DEB from the outside

By Maria Pozimski

When I first heard about the Dynamic Energy Budget theory, I was not a professional biologist like many others in the course, but I was studying for my Bachelor in Science in the, well, first semester. Primarily lead by an interest for theoretical biology I met Prof. Bas Kooijman. The DEB- course was just about to start so he invited me. “After this course you are going to know if you like the topic or not.”

Right at the start I heard that DEB is understandable on many different levels: What does DEB? How is it doing it? And is that really what we see in nature? These three phases of abstraction, translation in mathematics and again application to the real world form the basis of understanding the DEB theory. Not having any research I could apply DEB to, I set out to understand what DEB does to unify all kinds of species. Underlying the whole theory is the daring assumption that the metabolisms of all organisms are very similar. To prove this, rather different species need to be fitted into one system. To create a model there is a need to first find rules as a framework, which apply to the different species. The standard DEB theory describes 10 basic assumptions. The whole model is described by these premises and the conclusions which follow. That makes it relatively easy to understand the abstraction. Of course this is a simplification of the real world, but with this process of abstraction one comes closer to know what is important to understand a living organism. Making the model as simple as possible helps to really understand what happens inside an organism and to get deeper insights in biology. Otherwise the possibility can not be out ruled to have a right answer for a wrong cause. Of course this simplification has its limits, because the model still needs to be able to predict real world measurements. So if this understandable model would be able to calculate parameters that are found in the real world then the gained knowledge would be proven true. And it worked out. Numerous examples of species whose data fits the DEB model are given in the accompanying book, so one understands not only that the model works, but also how. So by applying the theory to more and more organisms it was proven that the metabolisms of a wide variety of species can be modeled in relatively simple terms. I say relatively simple, because the first 10 assumptions just clear the grounds for a variety of mathematical formulas which make the model precise. For me this was definitely the hardest part of the course, because I am not used to applying mathematical formulas, but it is noteworthy that not only biologists but also mathematicians and other professions participate regularly in the DEB course. It might not even be easier for either one of them, because to understand the model can challenge biologists as well as mathematicians to find new ways of understanding a problem.

However, with all its good sides exceptions can be found especially for the standard DEB model that assumes that individuals do not change in shape during growth. This phenomenon, called isomorphism, is astonishingly enough true for a lot of species, but to refine the model the follow up DEB theories abandoned the assumption that all individuals are basically isomorphic. After the model was successfully abstracted it can again be used to help researchers to understand energy fluxes in new organisms or systems. Under set circumstances it would now be possible to find out what happens to the energy the organisms take up in the form of food. Food is assimilated to form at least one reserve pool and the energy contributes in quantitatively fixed proportions to maintenance and growth as well as maturity and reproduction.

The great advantage of this theory is the unifying process. While most of biological research aims at collecting data to clarify the processes in more and more specialized fields, the DEB theory successfully finds the structures that connect different species and is able to secure its own correctness by using provable mathematical formulas. On one hand approaches like that secure that the huge amount of collected data concerning all kinds of species is not lost in a highly specific field, but can instead be applied, recognized and, in the best case, used by researchers form completely different fields. On the other hand allows DEB to compare even species in different levels of maturation so that biologists may have a starting point for new research. Although the theory is not as widely known as it would deserve it, new species and corrections to the first theory are added every year.

I started with very little knowledge about this part of biology, but it helped me even in a non-professional setting to see larger structures in biology. It is fascinating how much farther we can get by applying math to the field of biology. So far I think this course is really designed for professionals so they can apply it to their own research, but I think it would also be very helpful for people who are interested in biology in a non-professional setting to get an understanding how organisms work.