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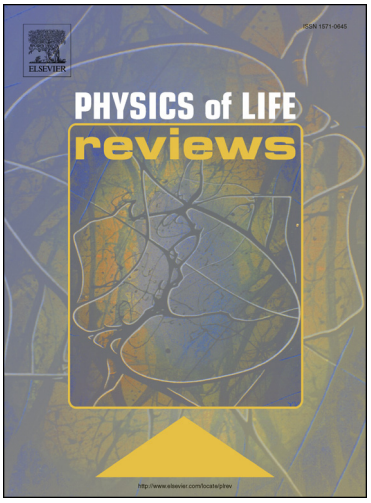

Homeostasis and the fuelling of metabolism

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Homeostasis and the fuelling of metabolism
Comment on "Physics of metabolic organization" by Marko Jusup et al

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The nice and lucid introduction by Jusup et al [2] to the standard model of Dynamic Energy Budget (DEB) theory aims, according to the authors, to serve both physicists and biologists. In my opinion, the authors have been very successful in this, and even for me, as founder of DEB theory, I found several new elements (see below).

The standard DEB model is the simplest non-degenerated model in the family of models in the context of DEB theory. I see it as a canonical form, and applies to most animals (see [1]). This is because animals are special organisms in the sense that they feed on other organisms, dead or alive, so a chemically complex substrate that covers all their metabolic needs. The differences in chemical composition between prey species for animals are less important than their amounts. Many organisms acquire the various substrates (energy, carbon, nutrients) independently of each other. The number of required reserves should match the number of independently acquired substrates to smooth out fluctuations in availability in the environment [5]. A single reserve is thus an evolutionary advanced situation [7]. Multiple reserves, required for most other organisms, come with additional complexity of linking their dynamics to respect stoichiometric constraints, involving some excretion of (transformed) reserve. I only learned how to get there in a natural way, after the discovery of Synthesizing Units (SUs) [4], basically a re-formulation of enzyme kinetics that avoids the use of the concept concentration and is fully based on fluxes.

Although the standard DEB model might seem complex to some, I think that it is extremely simple, given the complexity of its task to capture a bewildering biodiversity that exists. In my opinion it is not possible to strip it down any further, simplicity has been my top priority during its development, without substantially loosing performance to match data and to compare species on the basis of their parameter values, while still respecting biodiversity. I agree with the authors that the DEB book [6] may be hard to read for physicists and mathematicians because of the many biological 'details'. Being aware of the existing biodiversity, I constantly heard voices from my fellow biologists in the back of my mind while writing the book saying 'This is nonsense, don't you know of the existence of this or that species that does it differently?'. This would be a natural critique when you have the ambitious aim of capturing all life in one framework. I also thought that the details help to match the real and the abstract worlds, a key operation for modelling. My experience is that the 'details' easily confuse newcomers to the line of thinking, so I admire the courage of Jusup et al to strip most of them which makes it more easy to start with.

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