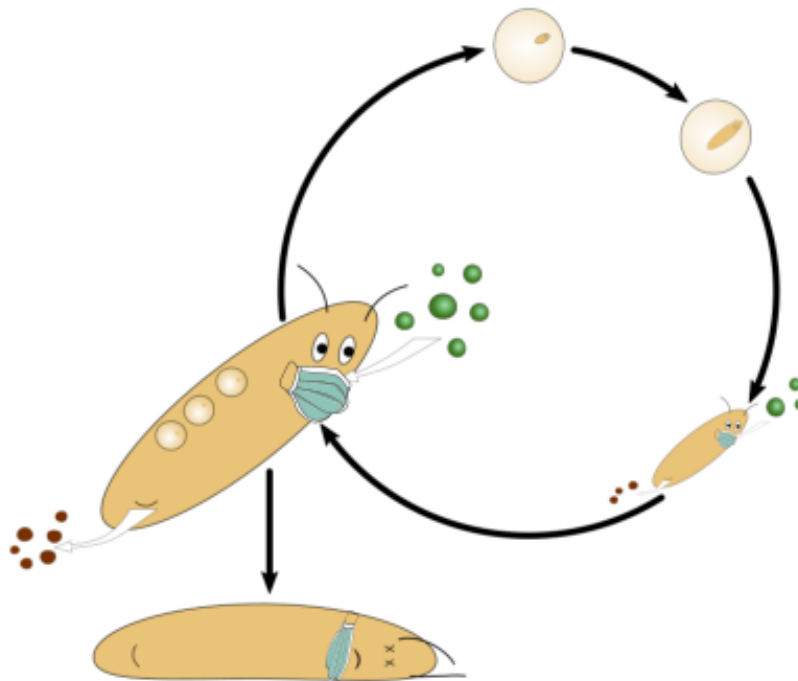# DEB2021 17-28 May 2021

Seventh International Symposium and Thematic School on DEB theory for metabolic organization

Book of Abstracts

About DEB2021

DEB2021 is the seventh edition of a series of tele-courses, schools, and symposia which take place every two years and for the first time (virtually) in North America.

Dynamic Energy Budget (DEB) theory aims at unifying commonalities of metabolic organization between all types of organisms (animals, plants, bacteria). The theory is based on a restricted number of assumptions, written out as mathematical formulas, which allow quantifying growth, development, reproduction of an organism during its life cycle as a function of available food and temperature. It also enables modelling the effects of stressors such as contaminants, pathogens, oxygen, and pH.

In the current context of biodiversity erosion, better understanding the relationship between physiological traits and organism performance is recognized as a crucial step in preserving structurally and functionally healthy ecosystems. Such a goal may only be achieved through interdisciplinarity. DEB theory emerged in 1979 in the context of improving environmental risk assessment, at the crossing of toxicology, physiology, and theoretical biology. Over the last 45 years of Research and development, the theory has been useful to simulate biological systems using parameters extracted from data. With more than 900 publications, DEB theory illustrates and promotes the positive feedback between experimental and monitoring data acquisition, and methods for the interpretation of data such as modelling, which is supported through interdisciplinary research. Aside from comparisons of species functional traits, applications comprise studies predicting effects of global change, understanding changes in species geographical distribution, quantifying and interpreting effects of environmental stressors, optimizing bio-production, aiding management of exploited resources, and more. What unifies these diverse applications is the need to quantitatively model the metabolism of living systems in a variable environment.

The theme of the 2021 edition is "Forecasting in a changing world". With an increased awareness of the threats posed by a changing climate and human impacts on the biosphere, numerical modelling is a tool on the rise for scientists, managers, and stakeholders. But the naturally dynamic characteristics of the biological, chemical and physical aspects of our world constitute a challenge that must be considered. DEB theory is rooted in a mechanistic description of the individual metabolic processes, which is crucial to connecting functional traits to predictive variables, therefore, ensuring the adaptability of models to changing conditions. Many applications of DEB theory have already demonstrated this aspect and been used to inform decision-making. This symposium will include the latest advances of this field of research and contribute to the emulation of ideas that will help forecasting in a changing world.

With the Covid-19 pandemic, travel restrictions and health safety guidelines in Canada made an in-person meeting impossible to organize this year. Instead, we are relying on online conferencing tools to hold the School and the Symposium virtually. This is new territory for all of us and this year's edition will be different than previous ones. But we hope that the usually fascinating, creative, and friendly interactions we all enjoy within the DEB community during these important bi-annual meetings will take form in one way or another.

The DEB2021 Organizers

Organization

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Monday, May 24th, 2021

15:00	**Welcome and opening**
15:05	*Session 1: Populations and Ecosystems in a Changing Climate*
	KEYNOTE
	Ben Martin, University of Amsterdam, Netherlands
	Understanding the effects of climate change on animal populations through the lens of organismal energetics
16:05	**Jean-Pierre Desforges**, McGill University, Canada
	Individual and population response to climate change in Arctic muskoxen
16:25	**Break**
16:35	**Lola De Cubber**, Laboratoire d'Océanologie et de Géosciences, France
	Investigating population dynamics, traits and shore distribution of two sympatric lugworm species...
16:55	**Wissam Barhdadi**, Ghent University, Belgium
	Extending DEB-IBM towards an eco-evolutionary modelling framework
17:15	**Ines Haberle**, Ruđer Bošković Institute, Croatia
	Can an individual tell us something about its population?
17:35	**Lynda Bradley**, Emory University, United States
	Predicting the effects of resource pulses on snail and human schistosome dynamics using a DEB-IBM
17:55	**General Discussion**
18:00	

Tuesday, May 25th, 2021

Time	
15:00	*Session 2: Theoretical & Methodological Developments and New applications*
	KEYNOTE
	Michael Kearney, University of Melbourne, Australia
16:00	What is the status of metabolic theory one century after Pütter invented the von Bertalanffy growth curve?
	Charlène Guillaumot, Université de Bourgogne Franche-Comté, France
16:20	Simple or hybrid? The performance of next generation ecological models to study the response of Southern Ocean..
16:30	**Break**
	Tom Martin, University of New York, United Kingdom
16:50	Modelling effects of variability in feeding rate on growth a vital step for DEB-TKTD modelling
	Juan Francisco Robles, Universidad de Granada, Spain
17:10	MultiCalib4DEB: a toolbox bringing multimodal optimization for DEB parameters calibration
	Eleni Livanou, University of Crete, Greece
17:30	Modelling nanoflagellates – bacteria interactions in the oligotrophic Eastern Mediterranean Sea
	Konrad Matyja, Wroclaw University of Science and Technology, Poland
17:50	The larvae, which eat polystyrene: growth, development, and survival analysis
	General Discussion
18:00	

Wednesday, May 26th, 2021

Time	
15:00	
	Poster session
16:20	
	Break
16:30	
	Marko Jusup, Tokyo institute of Technology, Japan
16:50	Let the concept of trait be theoretical
	Tin Klanjšček, Ruđer Bošković Institute, Croatia
17:10	DEB theory should not be a dead Christmas tree
	Joaquim Tomàs-Ferrer, Laboratori d'Investigacions Marines i Aqüicultura, Spain
17:30	Bayesian estimation of DEB parameters using STAN
	Gonçalo Marques, MARETEC Universidade de Lisboa, Portugal
17:50	Direct greenhouse gas emissions in livestock production
	General Discussion
18:00	

Thursday, May 27th, 2021

Time	
15:00	*Session 3: Effects of anthropogenic and environmental stressors*
	KEYNOTE
	Cheryl Murphy, Michigan State University, United States
	The complexity of mixture toxicity and multiple stressors:how incorporating suborganismal processes
16:00	**Benoit Goussen**, ibacon GmbH, Germany
	A DEB egg-laying module for birds exposed to pesticides
16:20	**Break**
16:30	**Kim Rakel**, Research institute gaiac, Germany
	Alive and kicking? - Earthworm cocoon test for TKTD Modelling in soil risk assessment of chemicals
16:50	**Sandrine Charles**, Laboratoire de Biométrie et Biologie Evolutive (LBBE), France
	Towards a facilitated use of Modelling in Environmental Risk Assessment
17:10	**José Moreira**, MARETEC Universidade de Lisboa, Portugal
	Impacts of climate change in temperate and sub-tropical fish species
17:30	**Tiago Domingos**, MARETEC Universidade de Lisboa, Portugal
	DEB modelling and IPCC accounting methods: a bridge between frameworks
17:50	**General Discussion**
18:00	

Friday, May 28th, 2021

Time	
15:00	*Session 4: Evolution & Biodiversity*
	KEYNOTE
	Sabrina Russo, University of Nebraska-Lincoln, United States
	Applying the Dynamic Energy Budget approach to models of plant resource allocation
16:00	**Sylvie Gaudron**, Laboratoire Océanologie et Géosciences (LOG), France
	Inferring functional traits in a deep-sea wood-boring bivalve using dynamic energy budget theory
16:20	**Break**
16:30	**Emilien Pousse**, NOAA NEFSC, United States
	Projecting the effect of ocean acidification and warming on two Atlantic surfclam...
16:50	**Isabel Smallegange**, University of Amsterdam, Netherlands
	Unusually paced life history strategies of marine megafauna drive atypical sensitivities to environmental change
17:10	**Charlotte Récapet**, Behavioural Ecology and Fish Population Biology Laboratory, France
	Intra-specific variation of life-history traits in Atlantic salmon: environmental and genetic factors
17:30	**Joany Mariño**, Memorial University, Canada
	Resource and seasonality drive interspecific variability in the Dynamic Energy Budget model
17:50	**Conclusion and Closing**
18:00	

Understanding the effects of climate change on animal populations through the lens of organismal energetics

Benjamin Martin *

Assistant professor at University of Amsterdam, Amsterdam, Netherlands.Department of Theoretical and Computational Ecology

Predicting how animal populations will respond to a warming climate is one of the central challenges for applied ecology. Temperature directly affects how animals are coupled to their environments through the exchange of energy and materials, and thus thermal stress can be naturally understood through the lens of organismal energetics. The energetic impacts of elevated temperatures on organismal energetics can then be scaled to the population level using mathematical models. Thus DEB-theory based approaches that connect organismal and population levels are a natural choice for predicting the effect of a changing climate of animal populations. However, this approach is currently limited by our understanding of the mechanisms that reduce organismal performance at elevated temperatures; in many cases the energetic mechanisms of thermal stress remain poorly understood and are not covered by core DEB theory. I review several case studies where accurate predictions of thermal stress required the development of new mechanistic theory at the organismal level. More generally, I argue that while energy budget models will be an important tool for predicting the impacts of climate change on animal populations, the usefulness of these tools will depend on better resolving mechanisms of thermal stress.

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Individual and population response to climate change in Arctic muskoxen

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Species conservation in a rapidly changing world requires an improved understanding of how individuals and populations respond to changes in their environment. Increased warming in the Arctic puts this region at particular risk for rapid environmental change, with potentially important impacts on resident wildlife such as the muskox (*Ovibos moschatus*). Here we use a dynamic energy budget linked individual based model (DEB-IBM) to explore two broad questions on how muskoxen respond to harsh Arctic conditions: 1) what are the energetic and fitness consequences of over-winter heterothermy? and 2) how do populations respond to temporally dynamic winter and summer forage availability? We show that the relatively small drop in overwinter body temperature observed in wild muskoxen (0.8 °C) equates to meaningful fitness benefits in terms of reduced daily energy expenditure and overall body mass and energy reserve loss, but benefits depended largely on whether ingestion rates were temperature regulated. Using continuous year-round environmental data (snow depth and normalized difference vegetation index (NDVI)) as proxies for food availability, we show how both winter and summer food availability as well as density-dependence drive seasonal dynamics of energy storage and thus life history and population dynamics of Northeast Greenland muskoxen. Specifically, winter forage accessibility (snow depth), more than summer forage availability (NDVI), was the primary determinant of muskox population dynamics through impacts on calf recruitment and longer-term carry-over effects of maternal investment. Impacts on recruitment were the cumulative result of condition-driven reproductive performance at multiple time points across the reproductive cycle (ovulation to calf weaning) as a trade-off between survival and reproduction. Altogether, results from these two studies reveal that muskoxen are indeed vulnerable to changes in climate parameters that influence their access to forage throughout the year, particularly during winter months when they rely heavily on stored energy reserves for survival and reproduction.

Keywords: Arctic, climate change, muskox, mammal, population dynamics, environmental conditions

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*Speaker

Investigating population dynamics, traits and shore distribution of two sympatric lugworm species over a latitudinal gradient with a Dynamic Energy Budget - Individual-Based Model

Lola De Cubber [*][†] [1,2], Daniel Schaffer [3], Sébastien Lefebvre [4], Hubert Loisel [3], Sylvie Gaudron [3,5]

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[4] UMR 8187 Laboratoire d'Océanologie et de Géosciences (LOG) – Univ. Lille, Univ. Littoral Côte d'Opale, CNRS – F-59000 Lille, France
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Dynamic Energy Budget models coupled to Individual-Based Models (DEB-IBMs) allow simulating both individual and population characteristics under an infinite variety of environmental conditions, constituting promising tools for ecologists. In this study, we have developed such models to investigate the environmental effects on two intertidal sympatric ecosystem engineers, *Arenicola marina* and *A. defodiens* (Annelida Polychaeta) that inhabit galleries within soft-sediment foreshores from the Mediterranean to the Arctic. Published DEB parameters were used for *A. marina* and a specific calibration was undertaken for *A. defodiens* using an abj-DEB model, combining literature data and new experimental and *in-situ* data. DEB-IBM simulations allowed following super-individuals' growth and reproduction while they were colonizing, migrating and dying over a simulated foreshore displaying specific characteristics. Migration and density rules were set according to the literature. Spawning was triggered by a combination of Sea Surface Temperature (1 °C decrease in 2 weeks and SST $\geq$ 10 °C) and gonado-somatic index (10% trigger threshold). Recruitment happened when individuals reached the juvenile life-stage. Density constrained the number of recruits. Mortality (0.008 ind.d^{-1}) was adjusted according to real *in situ* observations in various locations. Simulations were ran three times over 18 years for 28 sets of monthly values of planktonic chlorophyll-a concentrations (chl-a, 1 km^2 resolution : www.hermes.acri.fr) and daily values of SST (4 km^2 resolution : www.cersat.ifremer.fr) extracted from satellite data, corresponding to areas where lugworms were formerly recorded. Combinations of most extremes values of chl-a and SST were also used to explore the relative effects of these parameters over populations' dynamics. Population density, biomass, total reproductive output, maximum length, and length at puberty were then compared. Chl-a appears to display a key role to sustain lugworm populations. Further use of this model under climate change scenarios should lead to better insights on the populations' evolution over the next decades.

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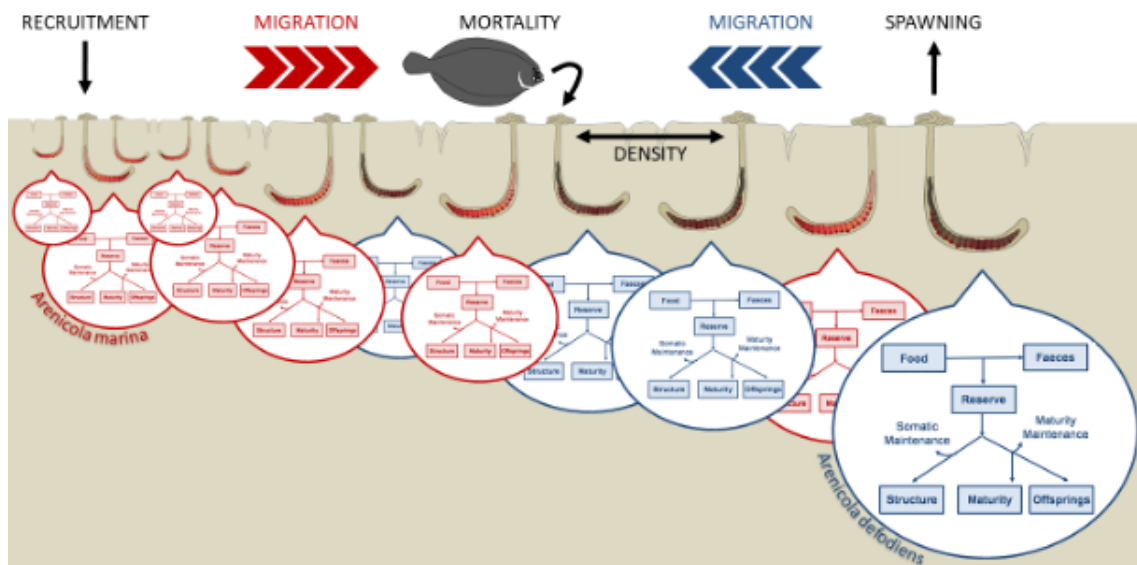
Extending DEB-IBM towards an eco-evolutionary modelling framework

Wissam Barhdadi [*†][1], Aisling Daly [1], Jan Baetens [1], Bernard De Baets [1]

[1] Department of Data Analysis and Mathematical Modelling (KERMIT) – Coupure links 653, B-9000 Ghent, Belgium

Ongoing environmental changes are significantly impacting population dynamics in ecosystems across the globe. Considering the importance of individual life histories to the vital rates of a population, the impact of a changing environment is significantly mediated by an individual organism's biology. The DEB-IBM framework has therefore proven to be an intuitive approach to model population dynamics facing changing environments by extrapolating the DEB-based life-history trait-environment relationship to the population level.
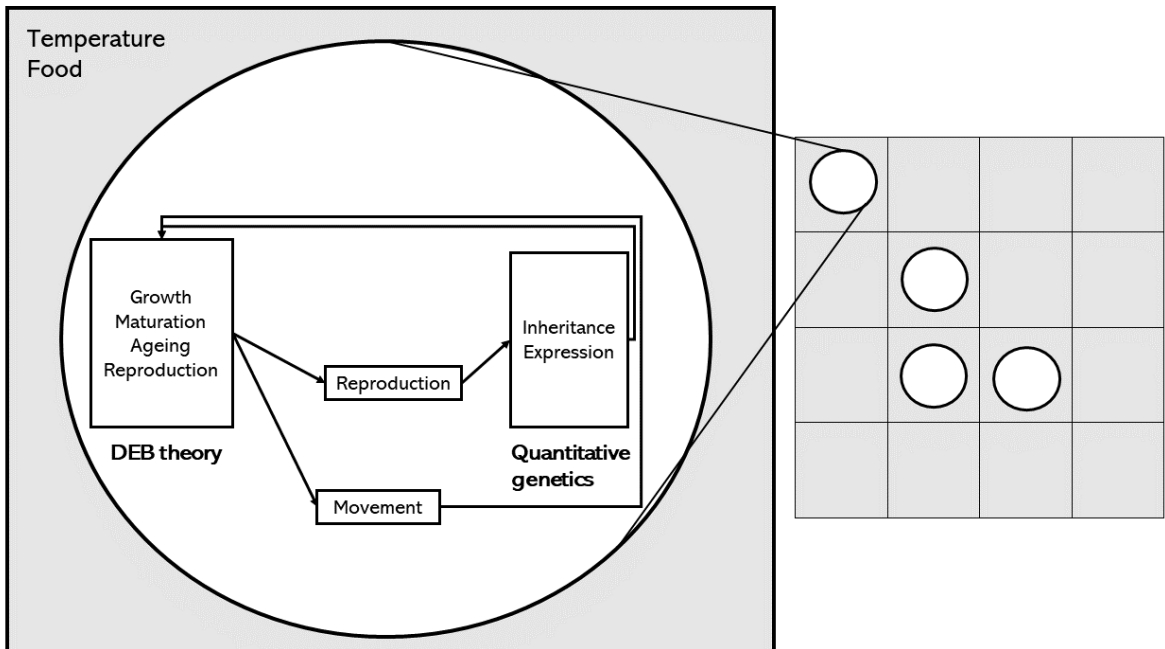
Mechanistic population models incorporating abiotic drivers, such as temperature or pH stress, often resort to a set of key demographic and physiological mechanisms to be included. Over the past years, the inclusion of evolutionary processes in ecological models has also gained popularity as modellers are increasingly acknowledging the potential of populations to adapt to novel environments, even on ecological time scales. This ability may have profound impacts on populations' long-term persistence and resilience. Among individual-based models (IBMs), a variety of approaches have been developed to integrate evolutionary mechanisms. However, DEB-IBMs have largely ignored genetic adaptation as a mechanism influencing population dynamics.

We propose an extension of the DEB-IBM framework to include genetic adaptation of heritable traits using a quantitative genetic approach in a two-dimensional environment. This extension allows for the modelling of spatially explicit eco-evolutionary dynamics of populations confronted with changing climate conditions. Using next-generation IBM analysis techniques, we analyze the behaviour of the extended DEB-IBM framework. With this proposed extension, we aim to contribute to improving structural realism of individual-based population models.

Keywords: eco, evolutionary, DEB, IBM, individual, based modelling, quantitative genetics, adaptation, micro, evolution, population

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Temperature
Food

Growth
Maturation
Ageing
Reproduction

DEB theory

Reproduction

Inheritance
Expression

**Quantitative
genetics**

Movement

Can an individual tell us something about its population?

Ines Haberle [*][†] [1], Lav Bavčević [2], Tin Klanjšček[‡] [1]

[1] Ruđer Bošković Institute (IRB) – Bijenicka cesta 54, 10010 Zagreb, Croatia
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Effective decision-making in wildlife management relies on accurate estimates of the current population status, as well as on predictions of its dynamic. The population dynamic is determined by vital rates of individuals, which depend on energy investment into growth and reproduction. The investments depend on the individual's energy budgets that can be estimated by observing weight and length of individuals. Translating such individual-level measurables to population dynamics, however, is confounded by ecological and environmental feedbacks.

We use a DEB-IBM model of European pilchard to look at how environmental conditions – including fishing – affect the relationship between population size and individual-level status. We model how fishing pressure and environmental food availability affect size, reproduction, energy reserves, condition index (CI) and abundance. As expected, both average energy content and average fish condition increase with food availability. Increased fishing mortality results in lower population levels, followed by an increase in energy reserves and CI. Counterintuitively, this implies that very good condition (high CI) of the fish could indicate overfishing.

Our results, therefore, suggest that CI may reflect the state of the population. Since CI is a simple metric calculated from commonly available biometric data, it has a great potential of becoming a very simple but powerful addition to existing tools in management of fisheries. We also discuss some limitations of the approach, and applicability to other wildlife.

Keywords: DEB IBM, condition index, population, fisheries, fishing mortality, carrying capacity
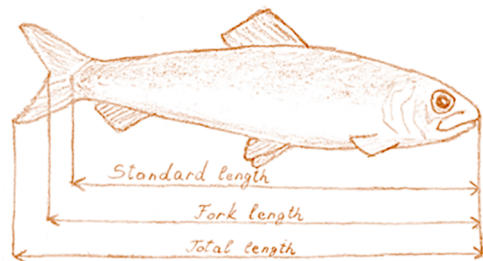
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$$\frac{W}{L^3}$$

Standard length

Fork length

Total length

Predicting the effects of resource pulses on snail and human schistosome dynamics using a DEB-IBM

L. M. Bradley *† [1], David Civitello [1]

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Resource pulses are ubiquitous and have cascading effects on population, community, and ecosystem dynamics. Predicting how resource pulses affect aquatic ecosystems is critical for basic ecological understanding and management. For example, agricultural runoff and nutrient pollution are implicated in increasing schistosomes produced by freshwater snail hosts because they increase the total number of snails as well as the per capita production of cercariae, the human-infectious life stage. DEB-based models could improve predictions of resource pulse effects on transmission potential because they naturally accommodate how hosts grow, reproduce, transmit, and survive in variable resource environments.

We conducted a simulation study of the effects of resource pulses on the population dynamics of snails and their schistosomes using a DEB-based individual based model (DEB-IBM). We simulated seasonal transmission scenarios in which a small number of founders (drawn uniformly from a realistic size distribution [4-16 mm]), consume logistically growing algae or nonreproductive detritus throughout a 120-day transmission season in daily time steps. We separately investigated two dimensions of detritus pulses: timing (one single pulse per simulation occurring on different weeks) and frequency (holding total input constant, adding resources every 1, 3, 7, 14, or 28 days). We hypothesized that resource pulse scenarios that substantially elevate host reserves will stimulate transmission potential, because well-fed hosts produce many parasites. Results from the timing simulations indicate that total transmission potential peaked when the single pulse occurred mid-season. The frequency simulations show that transmission potential increases with pulse frequency. Both findings can be explained through observing the DEB reserve density over time, which predicts when a pulse will "rescue" a snail population from starving—and if the population is mature, then also abundantly produce parasites. We are currently testing these hypotheses further with a mesocosm experiment, and will compare these results to the DEB-IBM simulation results.

Keywords: DEBIBM, IBM, disease ecology, resource pulses, water management, schistosomiasis

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DEB-IBM
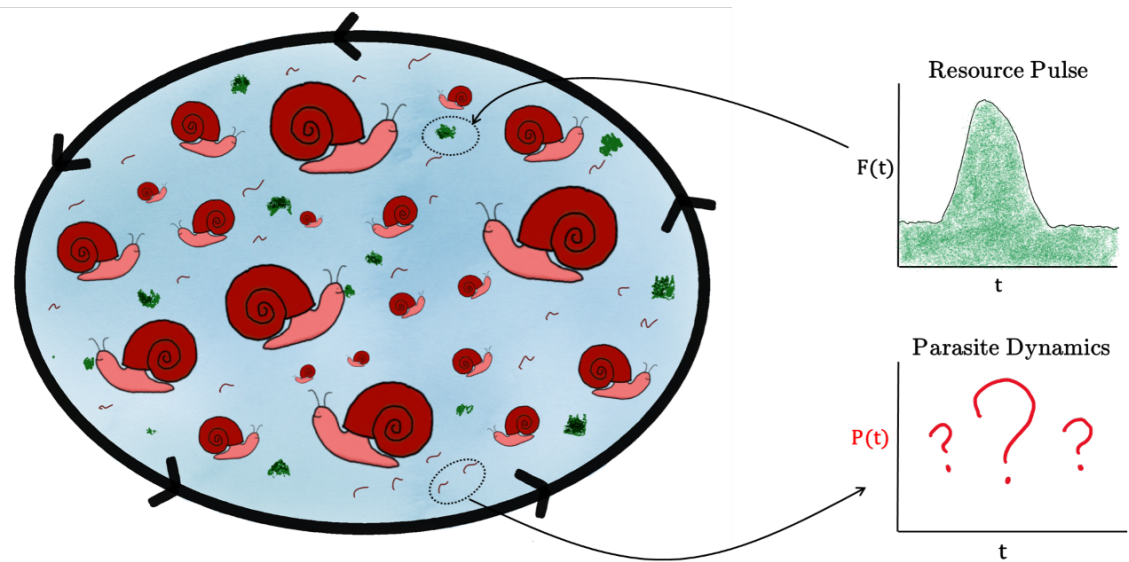
Resource Pulse

$F(t)$

t

Parasite Dynamics

$P(t)$

t

What is the status of metabolic theory one century after Pütter invented the von Bertalanffy growth curve?

Michael Kearney*

Professor at the University of Melbourne, Melbourne, Australia, Climatic and Metabolic Ecology

Metabolic theory aims to tackle ecological and evolutionary problems by explicitly including physical principles of energy and mass exchange, thereby increasing generality and deductive power. Individual growth models (IGMs) are the fundamental basis of metabolic theory because they represent the organisational level at which energy and mass exchange processes are most tightly integrated and from which scaling patterns emerge. Unfortunately, IGMs remain a topic of great confusion and controversy about the origins of the ideas, their domain and breadth of application, their logical consistency and whether they can sufficiently capture reality. It is now 100 years since the first theoretical model of individual growth was put forward by Pütter. His insights were deep, but his model ended up being attributed to von Bertalanffy and his ideas largely forgotten. In this talk I will review Pütter's ideas and trace their influence on existing theoretical models for growth and other aspects of metabolism, including those of von Bertalanffy, the Dynamic Energy Budget (DEB) theory and the Ontogenetic Growth Model (OGM). I show that the von Bertalanffy's model is a minor modification of Pütter's original model. I then synthesise, compare and critique the ideas of the two most-developed theories, DEB theory and the OGM, in relation to Pütter's original ideas. I trace the confusion and controversy regarding these theories to the notions of anabolism, catabolism, assimilation and maintenance, the connections to respiration rate, and the number of parameters and state variables their models require. The OGM model has significant inconsistencies that stem from the interpretation of growth as the difference between anabolism and maintenance, and these issues seriously challenge its ability to incorporate development, reproduction and assimilation. The DEB theory is a direct extension of Pütter's ideas but with growth being the difference between assimilation and maintenance rather than anabolism and catabolism. The DEB theory makes the dynamics of Pütter's 'nutritive material' explicit as well as extending the scheme to include reproduction and development. Future research on the connections between theory and data in the study of macrometabolic topics have the greatest potential to advance the status of metabolic theory and its value for pure and applied problems in ecology and evolution.

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Simple or hybrid? The performance of next generation ecological models to study the response of Southern Ocean species to changing environmental conditions

Charlène Guillaumot * [1,2], Jonathan Belmaker [3], Yehezkel Buba [3], Damien Fourcy [4], Philippe Dubois [5], Bruno Danis [5], Thomas Saucède [6]

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In the context of intensifying threats of climate change on marine communities, ecological models are widely used and applied for conservation strategies, though polar studies remain scarce given the limited number of datasets available. Among models, correlative models (e.g. Species Distribution Models, SDM) describe the occurrence-environment relationship; mechanistic (physiological) models (e.g. Dynamic Energy Budget models, DEB) study the influence of environmental conditions on organism metabolic performances and population dynamics. Integrating both approaches is powerful and complementary, as it allows to better estimate the species realised niche (assessed by correlative approaches), by adding the effect of environmental inputs on species physiology (the fundamental niche, estimated by mechanistic approaches).

Here, we used data from a long-term observing network located in the Kerguelen Islands, to implement for the first time, integrated models to predict the distribution of an endemic sub-Antarctic sea urchin, *Abatus cordatus* (Verrill, 1876) as a response to environmental drivers. We compared the performances of simple and integrated approaches to predict *A. cordatus* distribution according to seasonal variations. Two integrated approaches were studied and performed by either (1) including the spatial projection of the DEB model as an input layer inside the SDM ('integrated SDM-DEB' approach) or (2) using a Bayesian inference procedure to use DEB model outputs as priors of the Bayesian SDM ('integrated Bayesian' approach).

Results show higher performances of the 'integrated Bayesian' approach to evaluate *A. cordatus* realised niche compared to 'simple' and 'integrated SDM-DEB' methods. The influence of environmental conditions on model predictions is further captured with the 'integrated Bayesian' procedure and better highlights the seasonal effect on the species predicted distribution. These results are encouraging and the method promising for application to other data-poor case studies, in a context of climate change or for conservation issues.
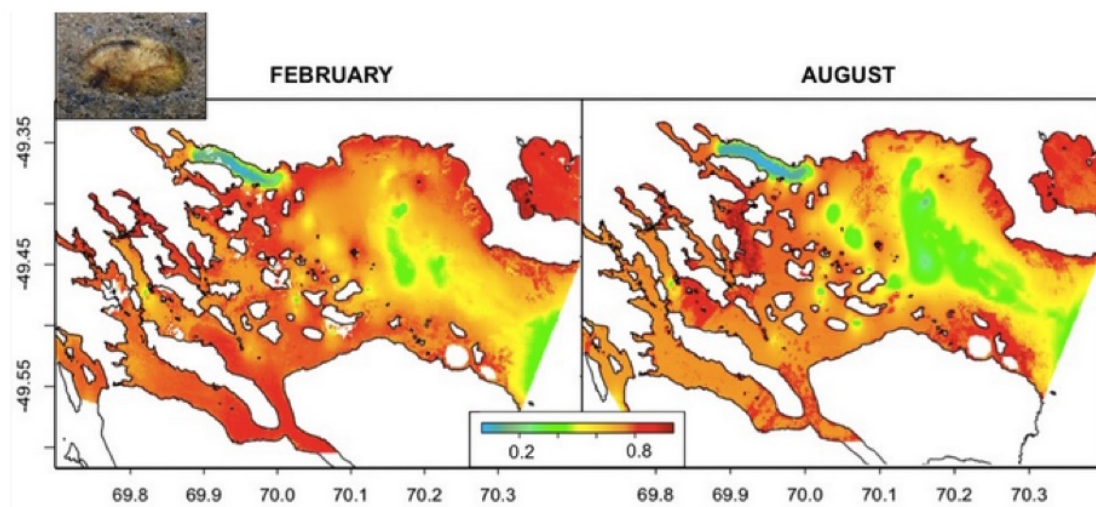
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*Presenter

Figure. Spatial projections of the 'integrated Bayesian' models for February (left) and August (right), averaged of 50 model replicates. The DEB output used as a prior in the Bayesian inference procedure is the amount of energy remaining from the reserve compartment that is available after paying for maintenance costs.

Modelling effects of variability in feeding rate on growth – a vital step for DEB-TKTD modelling

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A major limitation of dietary toxicity studies on rodents is that food consumption often differs between treatments. The control treatment serves as a reference of how animals would have grown if not for the toxicant in their diet, but this comparison unavoidably conflates the effects of toxicity and feeding rate on body weight over time. A key advantage of toxicity models based on dynamic energy budget theory (DEB) is that chemical stress and food consumption are separate model inputs, so their effects on growth rate can be separated.

To reduce data requirements, DEB convention is to derive a simplified feeding input, f, from food availability; its value ranges from zero (starvation) to one (food available *ad libitum*). Observed food consumption in dietary toxicity studies shows that, in fact, rats limit their food consumption, contradicting DEB assumptions regarding feeding rate. Relatively little work has focused on addressing this mismatch, but accurately modelling the effects of food intake on growth rate is essential for the effects of toxicity to be isolated. This can provide greater insight into the results of chronic toxicity studies and allows accurate extrapolation of toxic effects from laboratory data.

Here we trial a new method for calculating f, based on the observed relationships between food consumption and body size in laboratory rats. We compare model results with those of the conventional DEB method and a previous effort to calculate f using observed food consumption data. Our results showed that the new method improved model accuracy while modelled reserve dynamics closely followed observed body fat percentage over time. The new method assumes that digestive efficiency increases with body size. Verifying this relationship through data collection would strengthen the basis of DEB theory and support the case for its use in ecological risk assessment.

Keywords: Feeding rate, TK, TD, DEBkiss, Growth

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MultiCalib4DEB: a toolbox bringing multimodal optimization for DEB parameters calibration.

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Dynamic Energy Budget (DEB) theory has become a popular approach to mechanistically describe individual's bioenergetics throughout their life cycle. DEB can be applied to all species. However, the need to calibrate a large set of parameters is both a pitfall for the use of DEB models and one of the most challenging aspects of DEB modelling. Moreover, parameters have been estimated for thousands of species and DEB parameter calibration has become a core task, where different sets of estimated parameters' values can frequently yield the same fitting values. The introduction of the DEBtools toolbox (https://add-my-pet.github.io/DEBtool_M/docs/index.html) provided an accessible calibration framework and a vast library of functions and examples to use for parameter calibration and DEB models applications. The DEBtools toolbox was one of the reasons behind the success of DEB theory as it is being constantly updated to improve the modelling experience. But the existing calibration module within DEBtools toolbox has often been criticised because it is not able to deal with the challenges of the multimodal search space of the DEB parameters' calibration.

In this work we present a calibration toolbox based on evolutionary multimodal optimization algorithms called MultiCalib4DEB which is directly integrated with the existing DEBtools toolbox and its calibration framework. Evolutionary multimodal optimization based on niching genetic algorithms has been recognised as a powerful calibration tool offering an integral and interactive framework to calibrate diverse modelling methodologies while improving the validation of the results. The presented toolbox adds the potential of these effective evolutionary algorithms to the parameter calibration framework and the DEBtools toolbox library providing a wider range of outputs, different calibration solution alternatives, and specific tools to assess parameter uncertainty and validation. The MultiCalib4DEB toolbox can be directly applied to ongoing studies or existing DEB libraries of species to calibrate the model's parameters, assess their robustness, and perform visual sensitivity analyses in just one run of the algorithm. The outputs of this tool are compared with the standard outputs of the DEBtools toolbox.

Keywords: Multimodal optimization, Dynamic energy budget, DEBTools toolbox, Parameter calibration

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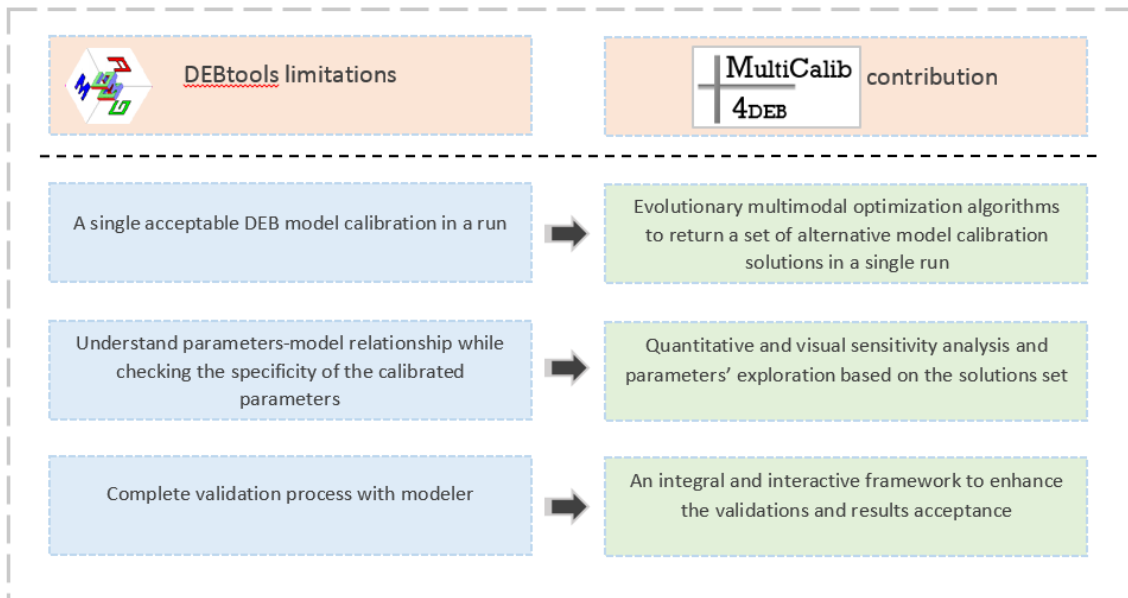
Modelling nanoflagellates – bacteria interactions in the oligotrophic Eastern Mediterranean Sea

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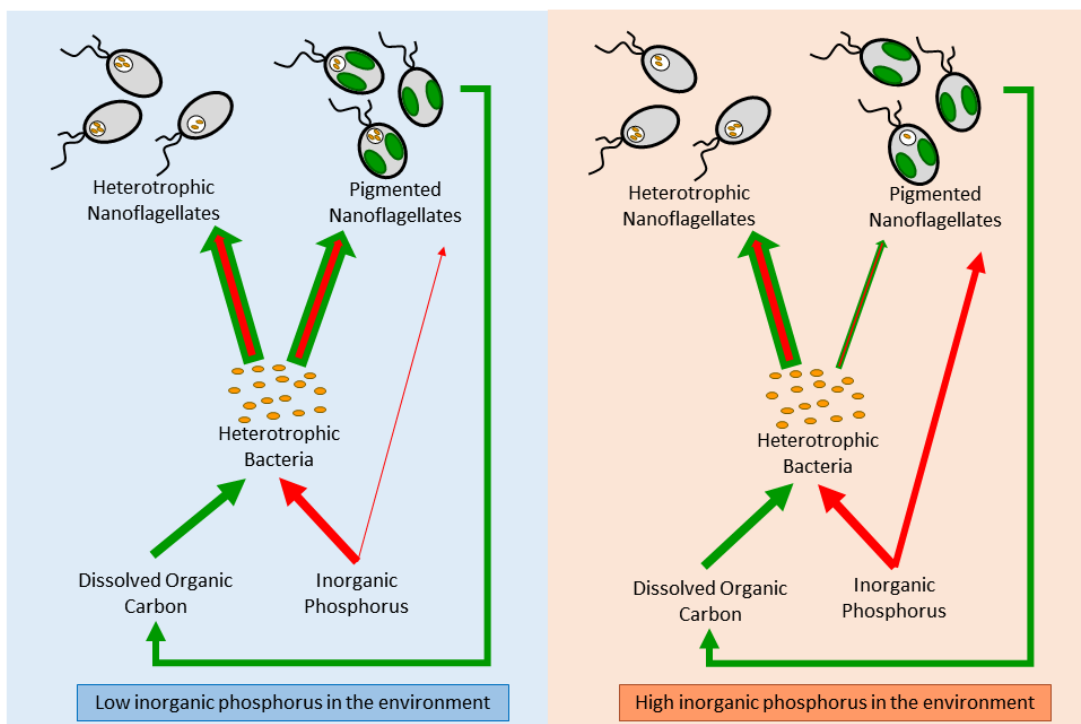
In the phosphorus (P) limited Eastern Mediterranean Sea (EMS) the microbial food web mediates most of the energy and matter flux. In this system, pigmented nanoflagellates (PNF) are important primary producers while, along with heterotrophic nanoflagellates (HNF), they are important consumers of heterotrophic bacteria (HB). In the present work, the combination of phototrophic and phagotrophic nutrition in PNF, termed mixotrophy, is modeled using the concept of the Synthesizing Unit, developed within the frame of DEB theory. The mathematical formulation of mixotrophy, which is P dependent for PNF in the EMS, is incorporated into a DEB model for photosynthetic cells that takes into account the excretion of dissolved organic matter under varying P availability. Finally, a simplified microbial food web model is formulated with the aim to qualitatively explore the pathways of carbon and phosphorus flow through the HB-PNF-HNF link in the EMS. Model simulations suggest that, under P limited conditions, PNF support bacterial production and P uptake by supplying HB with dissolved organic carbon. In turn, PNF fulfill their P requirements through HB consumption, thus holding a key role in P transfer through the microbial food web. Conversely, the relative role of HNF in bacterial grazing is enhanced under P replete conditions, as PNF lower their grazing rates upon HB. The present study highlights the importance of taking into account the flexible physiology of mixotrophic PNF in order to understand the functioning of oligotrophic systems and predict their response to global environmental changes.

Keywords: Eastern Mediterranean Sea, Mixotrophy, Nanoflagellates, Phosphorus limitation, Microbial food web model, DEB theory

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A conceptual model of nanoflagellates − bacteria interactions in the Eastern Mediterranean Sea

Heterotrophic
Nanoflagellates

Pigmented
Nanoflagellates

Heterotrophic
Bacteria

Dissolved Organic
Carbon

Inorganic
Phosphorus

Low inorganic phosphorus in the environment

Heterotrophic
Nanoflagellates

Pigmented
Nanoflagellates

Heterotrophic
Bacteria

Dissolved Organic
Carbon

Inorganic
Phosphorus

High inorganic phosphorus in the environment

The larvae, which eat polystyrene: growth, development, and survival analysis

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Polystyrene (PS), is widely used for the production of foamed insulation boards and packaging. The production of Styrofoam, the most popular form of PS, reaches over a million tons per year in Europe, which makes it one of the major plastic pollutants in the environment. It is easily spread by wind and floats on water, polluting shores and waterways. PS is hardly degradable and an efficient and environmentally friendly method of PS recycling is still needed. Involving living organisms (including microorganisms) in polystyrene degradation seems to be environmentally friendly and economically justified compared to other mechanical, chemical, and thermal methods. The main aim of this study was to assess if the larvae of *Tenebrio molitor* are able to use PS as a source of mass and energy and therefore if they can be used for utilizing polystyrene. The Dynamic Energy Budget (DEB) model was used to analyze the effects of food type on the survival, growth, and development of the larvae. Five possible modes of influence of PS diet on DEB model parameters including a decrease of food availability, an increase in somatic maintenance power, an increase in costs for structure, allocation of energy, and a decrease in somatic maintenance power were investigated. We concluded that changes in the development of larvae fed with PS are mainly caused by a decrease in reserve density and reaction of the organism to the insufficient food supply. Thus, the inability or difficulty in completing the life cycle of the mealworms fed with PS raises doubts about their application in Styrofoam utilization.

Keywords: polystyrene, mealworm, biodegradation, energy budget, modeling

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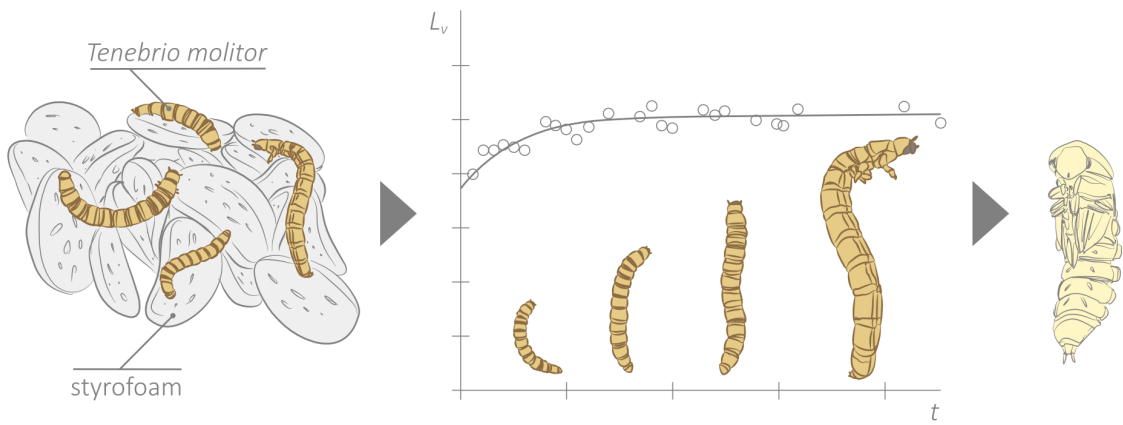
Let the concept of trait be theoretical

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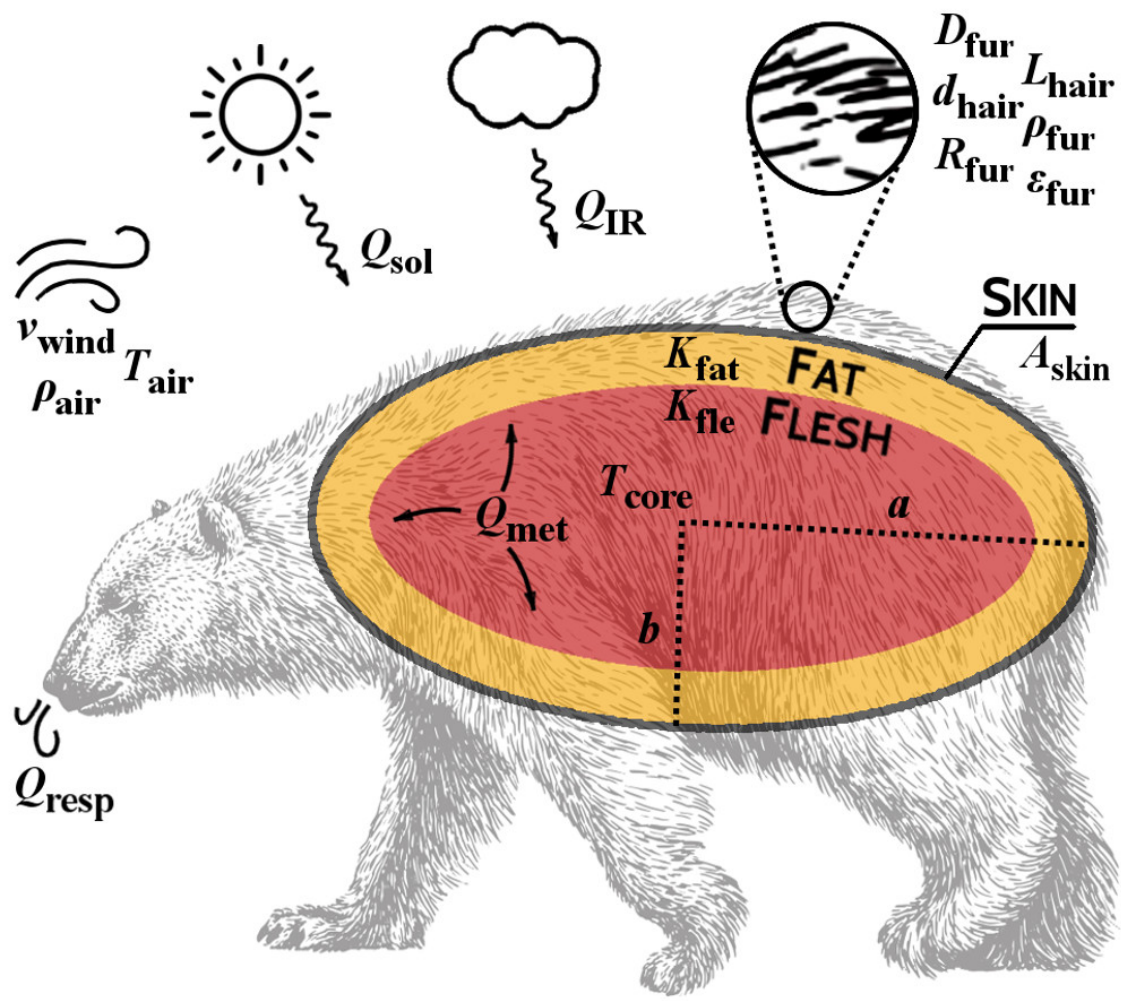[4] VU University Amsterdam – De Boelelaan 1105, 1081 HV Amsterdam, Netherlands
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Traits are increasingly important in ecology, giving birth to many initiatives to collate and integrate trait data into biodiversity databases. Functional traits, that is, those with a definite link to individual survival, development, growth, and reproduction, are of most interest. However, which functional traits should be prioritised and how should we characterise them? Here, we present the advantages of a theoretical perspective for defining functional traits in relation to dynamical systems models of energy and mass exchange that link organisms to their environments. We argue that the theoretical frameworks upon which such models are built (biophysical ecology and metabolic theory) provide clear criteria by which to decide upon functional trait definitions, measurement requirements, and associated metadata. The criteria in question naturally arise via their mathematical connection to model parameters and state variables, and thus to system performance (survival, development, growth, and reproduction). We distinguish between 'descriptive' and 'functional' traits by dividing the latter into four classes: parameter, model, threshold, and estimation, based on whether they are model parameters, define model structure, are threshold state variables, or can be used to estimate model parameters. For practical purposes, we develop a decision tree for this classification and illustrate it in three different contexts: mammalian heat exchange, water exchange, and energy balance. The use of theoretically driven criteria for prioritising the collection of functional trait data will maximise the generality, quality, and consistency of trait databases for comparative analyses. Such databases will simultaneously facilitate the development of integrated predictive modelling frameworks across multiple organisational scales from molecules to ecosystems.

Keywords: biological physics, life history, metabolic ecology, physiological ecology, mechanistic niche models, functional traits

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†Speaker

Q_{sol}

Q_{IR}

D_{fur} L_{hair}
d_{hair} ρ_{fur}
R_{fur} ε_{fur}

v_{wind} T_{air}
ρ_{air}

SKIN
A_{skin}

K_{fat} FAT
K_{fle} FLESH

T_{core}

Q_{met}

a

b

Q_{resp}

DEB theory should not be a dead Christmas tree

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DEB theory has been able to explain and – perhaps even more importantly – unify approaches to many hitherto confusing phenomena and processes, thus becoming undoubtedly THE most successful metabolic theory of life. Kooijman (2020) likens the standard model to a Christmas tree, unique in simplicity and plausibility; only a limited set of ornaments remain to be placed upon the tree. His proposition that no plausible alternatives to standard DEB exist is, however, dangerous - reminiscent of Michelson's thesis proclaiming end of progress in physics just a decade before quantum theory emerged. Despite successes of the standard DEB model, limitations abound that may be fundamental to its core structure. For example, (i) many scalings (e.g. of pM) are at odds with theoretical predictions, (ii) growth of at least some organisms reflects assimilation rather than energy reserves, and (iii) current assimilation rules imply physiologically unrealistic rates of dilution of ingested toxicants, hindering acute exposure modelling. Simple ornaments could resolve some issues, but some lack mechanistic underpinnings, and others threaten to topple the tree. We showcase a transport-based DEB model description that satisfies all existing stylized facts, but also a few more that standard DEB does not. We do not suggest replacing the tree, just that (i) alternatives are possible and should be investigated, and (ii) complacency, rather than excessive ornamentation, poses the greater threat towards DEB theory meeting the fate of a used Christmas tree. DEB theory must not only be alive, but its evolution must be one of our main courses of action. To this end, we should be brave in modifying the tree, and nourish new branches that look promising.

REFERENCE
Kooijman 2020. Ecological Modelling, Elsevier, vol. 428(C):109106

Keywords: general DEB, quick reserve turnover, multicompartmental toxicokinetics, sublethal toxicant effects, Christmass tree and ornaments

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*Speaker

Bayesian estimation of DEB parameters using STAN

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Parameter estimation of dynamic energy budget (DEB) models is a particularly challenging topic. The large number of parameters to be estimated has been claimed to be one of the main technical difficulties that are limiting the expansion of DEB applications. The "Covariation method" (Lika et al. 2011) was a relevant landmark for circumventing the problem. It has been recently revised (Marques et al. 2019) and several improvements in the loss functions have been implemented in DEBtool (Marques et al. 2018). However, (i) between-individual variability and (ii) parameters' uncertainty are not usually considered. The use of a Bayesian inference framework and mixed (hierarchical) models have shown promise for facing these two problems (Johnson et al. 2013; Boersch-Supan & Johnson 2019). Nevertheless, the need for numerically solving a system of coupled differential equations at each iteration may be a computational nightmare. STAN (https://mc-stan.org/), a recently released platform for statistical computing, is particularly appealing for estimating DEB parameters because it offers full Bayesian statistical inference using more efficient algorithms to move MCMC chains (NUTS). Moreover, STAN has some build-in function for numerical integration (e.g., the function integrate_ode_rk45). Here we show some of the technicalities needed for using STAN for DEB parameter estimation at individual level using simulated observational data sets, which allows assessing accuracy and precision. We focused in four particularly relevant parameters (kappa, nu, pAm and kM). Simulated but realistic data of fish length, body wet weight and gonad wet weight have been used as observable variables. The results obtained in a given trial are shown at Figure 1. The limitations of this approach are also discussed: computational time may be a limiting factor and between-parameter correlations (different combinations of values can result in the same observed patterns) may remain as a structural, unsolved problem of DEB modeling.

REFERENCES

Boersch-Supan, P.H. & Johnson, L.R. (2019). Two case studies detailing Bayesian parameter inference for dynamic energy budget models. J. Sea Res., 143, 57–69.

Johnson, L.R., Pecquerie, L. & Nisbet, R.M. (2013). Bayesian inference for bioenergetic models. Ecology, 94, 882–894.

Lika, K., Kearney, M.R., Freitas, V., Veer, H.W. Van Der, Meer, J. Van Der, Wijsman, J.W.M., et al. (2011). The " covariation method " for estimating the parameters of the standard

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[*]Speaker

Dynamic Energy Budget model I: Philosophy and approach. J. Sea Res., 66, 270–277.

Marques, G.M., Augustine, S., Lika, K., Pecquerie, L., Domingos, T. & Kooijman, S.A.L.M. (2018). The AmP project: Comparing species on the basis of dynamic energy budget parameters. PLOS Comput. Biol., 14, e1006100.

Marques, G.M., Lika, K., Augustine, S., Pecquerie, L. & Kooijman, S.A.L.M. (2019). Fitting multiple models to multiple data sets. J. Sea Res., 143, 48–56.

Keywords: Parameter estimation, between, individual variability, uncertainty, Bayesian inference, STAN
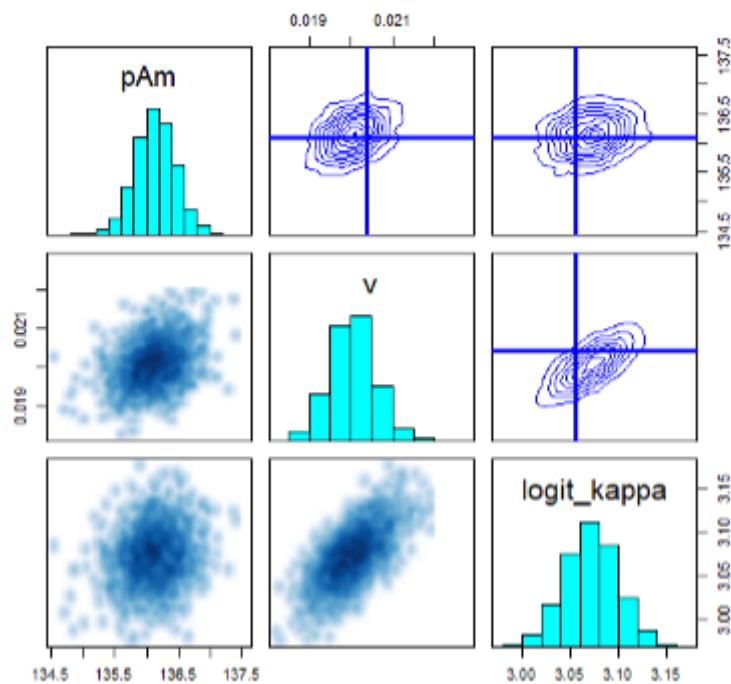

Figure 1: True versus estimated comparison demonstrating that STAN is able to accurately and precisely estimate DEB parameters from simulated but realistic data. The scatter plots show the MCMC values. The histograms show the posterior distributions. Contour plots define the credibility intervals of the parameter estimates. The lines show the true parameter values

Direct greenhouse gas emissions in livestock production

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Livestock production is one of the main contributors to global greenhouse gas (GHG) emissions. The tools provided by the Intergovernmental Panel on Climate Change to estimate GHG emissions (Tier 1 and Tier 2) cannot be used as a tool for advising farmers or national policy on how to minimize GHG emissions because these estimates are not explicitly related to any metabolic properties. For that, we need a metabolic model that obeys mass and energy balances and that models the trade-offs between different allocations of energy in the organism, throughout the life cycle, as a function of environmental variables such as temperature and the amount and type of food. The Dynamic Energy Budget (DEB) Theory ensures mass conservation and models the transformations of state variable and product formation, allowing for explicit GHG emissions estimates. Therefore, we used this theory to build models for different bovine breeds, including autochthonous breeds from Portugal, such as Alentejana, and more international breeds such as Angus. The goodness-of-fit of DEB models to data is good for all breeds. Differences in DEB breed specific parameters, such as the maximum reserve density and the maximum specific assimilation rate, explain differences in GHG emissions, among other metabolic traits. Accumulated methane and nitrogen production ranges between 0.2 and 2, and 0.1 and 0.7 kg per kg of body weight, respectively. In terms of accumulated direct GHG emissions, there is a strong dependence on breed and age.

Keywords: Climate change, Greenhouse gas emissions, Cattle metabolism

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*Speaker

The complexity of mixture toxicity and multiple stressors: how incorporating suborganismal processes into dynamic energy budgets can provide a path forward

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The discovery of widespread endocrine disruption led to a paradigm shift in toxicity testing – moving from whole organism dose response studies to high-throughput suborganismal, sub cellular assays to determine biological pathway perturbations. The adverse outcome pathway was formed to organize information so that these suborganismal responses could be anchored in whole organism responses. As the framework evolved, large, complex datasets were organized to inform predictive (quantitative) toxicity patterns. While the AOP framework has been immensely valuable for problem formulations, hypothesis testing, organization and communication, there are limitations related to cross-species extrapolations and life history responses. Additionally, variable environmental conditions such as food limitations and temperature are usually indicated as modulating factors and are not well characterized.. We show that these shortcomings could be overcome using DEB theory. Research in our group explored different approaches to link AOPs to DEB theory using case studies and specifically designed laboratory experiments that include multiple stressors and chemical mixtures. Our approaches indicate that these linkages are indeed possible and could be incorporated into ecological risk assessment.

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A DEB egg-laying module for birds exposed to pesticides

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Environmental risk assessment (ERA) of a commercially important fungicide (fluopyram) is currently based on the statistical analysis of data collected from standard OECD Guideline #206 bird reproduction experiments. These studies report feeding, growth and reproduction combined with observed F1 hatchling size and subsequent growth. We here focus on a model bird species: the bobwhite quail. The exposure in those laboratory studies (constant concentrations over 20 weeks) does not match the realistic exposure scenarios (short peak exposures) in the field, leading to differences in the expected effects over time between the two exposure situations. This impacts the capacity to (i) assess the risk of real-life applications of the fungicide to real world bird populations and (ii) limits to applicability of statistical methods to perform scenario analysis and optimize application rates. Dynamic Energy Budget (DEB) models applied to eco-toxicology overcome this challenge. DEB models are well tested for many bird species across all major bird phyla. In this study, we performed an in-depth literature search and then fit the DEB model to all relevant data simultaneously. We obtained remarkably good fits for: embryo development, growth, and reproductive output. Modelling results suggest that during the first few weeks, chicks eat more (or different food) compared to their later life. Furthermore, female quails eat more than predicted by the DEB model during egg-laying. New assumptions were implemented specifying how the extra food is allocated between maintenance, growth and reproduction. We then implemented a toxicokinetic-toxicodynamic (TKTD) module and estimated TKTD parameters from two separate standard bird reproduction studies. TD parameters such as the no effect concentration, coupled with TK parameters like the elimination rate, improve our understanding of possible effects on wild birds. We present our model fits to these detailed toxicity test data and discuss our results in the context of both bird eco-physiology and a next generation intelligent ERA.

Keywords: OECD birds reproduction experiment, egg, laying module, TKTD

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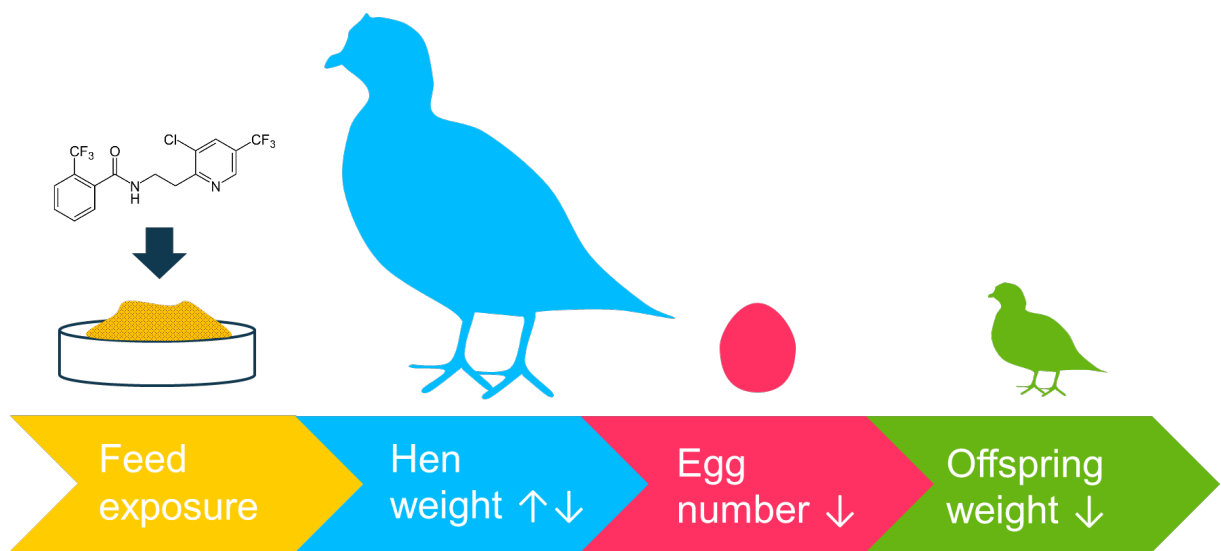
Feed exposure → Hen weight ↑↓ → Egg number ↓ → Offspring weight ↓

Alive and kicking? - Earthworm cocoon test for TKTD Modelling in soil risk assessment of chemicals

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In soil risk assessment, toxicokinetic-toxicodynamic (TKTD) modelling is considered to be not yet ready for use. Reasons include the heterogeneous environment, the more complex sampling methods which make it challenging to measure endpoints over time and unclear exposure. Especially data on biological data like growth and reproduction observed for multiple time points is scarce and chemical measurements are not required in the standard tests. However, TKTD modelling may provide a meaningful refinement also in soil risk assessments. Currently used in risk assessment for earthworms is the earthworm reproduction test OECD 222. We developed a test design which is aligned with the existing test setup of OECD 222 and, with small adaptions, provides data which are needed for TKTD modelling. In this study we show an example of how this new data with carbendazim and *Eisenia fetida* can feed a Dynamic Energy Budget Theory (DEB)-TKTD model and its possible future use in risk assessment.

On basis of the existing entry for *E. fetida* in the Add-my-Pet database, different physiological modes of actions were implemented to allow for parameterisation of the sublethal effects.

The new cocoon test showed a dose-response relationship for growth and reproductive performance.

The parameterized model was able to describe the patterns observed in the experiments. Increased somatic and maturity maintenance costs were assumed to be the primary mode of action resulting in reduced growth and production of neonates. As the number of juveniles per cocoon decreased with increasing exposure concentrations, hazard during oogenesis was employed as a secondary mode of action.

The proposed earthworm cocoon test with its temporally resolved biological data enables the use of DEB-TKTD modelling in soil risk assessment and can serve as possible refinement step. With this kind of modelling that modes of action of a substance can be discovered and well described.

Keywords: physiological modes of action, earthworm, ecotoxicology

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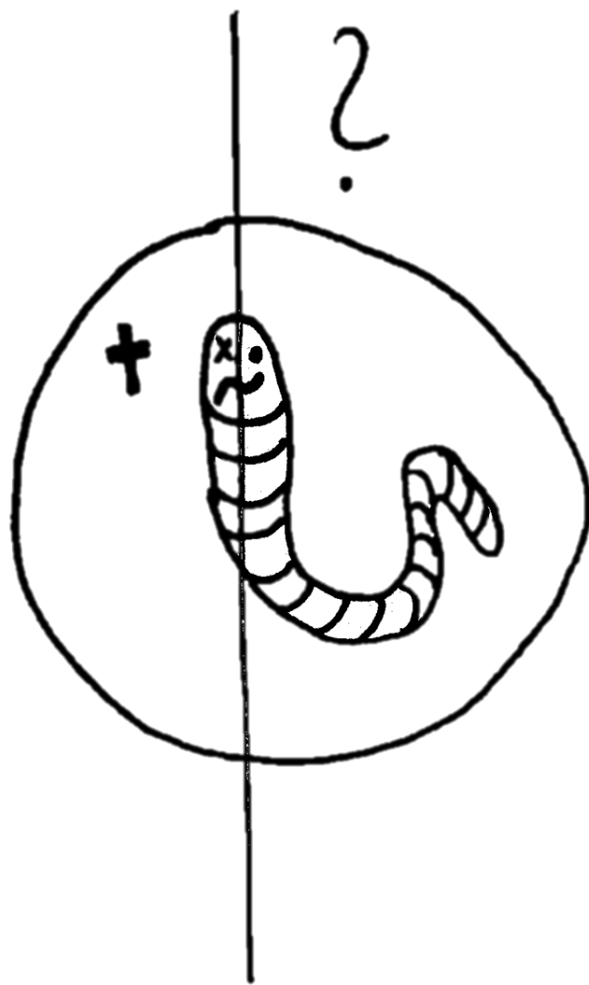
Impacts of climate change in temperate and sub-tropical fish species

José Moreira [*][†][1], Ana Luísa Maulvault [2,3,4], António Marques [2,4], Rui Rosa [3], Ana Mendes [4], Pedro Pousão-Ferreira [4], Patrícia Anacleto [2,3,4], Gonçalo Marques [1]

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Marine ecosystems are currently experiencing the effects of climate change, namely rising temperatures and ocean acidification, which are expected to aggravate over the next decades. To assess how these effects may impact the juvenile growth and maturity development of marine fish, a metabolic model based on the Dynamic Energy Budget (DEB) theory was built for two temperate species (*Diplodus sargus* and *Solea senegalensis*) and one subtropical/tropical species (*Diplodus cervinus*) to simulate how these respond to different environmental conditions. Parameters for the model were reestimated for both *Diplodus* species using the AmP estimation procedure, with additional data collected from farmed fish in a controlled environment, together with data already available on the AmP collection files and other references. Absent from the AmP collection, a new parameter estimation was conducted for *Solea senegalensis* with data from farmed fish and other references, using the same procedure. For each species, four different climate change scenarios were evaluated, these being the combinations of two different temperatures and two different pH levels, with values differing for each species. For all species, juvenile growth was shown to be earlier and/or at a faster rate for the specimens exposed to a higher temperature. For both *Diplodus* species, the pH level showed no relation with growth, while for *Solea senegalensis*, juvenile growth was shown to be delayed for the specimens exposed to a lower pH level.

Keywords: Climate change, Ocean acidification, Global warming, Fish metabolism

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DEB modelling and IPCC accounting methods: a bridge between frameworks

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Livestock production is one of the main contributors to global greenhouse gas (GHG) emissions. The tools provided by the Intergovernmental Panel on Climate Change (IPCC) to estimate GHG emissions (Tier 1 and Tier 2) cannot be used as a tool for advising farmers or national policy on how to minimize GHG emissions because these estimates are not explicitly related to any metabolic properties. Nevertheless, they provide important information that should be incorporated in a DEB framework to provide a more sophisticated metabolic model that obeys mass and energy balances and that models the trade-offs between different allocations of energy in the organism, throughout the life cycle. In this work we present a bridge between the IPCCC accounting methods and DEB modelling.

Keywords: Climate change, Greenhouse gas emissions, Cattle metabolism

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*Speaker

# Towards a facilitated use of Modelling in Environmental Risk Assessment

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Within EU only, more than 100000 man-made chemicals are awaiting assessment of their risk to the environment. Based on statistical analyses providing toxicity indices at different tiers, risk assessment faces today new challenges to meet all expectations in terms of regulatory requirements together with the use of advanced and sound statistical methods. In particular, EFSA today recommends a clear and unambiguously identification of uncertainty sources, the use of TKTD models to refine tier 2 risk assessment in particular for plant protection products acting on aquatic organisms when exposed to environmentally realistic concentration profiles and that models be documented in a transparent way ensuring reproducible results. If plenty ideas, methods and tools already exist in the academic world to meet these expectations, practitioners struggle in appropriate them for reasons mostly attributable to modelers themselves. These reasons mainly come from lacks of support: (1) to easily quantify uncertainties, then their propagation to model outputs and subsequent predictions; (2) to better accept changing paradigm using new modelling approaches often appearing as black boxes, together with a lack of support to fully perceive the concrete added-value of these novelties for their daily work; (3) to easily interpret goodness-of-fit criteria and therefore trust model results in their ability to support decisions from predictions; (4) to appropriate recent user-friendly turn-key facilities, while already recognized as automatically providing toxicity indices of interest in full compliance with regulatory guidelines and risk assessment decision criteria. Based on concrete case studies dealt with a suite of convenient and relevant tools freely available within an all-in-one facility, this presentation will illustrate how the above-mentioned difficulties can be overcome to facilitate the use of models in the environmental risk assessment (ERA).

Keywords: TKTD models, calibration, validation, prediction, uncertainty, accessibility

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[*]Speaker
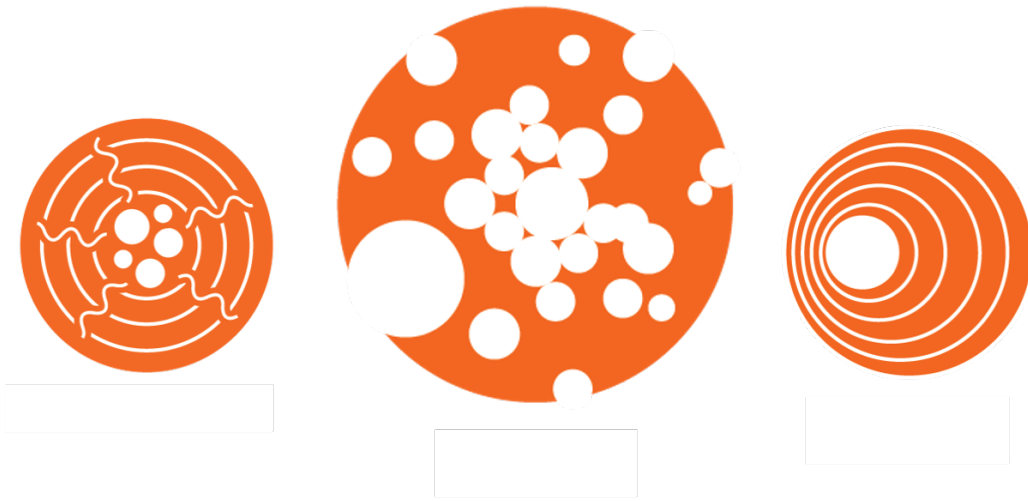
Dynamic Energy Budget Models: Fertile Ground for Understanding Resource Allocation in Plants?

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How an organism allocates its endogenous resources to alternative physiological functions strongly influences its fitness through effects on growth, survival, and reproduction. Because resource allocation is a zero-sum game, trade-offs arise that depend on environmental conditions. Moreover, because allocation of endogenous resources affects the acquisition of exogenous resources and subsequent growth, complicated feedbacks can arise between resource allocation and access. Empirically, resource allocation is very challenging to measure directly, and so has often been approached using mathematical models, such as Dynamic Energy Budget (DEB) models. Dynamic Energy Budget models offer a powerful and generalizable framework for modeling resource allocation, although they have been less applied to plants, making this fertile ground for expansion and development of DEB theory. The fact that all plants require a very similar set of exogenous resources, namely light, water, and nutrients, integrates well with the DEB modeling framework in which a small number of variables and fundamental processes linked through pathways represent an organism's state as it changes through time. A number of features of plants, many of which arise because they are sessile, make resource allocation particularly fundamental to their life histories, and many of these are thorny problems in plant biology that could be informed by a DEB approach. For example, the inability to flee herbivores and predators selects for resource allocation to defense, which may increase survival, but come at the cost of growth and reproduction. The inability to move if the environment becomes unfavorable selects for phenotypic plasticity or dormancy. The fact that a plant's largely indeterminant growth changes its own environment, particularly for long-lived plants like trees, selects for recycling and re-allocation of resources to different organs or tissues or even locations within the plant's body. Many plants' syntrophic relationships with nitrogen-fixing bacteria or mycorrhizal fungi in and on their roots extend the consideration of trade-offs in resource allocation to encompass the competing interests of both partners. There is much unrealized potential for using the DEB framework to address fundamental, yet unanswered questions about how plants have navigated evolutionary trade-off landscapes to produce the diversity of plant life history strategies that we see on Earth.

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Inferring functional traits in a deep-sea wood-boring bivalve using dynamic energy budget theory

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In the deep sea, there is a gap of knowledge on functional traits of species at all stages of their life cycle. Dynamic Energetic Budget (DEB) theory was proven to be an original framework to estimate functional traits by the way of modeling. An abj-DEB model was successfully developed in the deep-sea woodeater bivalve *Xylophaga atlantica* . Most of core and primary parameter values of the abj-DEB model of *X. atlantica* were in the range of those found in shallow marine bivalve species except for the energy conductance ($\dot{v}$), the energy required to reach puberty (E_H^p), and the maximum reserve capacity $[E_m]$. $\dot{v}$ and E_H^p, were much lower than in other bivalves for the same range of body size. $[E_m]$ was higher highlighting a better survival in starvation conditions. A series of functional traits were simulated in the deep-sea bivalve according to different scenarios of food density and temperature highlighting weak cumulative number of oocytes, slow von Bertalanffy growth rate and small maximum body size, but an extending pelagic larval duration at deep-sea environmental conditions. Moreover, DEB-modeling has helped explaining how some *X. atlantica* male individuals remain dwarfs while still reproducing by changing to 0.06 (instead of 0.73). The modeling of these traits is critical to decipher fundamental ecological knowledge and we suggest the use of DEB-modeling in further deep-sea studies.

Keywords: bivalve, deep sea, dispersal, dwarfism, traits, fitness

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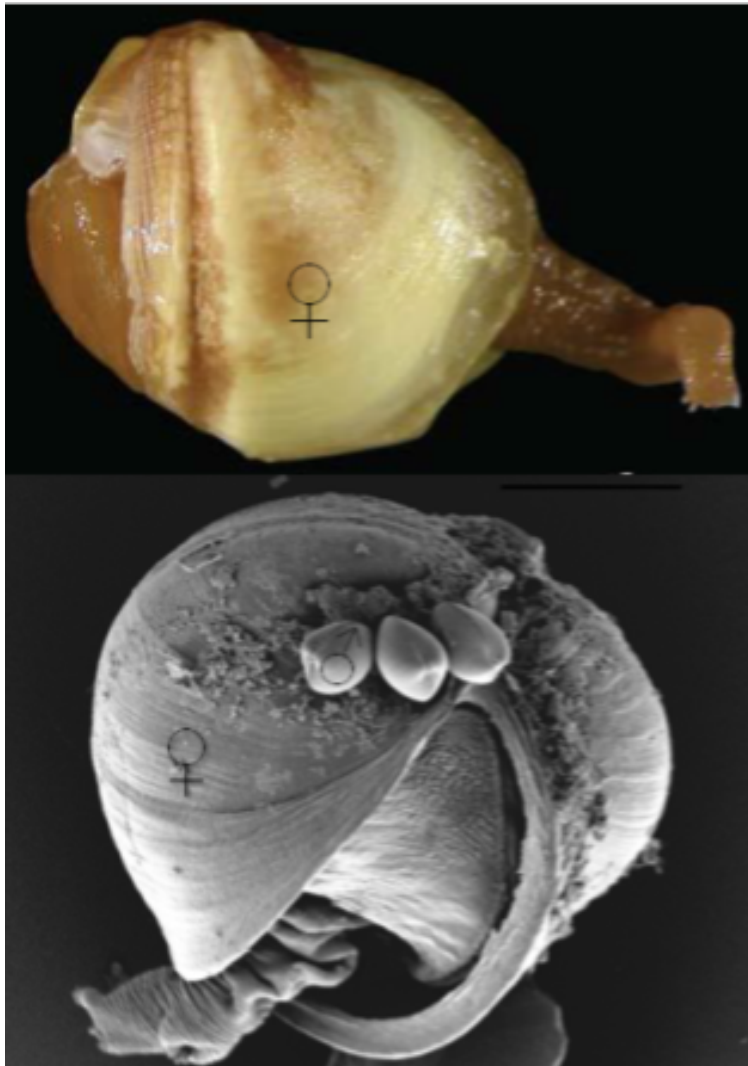
Projecting the effect of ocean acidification and warming on two Atlantic surfclam (*Spisula solidissima*) populations through a Dynamic Energy Budget model

Emilien Pousse * [1], Matthew Poach [1], Dylan Redman [1], George Sennefelder [1], David Veilleux [1], Melissa Krisak [1], Mark Dixon [1], Judy Li [1], Daphne Munroe [2], Deborah Hart [3], Daniel Hennen [3], Gary Wikfors [1], Shannon Meseck [1]

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Global carbon dioxide emissions have increased appreciably since the industrial revolution. The ocean absorbs one third of the CO_2 emitted, resulting in the ocean becoming less basic. Coastal ecosystems, where high nutrient levels and rapid growth and decomposition of plankton further reduce pH, are especially vulnerable to water acidification. When facing high CO_2 levels marine organisms may expend more energy to maintain homeostasis and to build and maintain shells. The Atlantic surfclam (*Spisula solidissima*), which supports an economically important fishery in the northwest Atlantic, is particularly sensitive to ocean acidification (OA), with lower growth and effects on physiological rates. A 12-week experiment was conducted in which 648 surfclams fed ad libitum were exposed to varied pCO_2 levels (566, 1380, 2164 ppm) at 16 °C. OA effects on bioenergetics were studied through a Dynamic Energy Budget (DEB) model. Respiration, excretion, feeding, and growth rate measurements were regularly measured. Results showed that OA induced a decrease in feeding rate and modified the catabolized energy (i.e. energy lost through respiration and excretion) with a threshold effect. With the assumptions that OA affects surfclam feeding and maintenance costs, a model scaling the OA effect as a function of its intensity was calibrated on those data. Growth and reproduction potential of two surfclam populations (Georges Bank and Mid-Atlantic Bight) were explored by forcing the calibrated model with pCO_2 and temperature projected by RCP scenarios from IPCC.

Keywords: Bivalves, Ocean Acidification, Climate change, Atlantic Surfclam

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Unusually paced life history strategies of marine megafauna drive atypical sensitivities to environmental change

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Predicting from life history strategies how populations respond to environmental change is a current challenge in demography. Marine megafauna display unusual combinations of life history traits: many rays, sharks and turtles are long-lived, characteristic of slow life histories, but turtles have high reproduction rates and juvenile mortality, characteristic of fast life histories. This raises the question if marine megafaunal responses to environmental variability follow conventional life history patterns, including the pattern that fast life histories are more sensitive to environmental autocorrelation than slow life histories. To answer this question, we used a functional trait approach, where growth and reproduction are described using an energy budget model, to quantify for different species of mobulid rays, cheloniid sea turtles and carcharhinid sharks how their life history, average size and population growth rate respond to changes in environmental autocorrelation and in the frequency of good environmental conditions. We found that the faster life histories were more sensitive to temporal frequency of good environment conditions, but both faster and slower life histories were equally sensitive, although of opposite sign, to environmental autocorrelation. These atypical patterns likely follow from the unusual megafaunal life-history traits. Our findings highlight how general patterns in life histories and population responses may not always be expected, and signify the importance of unravelling the mechanistic links between life history traits and population growth to accurately predict population responses to change.

Keywords: Carcharhinidae, Cheloniidae, dynamic energy budget, integral projection model, fast–slow life history speed continuum, Mobulidae

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Intra-specific variation of life-history traits in Atlantic salmon: environmental and genetic factors

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The mechanisms of energy acquisition and allocation impact organisms' life history strategies and their ability to react to environmental variations. Describing these bioenergetic mechanisms through the thermodynamic principles common to all living organisms has been shown to be extremely effective in predicting environmental effects (temperature, quality and quantity of food, for example), but this type of approach does not yet integrate intra-specific variation. In some species, such as salmonids, subtle quantitative variation in environmental conditions and genetic background can lead to striking differences in life-history traits, such as age at maturation, which are even referred to as alternative tactics and are crucial to the understanding of populations' dynamics and evolution. I will present my team's results investigating the sources of intra-specific life-history variation in Atlantic salmon, with a focus on (1) the effect of environmental variation (early-life conditions, inter-annual variation) on growth and life-history traits in a wild population and (2) the effect of artificial selection on DEB parameters.

Keywords: life history strategies, alternative reproductive tactics, intraspecific variation, salmon

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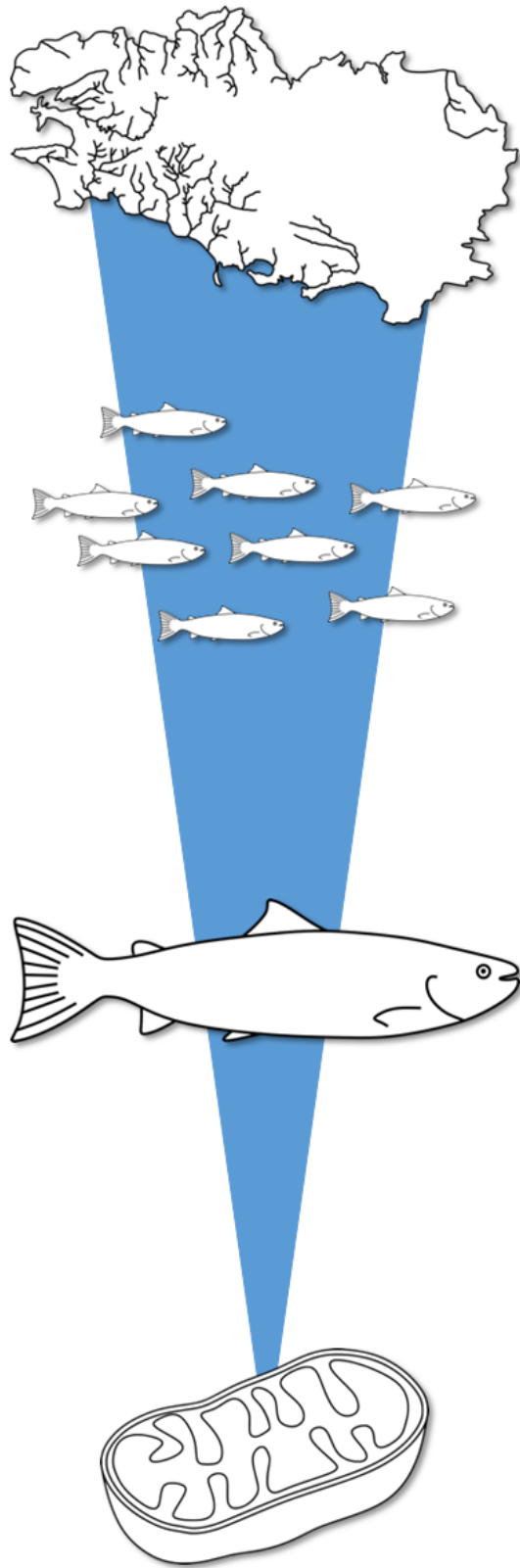
Resource and seasonality drive interspecific variability in the Dynamic Energy Budget model

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Resource and seasonality drive interspecific variability in the Dynamic Energy Budget model

Animals show a vast array of phenotypic traits in time and space. These variation patterns have traditionally been described as ecogeographical rules; for example, the tendency of size and clutch size to increase with latitude (Bergman's and Lack's rules, respectively). Despite considerable research into these patterns, the processes behind trait variation remain controversial. Here, we show how food variability, which determines individual energy input and allocation trade-offs, can drive interspecific trait variation. Using the standard dynamic energy budget (DEB) model, we simulated different food environments as well as interspecific variability in the parameters for energy assimilation, mobilization, and allocation to soma. We found that interspecific variability is greater when the resource is non-limiting in both constant and seasonal environments. Our findings further show that individuals can reach larger biomass and greater reproductive output in a seasonal environment than in a constant environment of equal average resource due to the peaks of food surplus. Our results agree with the classical patterns of interspecific trait variation and provide a mechanistic understanding that supports recent hypotheses which explain them: the resource and the eNPP (net primary production during the growing season) rules. The current alterations to ecosystems and communities make disentangling trait variation increasingly important to understand and predict biodiversity dynamics under environmental change.

Keywords: Bergman's rule, body size, eNPP, Lack's rule, trait variation, resource availability

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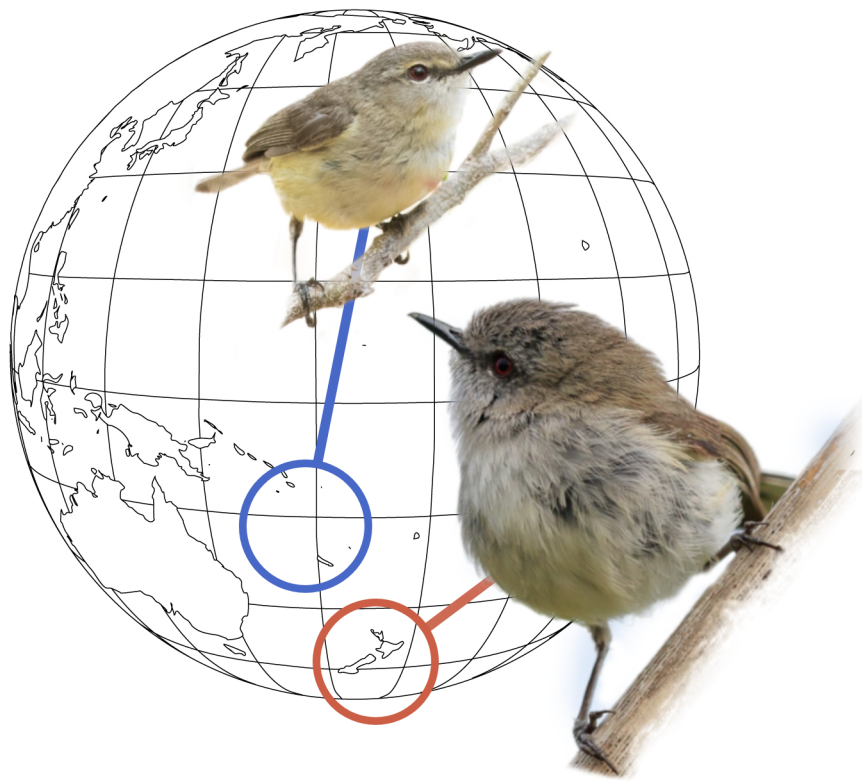
Figure 2: The fan-tailed gerygone (Gerygone flavolateralis) and the grey warbler (G. igata) serve as a case study to illustrate our findings. Both species reach similar adult sizes; however, the clutch size of the grey warbler from temperate areas of New Zealand is almost four times larger than that of the fan-tailed gerygone from tropical New Caledonia and Vanuatu.

Poster Presentations

Individual-based model of population dynamics in a sea urchin of the Kerguelen Plateau (Southern Ocean), Abatus cordatus, under changing environmental conditions

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The Kerguelen Islands are part of the French Southern Territories, located at the limit of the Indian and Southern oceans. They are highly impacted by climate change, and coastal marine areas are particularly at risk. Assessing the responses of species and populations to environmental change is challenging in such areas for which ecological modelling can constitute a helpful approach.
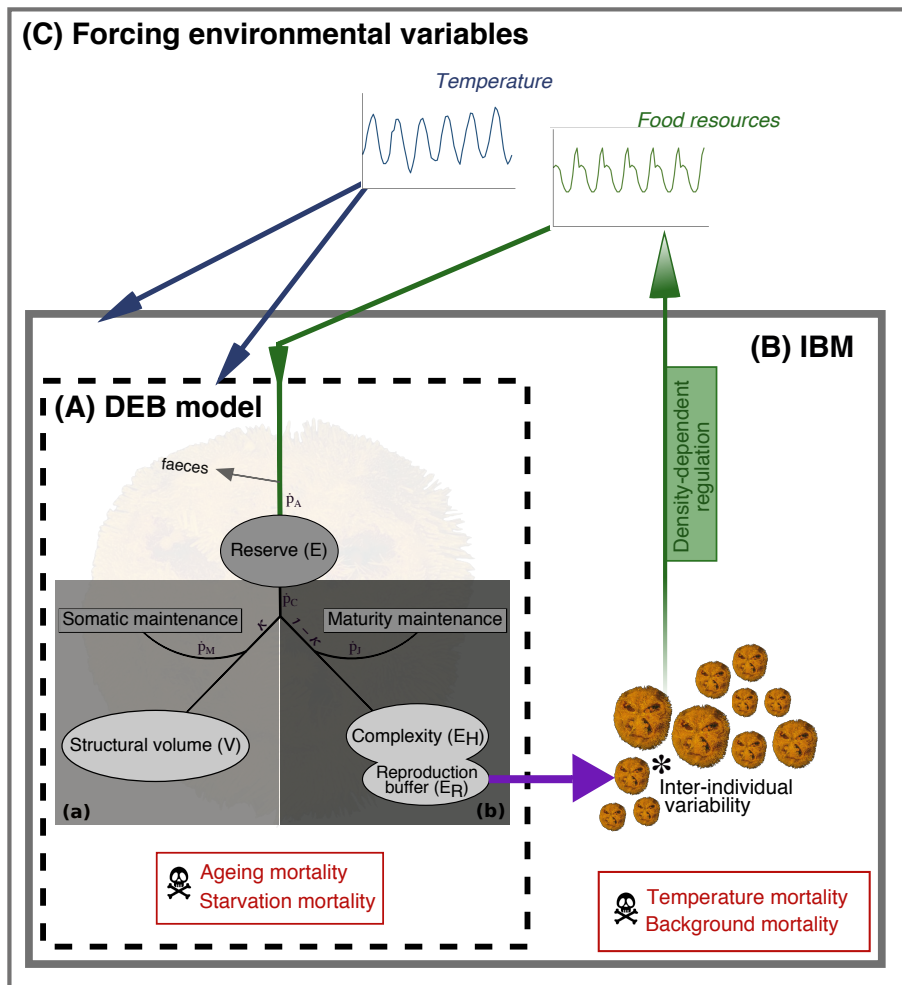
In the present study, a DEB-IBM model (Dynamic Energy Budget – Individual-Based Model) was generated to simulate and predict population dynamics of a common benthic species of shallow marine habitats of the Kerguelen Islands, the sea urchin *Abatus cordatus*. The model relies on a DEB model developed at the individual level. Upscaled to an individual-based population model (IBM), it then enables to model population dynamics through time as a result of individual physiological responses to environmental variations.

The model was successfully built for a reference site to simulate the response of populations to variations in food resources and temperature. Then, it was implemented to model population dynamics at other sites and for the different IPCC climate change scenarios RCP 2.6 and 8.5. Under present-day conditions, models predict a more determinant effect of food resources on population densities, and on juvenile densities in particular, relative to temperature. In contrast, simulations predict a sharp decline in population densities under conditions of IPCC scenarios RCP 2.6 and RCP 8.5 with a determinant effect of water warming leading to the extinction of most vulnerable populations after a 30-year simulation time due to high mortality levels associated with peaks of high temperatures.

Such a dynamic model is here applied for the first time to a Southern Ocean benthic and brooding species and offers interesting prospects for Antarctic and sub-Antarctic biodiversity research. It could constitute a useful tool to support conservation studies in these remote regions where access and bio-monitoring represent challenging issues.

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(C) Forcing environmental variables

Temperature

Food resources

(B) IBM

Density-dependent regulation

(A) DEB model

faeces

$\dot{p}_A$

Reserve (E)

$\dot{p}_C$

Somatic maintenance

κ

$1-\kappa$

Maturity maintenance

$\dot{p}_M$

$\dot{p}_J$

Structural volume (V)

Complexity (E_H)

Reproduction buffer (E_R)

(a)

(b)

Inter-individual variability

Ageing mortality
Starvation mortality

Temperature mortality
Background mortality

Keywords: Kerguelen Islands, climate change, model sensitivity, endemic echinoderm

2

Enchytraeus crypticus, a suitable soil species for DEB-TKTD modelling

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The Dynamic Energy Budget Theory (DEB) enables modelling the effects of chemical stressors on organism life cycle though the coupling with toxicokinetic-toxicodynamic (TK-TD) models. While good progress has been made in the development of DEB models for aquatic organism, DEB models for soil fauna are scarce and underdeveloped. Enchytraeids (Annelida: Clitellata) are model organisms in soil ecology and ecotoxicology, recognized as indicators of biological activity in soil, and chemical stress in terrestrial ecosystems. Despite that, there is no DEB model for this family yet, to assess the impact of chemicals on soil ecosystem (as far as we know, and according to the add-my-pet database). We here aimed at developing a DEB model for *Enchytraeus crypticus,* and use it to simulate the impact of chemicals on its life cycle. We first collected data on growth and reproduction at 3 different feeding levels to parametrize a DEBkiss model (a reserve-less DEB model). The only required modification from the standard DEBkiss model was the addition of a size-dependent food limitation for juveniles, because, like nematodes or earthworms, *E. crypticus* presents a slow initial growth phase which does not fit the von Bertalanffy growth curve under constant conditions. We next used the model to assess the effects of a toxic compound for *E. crypticus* (cypermethrin) on its life cycle (under *ad libitum* feeding condition based on the first experiment) with a DEBkiss-TKTD model. Model simulations showed good fits of the data for all treatments including the control, and highlighted that the more likely physiological mode of action (pMoA) for this insecticide was an increase of the growth energy cost. *E. crypticus* appeared as a suitable soil species for DEB-TKTD modelling to improve the ecological risk assessment for terrestrial ecosystems.

Keywords: Soil organisms, potworms, toxicokinetic, toxicodynamic, DEBtox.

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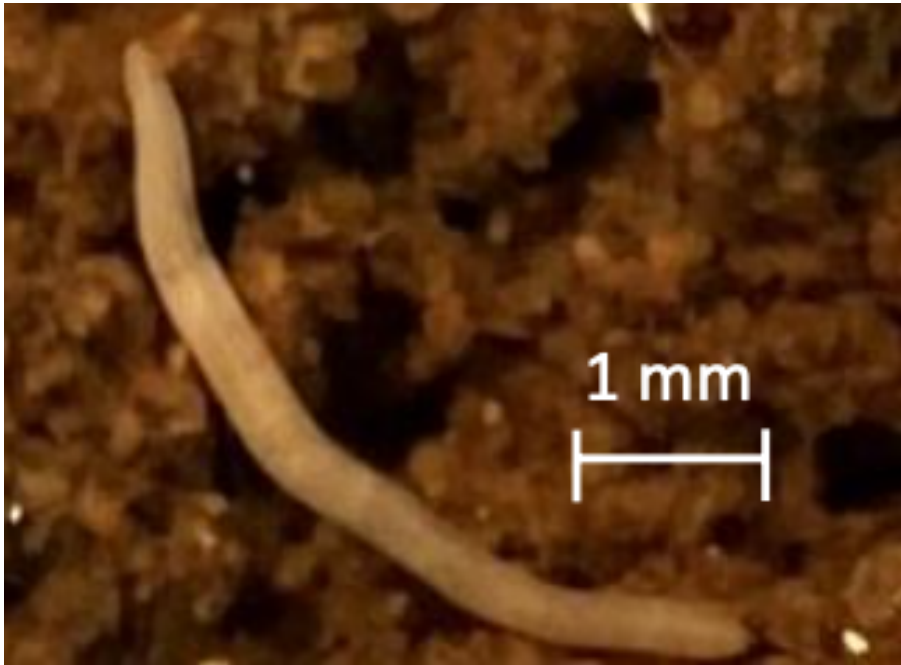
Conceptual DEB coupled agent-based model for ticks' species.

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Ticks are vectors of multiple pathogens responsible for zoonoses and significant economic losses in livestock. For the monitoring of vector-borne diseases, further studies on the population dynamics of ticks and their interaction with the environment are essential. Agent-Based Models (ABMs) are widely used in decision-making and for simulating tick-borne diseases and tick's population. Hence, the purpose of our work is to develop a conceptual ABM model following the ODD (Overview, Design concepts, and Details) protocol to evaluate the influence of climate factors on the dynamics of ticks in the first place and, secondly, to assess the most effective tick control strategy in monitoring the tick population. The underlying mechanisms of life-stage transitions of ticks are based on Dynamic Energy Budget DEB theory. The preliminary results allow to have a conceptual model that will be evaluated computationally in a further study. They will help determine the distribution of common ticks' species in Tunisia and the best monitoring strategy. Also, they will explain the relative importance of the interaction of tick population density, host dispersal (food availability) and environmental conditions.

Keywords: DEB theory, tick life cycle, agent based models, ticks monitoring, Climate change

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Std instead of abj type DEB model should be assumed when fitting freshwater crayfish ontogeny

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Freshwater crayfish have evolved from marine crustaceans, losing a larval (planktonic) stage along the way. This resulted in a shorter and simpler ontogeny compared to their marine relatives: the little crayfish stay attached to their mother after hatching, and at the onset of feeding ("birth" in DEB) they already physically resemble juveniles. Most of the crustaceans in the AmP database are, however, marine decapods, and the prevailing model type for crustaceans is therefore the abj-type DEB model. Unlike the standard model which assumes a constant metabolism throughout the life cycle, the abj model has a slower embryonic phase, with metabolism accelerating between birth and the turning point called metabolic metamorphosis. The metabolic metamorphosis most often (but not always) coincides with physical metamorphosis, i.e., the individual transforming from the larval into the juvenile stage. In this study, we compared performances of abj and std types of DEB model for freshwater crayfish. We applied the std-type model and compared its fit to abj-type model for the two existing freshwater crayfish entries in AmP database (signal crayfish, *Pacifastacus leniusculus* and noble crayfish, *Astacus astacus*), as well as for an additional species we added to the database (marbled crayfish, *Procambarus viriginalis*). For marbled crayfish, we included temperature sensitivity via multi-parameter Arrhenius correction. For all crayfish, we allow for a delay in onset of embryonic development, or a time needed to build up the reserve mobilization pathways - parameter t_0. We find that the std model fully describes the ontogeny of freshwater crayfish, resulting in predictions that match the observations of growth (age-length, age-weight), development (age at hatching, birth, puberty), and energetics (initial energy in an egg). We therefore suggest that the simpler std-type model be preferentially used over the abj-type model when fitting parameters for freshwater crayfish.

Keywords: freshwater crayfish, metamorphosis, metabolic acceleration, model selection
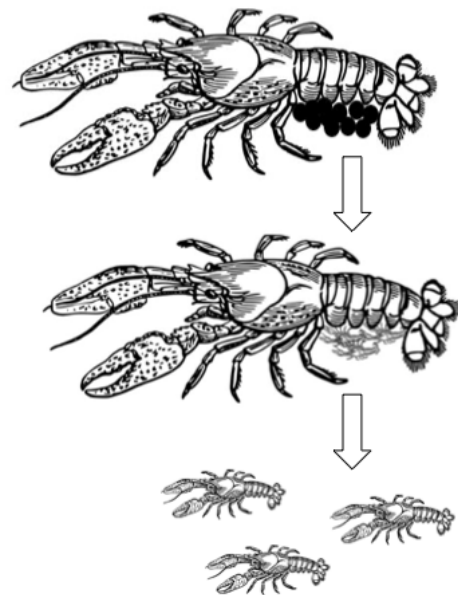
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MARINE – abj type model
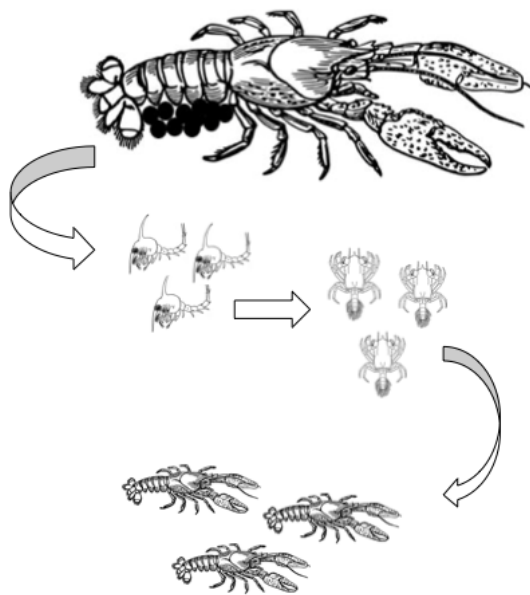
FRESHWATER - std OR abj type model ?

Building a Dynamic Energy Budget for A. poculata: modeling and parameterizing facultative symbioses

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Under global change conditions, many tropical corals have experienced a breakdown of their obligate relationship with their endosymbiont, leading to dysbiosis (bleaching) and ultimately mortality. At the edges of their physiological limits, corals may be more vulnerable to mortality due to increased energy expenditure necessary for survival in these challenging environments. But how much energy is needed to survive? A dynamic energy budget (DEB) is a computationally-heavy mathematical model of the energetic intake and expenditures of an organism. Modelling a coral's DEB is therefore a useful tool for evaluating its resilience to global change. DEBs can provide insight into whether corals have the necessary resources to develop, reproduce, and maintain homeostasis in changing environments. The temperate coral *Astrangia poculata* is found across the Atlantic US, and the northern end of its range is Massachusetts, which is highly vulnerable to ocean warming. *A. poculata* provides a unique opportunity to investigate the energetic costs and benefits of coral-algal associations because it is facultatively symbiotic, occurring both with (symbiotic) and relatively without (aposymbiotic) endosymbionts. We propose a DEB model to examine energy flux in symbiotic and aposymbiotic *A. poculata* corals, building upon existing physiological data and adding remaining empirical measurements needed to comprehensively complete energy calculations. This custom-built model will enable parameterization to test the effects of stress (e.g. increasing temperatures, ocean acidification, etc) on the physiology (growth rate, respiration rate, photosynthetic efficiency) of any facultatively symbiotic coral.

Keywords: Corals, facultative symbiosis, ecophysiology, global change

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Can DEB models infer metabolic differences between intertidal and subtidal morphotypes of the Antarctic limpet *Nacella concinna* (Strebel, 1908)?

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In the context of intensifying threats of climate change on marine communities, ecological models are widely used and applied for conservation strategies, though polar studies remain scarce given the limited number of datasets available. Among models, correlative models (e.g. Species Distribution Models, SDM) describe the occurrence-environment relationship; mechanistic (physiological) models (e.g. Dynamic Energy Budget models, DEB) study the influence of environmental conditions on organism metabolic performances and population dynamics. Integrating both approaches is powerful and complementary, as it allows to better estimate the species realised niche (assessed by correlative approaches), by adding the effect of environmental inputs on species physiology (the fundamental niche, estimated by mechanistic approaches).

Here, we used data from a long-term observing network located in the Kerguelen Islands, to implement for the first time, integrated models to predict the distribution of an endemic sub-Antarctic sea urchin, Abatus cordatus (Verrill, 1876) as a response to environmental drivers. We compared the performances of simple and integrated approaches to predict A. cordatus distribution according to seasonal variations. Two integrated approaches were studied and performed by either (1) including the spatial projection of the DEB model as an input layer inside the SDM ('integrated SDM-DEB' approach) or (2) using a Bayesian inference procedure to use DEB model outputs as priors of the Bayesian SDM ('integrated Bayesian' approach). Several DEB outputs were used and compared, including the predicted available energy in the reserve compartment, the predicted amount of energy required for somatic maintenance, and the energy remaining from the reserve for growth, after paying for maintenance costs.

Results show higher performances of the 'integrated Bayesian' approach to evaluate A. cordatus realised niche compared to 'simple' and 'integrated SDM-DEB' methods. The influence of

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environmental conditions on model predictions is further captured with the 'integrated Bayesian' procedure and better highlights the seasonal effect on the species predicted distribution. Model performance are good for the different seasonal simulations and uncertainty in predictions are well highlighted. These results are encouraging and the method promising for application to other data-poor case studies, in a context of climate change or for conservation issues.

A bioenergetic model to predict changes in evolutionary potential with age

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The heritability of a given trait vary among populations, but also during the life of an organism. According to empirical studies, the heritability and the genetic variance of life-history traits can increase with age. Various hypotheses have been put forward to explain these variations, such as a decrease in environmental or maternal effects with age, or the convergence of growth trajectories toward a genetically-determined maximal size, but it is not currently possible to test them because there is no theoretical approach to predict them. In particular, the physiological mechanisms that link genotype and phenotype are generally neglected. Therefore, the objective of this study is to use a DEB model to predict the variation in evolutionary potential with age and thus find the origins of these variations. To this aim, we will simulate size and reproductive output of *Daphnia magna* under different regimes of variation in food, temperature and energy in the egg corresponding to the hypotheses above. The model analysis will be analytical (constant environment for a given individual) or with simulations (environmental fluctuations within an individual lifetime). We will then compare the resulting age-dependence in the variance-covariance matrix of those traits, to conclude on the potential contribution of different hypothesized mechanisms.

Keywords: evolutionary potential, heritability, genetic variance, environmental variations, maternal effects

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Modelling growth and reproductive traits of green-lipped mussel under contrasting climate scenarios in 2100 and 2150

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The dynamic energy budget (DEB) model of Green-lipped mussel was applied to investigate climate change impact on mussel energetics. Most model parameters were kept the same as in the existing model by Ren et al. (2020), but pH-related parameters were slightly modified to accommodate the experimental conditions of the present study. Mesocosm experiments have been conducted to investigate climate change impact on phytoplankton growth. The experimental results were incorporated into the model for scenario simulations including current seawater condition, reduced pH only in 2100 and 2150, reduced pH and elevated temperature in 2100 and 2150. For scenarios in 2150, there are two projected temperatures in which temperature was elevated by 3.5 °C and 4.5 °C respectively. The application of the model has shown that the phytoplankton biomass was higher in reduced pH than in ambient conditions, but the direct effect of reduced pH is more than indirect effect of increased phytoplankton biomass on mussel energetics. This leads to reduction in growth and reproduction of mussels. However, the combination of elevated temperature and pCO_2 would cause significant increases of growth and reproduction, particularly in 2150. The model predicts that the flesh weight would increase from $\sim$30% to $\sim$150%, while the reproductive capacity would increase from $\sim$80% to $\sim$280%, respectively in 2100 and 2150. The present modelling work helps understand the effect of climate change on mussel energetics and provides an important component of ecosystem models to investigate climate change impact on coastal ecosystems.

Keywords: DEB model, climate change, phytoplankton growth, Pena canaliculus, energetics

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Parameterization of a DEB model for the Taiwanese smooth skink (Scincella formosensis): life history responses of a winter-active lizard to temperature

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Climate change affects the distribution range, activity time and population dynamics of reptiles. In this context, physiological ecology experiments and dynamic energy budget models are useful to explore an individual's response to temperature and ultimately, to predict how climate affects the species. The Taiwanese smooth skink, *Scincella formosensis* is a forest-species, and is the only skink with adults active in the cool season in sub/tropical Taiwan. Their egg-laying and hatching occurs from late March to June and juveniles develop during summer. The largest part of the development occurs in summer, making embryos and juveniles potentially more vulnerable to rising temperatures. This study measured how various aspects of *S. formosensis*' life history and physiology responded to temperature, including embryonic development, juvenile growth and rate of CO_2 production, in order to parameterize a DEB model. Our data showed a decline of growth at temperatures ≥ 28 °C, although CO_2 production did not show any obvious sign of decline at these temperatures. This observation suggests that the ingestion rate responds to high temperatures in a different way than other rate parameters. We included this finding by parameterizing two temperature correction functions, which produced a model that captures very well the major patterns of individuals' thermal physiology and life history. The fully parameterized model enables prediction of the full life history expressed by individuals under different temperature scenarios. For future application, we are planning to use this model in conjunction with a biophysical model and field data to predict how global climatic changes may affect the timing of life history event within the annual cycle and the challenges this could pose to this species.

Keywords: Reptile, Subtropical species, Thermal sensitivity, Thermal tolerance

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The DEB theory as a framework to approach the mass mortalities of *Pinna Nobilis* in the Mediterranean sea

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The fan mussel *Pinna nobilis* largest bivalve in Mediterranean, is an endangered IUCN protected species that is currently threatened by mass mortalities due to infections by a range of pathogens. The *Haplosporidium pinnae, Mycobacterium spp.*, and *Vibrio* spp were recently identified as infection agents. In order to conserve, regenerate and enhance the limited survived Pinna populations, it is important to understand how the environmental factors are triggering the pathogens–host interactions. The Dynamic Energy Budget (DEB) theory is a powerful framework to examine the energy flow during the lifecycle of the endangered bivalve under different infectious agents' attacks.

Data sets from the literature and eco-physiological experiments targeting stress/immune response indicators, environmental factors (emphasis on temperature and salinity that affect the pathogen–host interaction), and physiological history (shell growth bands), are used to link the *Pinna* sub-organismal (physiological) processes under pathogen infections to organismal performance at a population and ecosystem level.

Several environmental scenarios in Maliakos and Thermaikos gulf (Aegean Sea) are carried out as case studies, in order to build blocks for modeling the threatened fan mussel populations. Furthermore, the energy budget of *Pinna nobilis* individuals are examined at the specific environmental conditions of these ecosystems/regions. Potential knowledge gaps will be identified for further research development during the project "Innovative Actions For The Monitoring-Recovering – Enhancement of The Natural Recruitment of The Endangered Species (Fan mussel) *Pinna nobilis*, funded by the Operational Program for Fisheries and Maritime 2014-2020 (Measure 6.1.16) & EMMF, grant number (MIS) 5052394".

Keywords: Pinna nobilis, fan mussel, mass mortalities, disease, mediterranean sea, aegean, DEB

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Integrating earthworm movement and life history through dynamic energy budgets

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Earthworms are considered ecosystem engineers and, as such, they are an integral part of the soil ecosystem. Until recently, it has been assumed that the life-history of earthworms cannot be simulated using the assumptions of dynamic energy budget (DEB) theory. It was argued that the kappa-rule of the standard DEB model was not applicable to earthworm life cycles. In 2020, Rakel et al. were able to show that the standard DEB model is indeed able to reproduce the growth and reproduction of the earthworm *Eisenia fetida* under variable feeding regimes.

However, for earthworms, not only growth and reproduction can be affected by abiotic factors, such as the availability of food, but also their movement. The burrowing activity of earthworms, especially of endogeic species such as *Aporrectodea caliginosa*, is significantly influenced by abiotic factors. These factors include the moisture level, temperature, and the organic matter content. In laboratory experiments, earthworms showed a decrease in burrowing activity with decreasing moisture levels and even avoidance behavior of these unfavorable moisture environments. Furthermore, experimental results indicate that earthworm movement ceases completely at low moisture levels. At these conditions, individuals enter an inactive state, also described as diapause or aestivation (Holmstrup 2001). Moreover, the burrowing activity of earthworms is affected by temperature, for which the amount of casts produced per earthworm was used as a proxy in laboratory experiments. Last but not least, the organic matter content plays a significant role for the burrowing and movement of earthworms.

Here, we present a dynamic energy budget model for the endogeic earthworm *Aporrectodea caliginosa*. We will highlight how we integrated the effect of the abiotic factors moisture, organic matter content, and temperature simultaneously on earthworm movement and general life-history through dynamic energy budgets.

REFERENCES:

Rakel KJ, Preuss TG, Gergs A. 2020. Individual-based dynamic energy budget modelling of earthworm life-histories in the context of competition. Ecological Modelling. 432:109222. doi:10.1016/j.ecolmodel.2020.109222.

Holmstrup M. 2001. Sensitivity of life history parameters in the earthworm Aporrectodea caliginosa to small changes in soil water potential. Soil Biology and Biochemistry. 33(9):1217–1223. doi:10.1016/S0038-0717(01)00026-8.

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Modeling the energetic implications of early life responses to ocean acidification in an estuarine fish

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Ocean acidification, declining seawater pH due to increasing carbon dioxide, is occurring alongside warming and deoxygenation. Acidification causes variable, often subtle, responses in marine fishes, mainly in the early life stages. This presents challenges in understanding how organismal responses will affect populations, which are central to fisheries management. Understanding ocean acidification effects at higher levels of biological organization requires accounting for stage-specific effects, and Dynamic Energy Budget (DEB) theory facilitates this by incorporating differing energetic inputs and demands for each life stage. We use data on metabolism and growth of an ecologically important estuarine fish, the Atlantic silverside (*Menidia menidia*), to model the implications of early life responses for the full life-cycle energy budget. In a series of experiments, embryos and larvae were reared in ambient or elevated CO_2 levels, in combination with temperature and oxygen treatments. Acidification increased metabolic rate and hypoxia sensitivity of metabolism in embryos, but not larvae. Additionally, early life growth was reduced under acidification. We are using DEB models to test the hypothesis that acidification increases homeostasis costs early in life. Because of the interacting metabolic effects of CO_2 and hypoxia, we are also interested in testing the hypothesis that CO_2 affects fish energetics by reducing capacity for oxygen uptake and hypoxia tolerance, leading to increased reliance on anaerobic metabolism. Using DEBtool, we are obtaining estimates of model parameters using data from literature and our controls. We then narrow our focus and use the DEBkiss framework with a damage dynamics module to quantify energetic consequences of damage accumulation under simultaneous CO_2 and hypoxia. Using our detailed fits to the early life stages and taking parameters for later life stages from our DEBtool analysis, we will ultimately use the results to predict silverside population growth rates in realistic near-future scenarios of acidification and hypoxia.

Keywords: marine fish, DEBkiss, estuarine, ocean acidification, metabolism, hypoxia

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rDEBtktd, an R-package for sublethal effect modelling based on Dynamic Energy Budget theory

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Environmental Risk Assessment (ERA) of chemicals is based on standard laboratory toxicity tests with living organisms which ensure controlled experimental conditions and reproducibility. These toxicity tests are usually carried out under constant exposure concentrations, which can be far from reality of environmental exposure regimes as foreseen by the practical use of chemicals. In that respect mechanistic effect modelling, such as Toxicokinectic – Toxicodynamic (TKTD) modelling, has recently been playing an increasing role in the extrapolation of effects from constant controlled exposure conditions to time-variable exposure, closer to real environmental conditions. Among TKTD models, models based on the Dynamic Energy Budget theory adapted for ecotoxicology (DEB-TKTD models) offer a comprehensive framework to analyse and extrapolate sublethal effects (growth and reproduction) of chemicals on individual organisms across their whole life cycle. While DEB-TKTD models are considered as valuable tools for ERA, their full acceptance by stake-holders still requires the development of standardized and user-friendly tools. To bridge this gap, we developed ready-to-use functions within a new R package "rDEBtktd". This package takes advantage of the general Bayesian framework thus enabling the estimation of probability distributions for physiological DEB parameters and TKTD parameters, from which uncertainties can be easily quantified to be then propagated to forward-predictions for untested time-variable exposure scenarios. The physiological part of the DEB-TKTD model we implemented follows the original definition of the DEB model, which allows using the parameter values available for more than 1000 species in the Add-my-Pet database as prior information for the Bayesian inference process. This illustrates: (1) how to simply simultaneously estimate all the parameters of the DEB-TKTD model from one or several growth and reproduction datasets, (2) how to produce informative summaries to assess the results of the Bayesian inference and check all goodness-of-fit criteria, (3) how to make growth and reproduction predictions for untested time-variable exposure scenarios, (4) and finally the influence of both data quantity and design on the precision of parameter estimates.

Keywords: DEB, TKTD, TKTD, effect modelling

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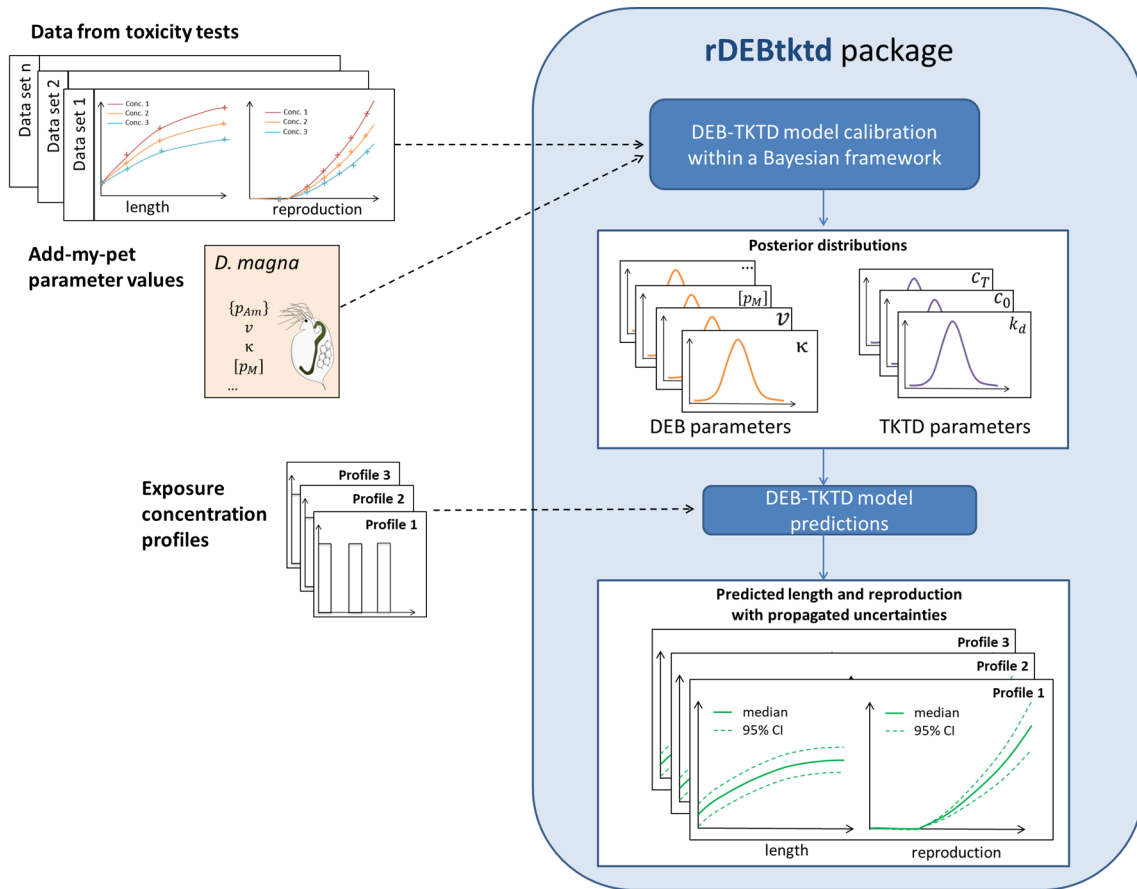
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