life-cycle, bioenergetic models for individual organisms [3, 4, 5, 6], as well as on (ii) the potential for future developments in this field [7, 8, 9, 10, 11]. Other, more specialized topics include (iii) the importance of tracking the maturity level of individuals [12], (iv) the difficulties of parameter estimation in relatively large phase spaces [13], and (v) a need for more approachable expositions of theoretical foundations if a broad acceptance among non-specialists is to be achieved [14]. For a reader interested in a succinct, yet remarkably thorough overview of the current state of affairs in the field, there is hardly a better resource than [15].

Criticizing the very fundamentals of [1], Martyushev [3] proposed an intriguing hypothesis that organisms should be viewed as maximizers of entropy production. We believe that a skeptical mind can neither discard this hypothesis lightly, nor accept it at face value without a deeper consideration. As it is seen from Eq. (8) in [1], a mere exchange of materials and energy with the environment for the purpose of accumulating reserve, building structure, and performing the necessary maintenance, demands that entropy is produced. Thus, we are in complete agreement with Schrödinger [16] in that organisms avoid decay by producing entropy and by freeing themselves from this entropy in some way. As explained in Section 5.4 of [1], heterotrophic aerobes get rid of entropy by dissipating heat, i.e., $T\sigma = -\dot{Q}$ (the need for a minus sign in this equation was nicely spotted and explained in [13]). In fact, we are also in agreement with Emden [17] in that the law of energy conservation provides us with little more than a means for bookkeeping, i.e., balancing inputs and outputs; the law indeed tells us nothing about *why* organisms do what they do. To answer the question *why*, Martyushev [3] invokes the principle of maximal entropy production.

The exposition in [1] steers clear of the question *why* and takes a more pragmatic approach of accounting for what organisms are readily observed to do. The two most fundamental observations on which we base our theoretical developments are very precisely stated in [4]: organisms change their chemical composition in response to the nutritional status and possess metabolic memory in the sense of provisioning for life stages (e.g.,

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Email address: `mjusup@gmail.com` (Marko Jusup) embryo) or periods (e.g., starvation) when outside food is unavailable. The simplest possible—and admittedly stylized—way to account for these observations is to assume that an organism consists of two material pools, both of which are of constant chemical composition. One pool (i.e., reserve) accounts for the metabolic memory, while the change in ratio between the two pools accounts for the changes in chemical composition. This stylized description is possible in the case of heterotrophic aerobes simply because they have evolved to feed on what—for all practical intents and purposes—is a single substrate, containing all the necessary nutrients for normal ontogenetic development [4, 18]. To give an intuitive example, a bluefin tuna feasting on small pelagic fish is essentially consuming the miniature versions of itself. We thus avoid invoking any kind of maximization principle in constructing a theory that leads to a general class of full life-cycle bioenergetic models for individual organisms. Is our theory in conflict with the entropy production maximization principle emphasized by Martyushev [3]? Not necessarily—after all, entropy production is an integral part of our framework—but even if there *was* a conflict, valuable lessons could be learned by exploring at which point the two approaches depart from one another. Indeed, any discrepancy between the principle and a theory successful in capturing observations would put more strain on the principle than the theory.

Other important issues regarding the entropy of living organisms is that it should be (i) different from the entropy of dead biomass and (ii) a function of more than just chemical composition and temperature [19]. To justify these expectations without contradicting modern thermodynamics or reviving the ideas of vitalism—as implied in [3]—let us consider a simplified example. Imagine a metallic cube with two opposite sides subjected to different but constant temperatures, and the other four sides covered by a perfect thermal insulator. Heat will flow from the higher temperature to the lower temperature side of the cube and, after a while, a steady-state temperature gradient will be established in the cube. In this steady state, the cube will be characterized by a certain entropy. At some later point in time, the insulating material is added to the previously non-insulated sides, making the cube a completely isolated system. The system subsequently evolves to an equilibrium. During this evolution, entropy production steadily increases the entropy of the cube. In equilibrium, therefore, entropy will be higher than the steady-state entropy, although the total energy and mass of the cube are the same as before. The reason for the change in entropy is the disappearance of the internal temperature gradient in the described process. Analogously, when an organism dies, its internal gradients fade away and entropy changes accordingly. In many respects, death could be *defined* as disappearance of these internal gradients. As [3] notes, entropy of the dead tissue is not yet maximized: complex molecules still contain order that can be used to produce entropy. In other words, complex dead tissue molecules can be degraded to fuel life—a fact used extensively in Dynamic Energy Budget (DEB) theory whenever considering food intake.

In addition to discussing the theoretical foundations laid out in [1], another universality concern expressed by some of the commentators [5, 6] pertains to the von Bertalanffy growth curve as a solution to the standard DEB model (see Section 6 of [1]). It is interesting that a very similar concern has arisen from presumably quite different modeling experiences; the authors of [5] and [6] have been developing the DEB models for insects (e.g., [20, 21]) and fish (e.g., [22, 23]), respectively. To see why the von Bertalanffy curve should be considered only a “first-order” approximation to growth data, we emphasize that the standard DEB model, of which this curve is just one possible solution, is the simplest non-degenerate model [4, 24] that can be constructed based on the principles of physiological energetics outlined in our review and elsewhere [2, 25, 26, 27]. The standard DEB model represents a canonical form that can account for the variability of chemical composition and metabolic memory in heterotrophic aerobes because these organisms, as explained above, feed on a single substrate with all the necessary nutrients for normal ontogenetic development. The von Bertalanffy growth curve as a simple solution to the simplest model captures many observed curves remarkably well. However, given the huge variety in life history of heterotrophic aerobes and other types of organisms, it would be naive to expect that such a simple model should be capable of perfectly capturing all the available data without modifications, extensions, or other tweaks. The five most common tweaks of the standard DEB model that have proven effective in explaining the existing data are referred to as the types of metabolic acceleration [28]:

- Type R acceleration is an increased allocation to soma whereby the value of parameter κ becomes relatively high during a particular life stage or phase. When κ eventually decreases, growth slows down, but respiration and maturation become faster.

- Type X acceleration is an improvement in food quality. In this type of acceleration, the parameter values of an individual are constant, yet the value of food density X improves, generally with size, as this individual becomes able to ingest previously inedible food items from the environment.

- Type A acceleration is an increase in energy assimilation, i.e., the value of parameter $\{\dot{p}_{Am}\}$ keeps increasing during a life stage or phase. A consequence is that the reserve capacity becomes higher, leading to a higher reserve density, and faster energy utilization. Type A acceleration improves the ability to survive starvation and manifests as a change in body composition.

- Type $\mathcal{M}$ acceleration is a simultaneous increase in assimilation and utilization of energy reserve, i.e., parameters $\{\dot{p}_{Am}\}$ and $\dot{v}$ keep increasing during the period between birth and metamorphosis [29]. In this type of acceleration reserve turnover speeds up, but reserve density remains unaffected, thus preserving weak homeostasis.
- Type T acceleration is a gradual increase in body temperature, especially in endotherms. All of endotherms function as ectotherms in the embryonic stage, but later in life gain the ability to maintain relatively constant body temperature above that of the surroundings. This increase in temperature is responsible for speeding up all metabolic rates simultaneously and is implemented in the model as a temperature correction of all rate parameters (i.e., those that have dimension time^{-1}).

Finally, departures from the von Bertalanffy curve may originate from changes in shape during ontogenesis, which are not necessarily isolated from metabolic acceleration. For example, changes in body shape often accompany type $\mathcal{M}$ acceleration [22, 30].

In discussing future prospects, an interesting theme brought forward by the commentators were the DEB models of metabolically "exotic" organisms [7, 8]. Comment [7], for example, emphasizes the need for mechanistically based models of primary producers in marine environments, specifically phytoplankton. One may wonder why phytoplankton would be considered "exotic" given that it is ubiquitous and resides relatively low on an evolutionary scale, yet this is precisely the root of the difficulty. To illustrate this problem, let us briefly return to the other end of the evolutionary scale, i.e., to a top predator such as bluefin tuna. As explained, a bluefin tuna will typically feast on anchovies, sardines, or herrings all of which could be characterized as scaled-down versions of the tuna itself in the sense that all necessary nutrients are already present in the diet. A consequence is that the tuna can roam the seas freely while maintaining a strict stoichiometric homeostasis without provisioning much for the "rainy days". Phytoplankton are, by contrast, forced to make use of what is available in their immediate environments, and when a nutrient is missing, there is little choice but to provision those nutrients that are available, while waiting for the missing nutrient to appear. Stoichiometry of phytoplankton can thus vary wildly depending on the environmental conditions [31]. As a general rule, the number of reserves should match the number of independently acquired nutrients [32]. In terms of mathematical modeling, therefore, bluefin tuna is—although arguably more evolved—simpler to describe because only a single energy reserve needs to be considered. A model for phytoplankton, however, would require multiple reserves and, consequently, end up being much more complicated than its tuna counterpart. Moreover, for the dynamics of multiple reserves to respect stoichiometric constraints, it is necessary to implement the concept of Synthesizing Units (SUs) into the model [4, 33], which add to the complexity. Similar considerations complicate development of DEB models of "exotic" metabolisms suggested by [8]; the development is further stifled by the required intimate knowledge of the metabolisms. We hope that these obstacles can be overcome by future advances in DEB theory and, even more importantly, closer collaboration between modelers and experts with the required biochemical knowledge. Our review and the ensuing discussion hopefully contribute to the understanding that the required effort is worth investing.

One promising line of research utilizing DEB theory are evolutionary considerations emphasized in [9]. Here, we briefly propose a formalism that systematically couples an individual-level growth model—such as the standard DEB model—with a population dynamics model in order to generate outputs subsequently used in an evolutionary dynamics model. We begin by assuming that an individual's growth is captured using the standard DEB model or some other conceptual equivalent that can be represented schematically as:

$$\frac{dl}{da} = \dot{G}(\text{e-state}, \text{i-state}; \lambda), \tag{1}$$

where l is the organism's size, a is age, e-state is a set of all relevant environmental state variables (e.g., food availability, temperature, light, toxicants, etc.), i-state is a set of all relevant organismal state variables (e.g., size, condition, stage, etc.), and λ is a model parameter interpreted as an evolving trait. Function $\dot{G}$ determines the organism's growth rate. In a full life cycle model, this function is appended with fecundity, $\dot{F} = \dot{F}(l)$, and survival $S = S(l)$. Because the individual-level growth model generates conversion function $l = l(a; \text{e-state}, \text{i-state}, \lambda)$, necessary ingredients for calculating population growth rate $\dot{r}_\lambda$ are all available. This calculation can be performed by solving, for example, the Euler-Lotka characteristic equation

$$1 = \int_0^t da e^{-\dot{r}_\lambda a} S\left(l(a)\right) \dot{F}\left(l(a)\right). \tag{2}$$

Natural selection for the continuous trait, λ, can thereafter be mathematically expressed using replicator equation:

$$\frac{\partial x}{\partial t} = \left(\dot{r}(\lambda) - \langle \dot{r} \rangle\right) x(\lambda, t) + D\frac{\partial^2 x}{\partial \lambda^2}, \tag{3}$$

where $x = x(\lambda, t)$ is the trait density distribution function, t is the evolutionary time, $\langle \dot{r} \rangle$ is the average population growth rate taken across all trait values, and D is a "diffusion coefficient" that quantifies how fast genotypic variation leads to phenotypic variation. The system of Eqs. (1–3) describes the evolution of trait λ in time depending on the state of the environment as specified by e-state.

Applications of the standard DEB model—or its extensions—to marine science have been particularly successful. Some examples in this context include (i) reconstructing individual food and growth histories from biogenic carbonates [34], (ii) back-calculating the feeding history and energy conversion efficiencies of captive bluefin tuna from growth data [35], (iii) estimating the impact of a top predator on wild pelagic fish populations [36], (iv) inferring the physiological energetics of an endangered marine turtle species from scarce and disjointed data [37], and (v) predicting the potential of future growth and calcification for a coccolithophore in an acidified ocean [38]. The additional value that mechanistic modeling may yet bring to fisheries science was recognized in comment [10]. Particularly intriguing is the possibility to use the derivatives of the standard DEB model in conjunction with biologging data. This would allow us, for example, to better understand the bioenergetic advantage of choosing one life history over the other, including the subsequent differences in ontogenetic development. Understanding these differences is important in the case of a migratory species such as skipjack tuna, the individuals of which can choose to stay in tropical waters or embark on a northward migration—a choice that has major consequences for the feeding ecology of an individual fish [39]. Similarly, some juvenile loggerhead turtles opt for an energetically more favorable neritic foraging strategy that trades the small disadvantages in survivorship for the relatively large advantages in growth and fecundity compared to the alternative, oceanic strategy, which guarantees a slower but safer life history [40].

Comment [14] presents a brief but sharp critique that for a wider acceptance among non-specialists, introductory materials on the standard DEB model need to be more concise and mathematically "gentler". Such a position is understandable in the sense that researchers have a limited time to devote to studying unfamiliar methodologies and not everyone appreciates the mathematical minutiae of a rigorous theoretical exposition. However, there is a price to be paid for cutting corners in terms of the depth to which the studied subject-matter can be understood. We illustrate this point using an example. In [41] it is assumed that the reserve density, $[E]$, follows first-order dynamics. This assumption effectively reduces our Eq. (23) to a much simpler form:

$$\frac{d\,[E]}{dt} = \frac{\dot{p}_A}{L^3} - C\,[E]\,, \tag{4}$$

where $\dot{p}_A$ is the assimilation energy flow, L is the organism's structural length, and C is a proportionality constant that can readily be determined from the equilibrium condition $\frac{d[E]}{dt} = 0$, which holds at some point $[E] = [E^*]$. It follows that $C = \frac{\{\dot{p}_{Am}\}f}{L[E^*]}$. When $f = 1$, the reserve density is at its maximum, $[E_m]$, and we immediately obtain $C = \frac{\{\dot{p}_{Am}\}}{L[E_m]}$ and

$$\frac{d\,[E]}{dt} = \frac{\{\dot{p}_{Am}\}}{L}\left(f - \frac{[E]}{[E_m]}\right). \tag{5}$$

The last equation completely determines the dynamics of the reserve density. An implication is that, by accepting the assumption that the reserve density is regulated by a first-order process, much of the discussion in Section 6 of [1] is rendered unnecessary. In an introduction aimed at non-specialists, such an explanation may be successful because non-specialists are often more willing to take the most direct path to applications than to spend too much time dwelling on theoretical fundamentals. However, even among those interested mostly in applications, there is bound to be someone who will ask *why* first-order dynamics. What is the motivation behind such an assumption? Unfortunately, there does not seem to be a short and satisfactory answer to this question. The described simplification may thus be easier to understand, but the resulting exposition may fail to convince an inquisitive reader of the generality of the approach.

Finally, we would like to address a remark in [13] on moles vs. C-moles by clarifying how to interpret Eq. (6) in [1]. For this purpose, we use glucose as an example, and note that 1 mole of glucose is equivalent to 6 C-moles of the same substance. Put differently, glucose is represented as $C_6H_{12}O_6$ when we talk about moles, but CH_2O when we are referring to C-moles. In our Table 1, organic molecules (generalized compounds) are written in C-moles. This should have no effect on the mass balance as long as the number of atoms of C, H, O, and P is equal on both sides. Let us write the simplest representation of photosynthesis in the following two ways:

$$6CO_2 + 6H_2O \rightarrow C_6H_{12}O_6 + 6O_2 \tag{6}$$

and

$$CO_2 + H_2O \rightarrow CH_2O + O_2. \tag{7}$$

Either way the mass balance is fully specified. We can say that 6 moles of water are needed to build 1 mole of glucose or that 1 mole of water is needed to build one C-mole of glucose. These two statements are equivalent and, by extension, consistent with one another.

Even as adoption of DEB theory is accelerating, quite a few issues in theory and applications remain. We view these as opportunities for advancement of our understanding of life. This advancement will require considerable effort and ever-closer collaboration between scientific disciplines. We hope that review [1] and the related discussion has helped to convince the reader to join us.

[1] M. Jusup, T. Sousa, T. Domingos, V. Labinac, N. Marn, Z. Wang, T. Klanjšček, Physics of metabolic organization, Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.001.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.001`

[2] R. M. Nisbet, E. B. Muller, K. Lika, S. A. L. M. Kooijman, From molecules to ecosystems through Dynamic Energy Budget models, J. Anim. Ecol. 69 (6) (2000) 913–926.

[3] L. M. Martyushev, Entropy production guides energy budget: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.015.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.015`

[4] S. A. L. M. Kooijman, Homeostasis and the fuelling of metabolism: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.007.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.007`

[5] J. L. Maino, M. R. Kearney, The universality of the von Bertalanffy growth curve: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.010.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.010`

[6] L. Pecquerie, K. Lika, Is reproduction limiting growth?: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.026.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.026`

[7] S. Geček, Autotrophs' challenge to Dynamic Energy Budget theory: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.019.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.019`

[8] P. Holden, DEB modeling for nanotoxicology, microbial ecology, and environmental engineering: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.013.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.013`

[9] R. M. Nisbet, Challenges for dynamic energy budget theory: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.018.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.018`

[10] T. Kitagawa, Y. Aoki, Viewpoints of high migratory tuna species ecology: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.002.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.002`

[11] N. Galić, V. E. Forbes, The role of Dynamic Energy Budget theory in predictive modeling of stressor impacts on ecological systems: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.008.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.008`

[12] S. Augustine, Maturity as quantifier for physiological time: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.009.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.009`

[13] G. M. Marques, Constraints and DEB parameter estimation: Comment on "Physics of metabolic organization" by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.009.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.009`

[14] Y. Iwasaki, More practical and gentler guides are required for non-mathematicians in ecotoxicology and beyond: Comment on “Physics of metabolic organization” by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.017.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.017`

[15] P. Klepac, Linking levels of life: Comment on “Physics of metabolic organization” by Marko Jusup et al., Phys. Life Rev. [in this issue]. doi:10.1016/j.plrev.2017.01.024.
URL `http://dx.doi.org/10.1016/j.plrev.2017.01.024`

[16] E. Schrödinger, What is Life? The Physical Aspects of Living Cell with Mind and Matter and Autobiographical Sketches, Cambridge University Press, 1967.

[17] R. Emden, Why do we have winter heating?, Nature 141 (1938) 908–909.

[18] S. A. L. M. Kooijman, T. A. Troost, Quantitative steps in the evolution of metabolic organisation as specified by the Dynamic Energy Budget theory, Biol. Rev. Camb. Philos. Soc. 82 (2007) 113–142.

[19] T. Sousa, R. Mota, T. Domingos, S. A. L. M. Kooijman, Thermodynamics of organisms in the context of Dynamic Energy Budget theory, Phys. Rev. E 74 (2006) 051901.

[20] J. L. Maino, M. R. Kearney, Testing mechanistic models of growth in insects 282 (1819) (2015) N/A.

[21] J. L. Maino, M. R. Kearney, Ontogenetic and interspecific scaling of consumption in insects, Oikos 124 (2015) 1564–1570.

[22] L. Pecquerie, P. Petitgas, S. A. L. M. Kooijman, Modeling fish growth and reproduction in the context of the Dynamic Energy Budget theory to predict environmental impact on anchovy spawning duration, J. Sea Res. 62 (2009) 93–105.

[23] K. Lika, S. A. L. M. Kooijman, N. Papandroulakis, Metabolic acceleration in Mediterranean perciformes, J. Sea Res. 94 (2014) 37–46.

[24] K. Lika, S. A. L. M. Kooijman, The comparative topology of energy allocation in budget models, J. Sea Res. 66 (2011) 381–391.

[25] T. Sousa, T. Domingos, S. A. L. M. Kooijman, From empirical patterns to theory: A formal metabolic theory of life, Phil. Trans. R. Soc. B 363 (1502) (2008) N/A.

[26] T. Sousa, T. Domingos, J.-C. Poggiale, S. A. L. M. Kooijman, Dynamic Energy Budget theory restores coherence in biology, Phil. Trans. R. Soc. B 365 (1557) (2010) N/A.

[27] S. A. L. M. Kooijman, Dynamic Energy Budget theory for metabolic organisation, Cambridge University Press, 2010.

[28] S. A. L. M. Kooijman, Metabolic acceleration in animal ontogeny: An evolutionary perspective, J. Sea Res 94 (2014) 128–137.

[29] S. A. L. M. Kooijman, L. Pecquerie, S. Augustine, M. Jusup, Scenarios for acceleration in fish development and the role of metamorphosis, J. Sea Res. 66 (2011) 419–423.

[30] M. Jusup, T. Klanjscek, H. Matsuda, S. A. L. M. Kooijman, A full lifecycle bioenergetic model for bluefin tuna, PLoS ONE 6 (7) (2011) e21903.

[31] C. A. Klausmeier, E. Litchman, S. A. Levin, Phytoplankton growth and stoichiometry under multiple nutrient limitation, Limnol. Oceanogr. 49 (2004) 1463–1470.

[32] S. A. L. M. Kooijman, Quantitative aspects of metabolic organization: a discussion of concepts, Phil. Trans. R. Soc. B 356 (1407) (2001) N/A.

[33] S. A. L. M. Kooijman, The synthesizing unit as model for the stoichiometric fusion and branching of metabolic fluxes, Biophys. Chem. 73 (1998) 179–188.

[34] L. Pecquerie, R. Fablet, H. De Pontual, S. Bonhommeau, M. Alunno-Bruscia, P. Petitgas, S. A. L. M. Kooijman, Reconstructing individual food and growth histories from biogenic carbonates, Mar. Ecol. Prog. Ser. 447 (2012) 151–164.

[35] M. Jusup, T. Klanjšček, H. Matsuda, Simple measurements reveal the feeding history, the onset of reproduction, and energy conversion efficiencies in captive bluefin tuna, J. Sea Res. 94 (2014) 144–155.

[36] E. Van Beveren, J.-M. Fromentin, S. Bonhommeau, A.-E. Nieblas, L. Metral, B. Brisset, M. Jusup, R. K. Bauer, P. Brosset, C. Saraux, Prey predator interactions in the face of management regulations: changes in Mediterranean small pelagics are not due to increased tuna predation, Can. J. Fish. Aquat. Sci. [in press]. doi:10.1139/cjfas-2016-0152.
URL `http://dx.doi.org/10.1139/cjfas-2016-0152`

[37] N. Marn, S. A. L. M. Kooijman, M. Jusup, T. Legović, T. Klanjšček, Inferring physiological energetics of loggerhead turtle (*Caretta caretta*) from existing data using a general metabolic theory, Mar. Environ. Res. [in press]. doi:10.1016/j.marenvres.2017.01.003.
URL `http://dx.doi.org/10.1016/j.marenvres.2017.01.003`

[38] E. B. Muller, R. M. Nisbet, Dynamic energy budget modeling reveals the potential of future growth and calcification for the coccolithophore *Emiliania huxleyi* in an acidified ocean, Global Change Biol. 20 (2014) 2031–2038.

[39] Y. Aoki, T. Kitagawa, H. Kiyofuji, S. Okamoto, T. Kawamura, Changes in energy intake and cost of transport by skipjack tuna (*Katsuwonus pelamis*) during northward migration in the northwestern Pacific Ocean, Deep-Sea Res. Pt. II [in press]. doi:10.1016/j.dsr2.2016.05.012.
URL `http://dx.doi.org/10.1016/j.dsr2.2016.05.012`

[40] S. H. Peckham, D. Maldonado-Diaz, Y. Tremblay, R. Ochoa, J. Polovina, G. Balazs, P. H. Dutton, W. J. Nichols, Demographic implications of alternative foraging strategies in juvenile loggerhead turtles *Caretta caretta* of the North Pacific Ocean, Mar. Ecol. Prog. Ser. 425 (2011) 269–280.

[41] J. van der Meer, An introduction to Dynamic Energy Budget (DEB) models with special emphasis on parameter estimation, J. Sea Res. 56 (2006) 85–102.