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

Organizing Committee:

**Romain Lavaud** - Louisiana State University AgCenter, Baton Rouge, LA, United States

**Starrlight Augustine** - Akvaplan Niva, Tromso, Norway

**Ramón Filgueira** - Dalhousie University, Halifax, Canada

**Leah Strople** - Dalhousie University, Halifax, Canada

**Laura Steeves** - Dalhousie University, Halifax, Canada

Scientific Committee:

**Jonathan Flye-Sainte-Marie** - University of Brest, Brest, France

**Tin Klanjšček** - University of Zagreb, Zagreb, Croatia

**Romain Lavaud** - Louisiana State University AgCenter, Baton Rouge, LA, United States

**Nina Marn** - University of Zagreb, Zagreb, Croatia

**Roger Nisbet** - University of California, Santa Barbara, CA, United States

**Jean-Christophe Poggiale** - Aix-Marseille University, Marseille, France

**Tânia Sousa** - University of Lisbon, Lisbon, Portugal

**Jaap van der Meer** - Wageningen University and Research, Wageningen, Netherlands

Funding & Sponsors:
Monday, May 24th, 2021

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>15:00</td>
<td>Welcome and opening</td>
</tr>
<tr>
<td>15:05</td>
<td>Session 1: Populations and Ecosystems in a Changing Climate</td>
</tr>
<tr>
<td></td>
<td><strong>KEYNOTE</strong></td>
</tr>
<tr>
<td></td>
<td>Ben Martin, University of Amsterdam, Netherlands</td>
</tr>
<tr>
<td></td>
<td>Understanding the effects of climate change on animal populations through the lens of organismal energetics</td>
</tr>
<tr>
<td>16:05</td>
<td>Jean-Pierre Desforges, McGill University, Canada</td>
</tr>
<tr>
<td></td>
<td>Individual and population response to climate change in Arctic muskoxen</td>
</tr>
<tr>
<td>16:25</td>
<td>Break</td>
</tr>
<tr>
<td>16:35</td>
<td>Lola De Cubber, Laboratoire d’Oceanologie et de Geosciences, France</td>
</tr>
<tr>
<td></td>
<td>Investigating population dynamics, traits and shore distribution of two sympatric lugworm species...</td>
</tr>
<tr>
<td>16:55</td>
<td>Wissam Barhdadi, Ghent University, Belgium</td>
</tr>
<tr>
<td></td>
<td>Extending DEB-IBM towards an eco-evolutionary modelling framework</td>
</tr>
<tr>
<td>17:15</td>
<td>Ines Haberle, Rudjer Boskovic Institute, Croatia</td>
</tr>
<tr>
<td></td>
<td>Can an individual tell us something about its population?</td>
</tr>
<tr>
<td>17:35</td>
<td>Lynda Bradley, Emory University, United States</td>
</tr>
<tr>
<td></td>
<td>Predicting the effects of resource pulses on snail and human schistosome dynamics using a DEB-IBM</td>
</tr>
<tr>
<td>18:00</td>
<td>General Discussion</td>
</tr>
</tbody>
</table>
**Tuesday, May 25th, 2021**

<table>
<thead>
<tr>
<th>15:00</th>
<th>16:00</th>
<th>16:20</th>
<th>16:30</th>
<th>16:50</th>
<th>17:10</th>
<th>17:30</th>
<th>17:50</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Session 2: Theoretical &amp; Methodological Developments and New applications</strong></td>
<td><strong>KEYNOTE</strong></td>
<td><strong>Charlène Guillaumot</strong>, Université de Bourgogne Franche-Comté, France</td>
<td><strong>Break</strong></td>
<td><strong>Tom Martin</strong>, University of New York, United Kingdom</td>
<td><strong>Juan Francisco Robles</strong>, Universidad de Granada, Spain</td>
<td><strong>Eleni Livanou</strong>, University of Crete, Greece</td>
<td><strong>Konrad Matyja</strong>, Wrocław University of Science and Technology, Poland</td>
</tr>
<tr>
<td></td>
<td><strong>Michael Kearney</strong>, University of Melbourne, Australia</td>
<td><em>What is the status of metabolic theory one century after Pütter invented the von Bertalanffy growth curve?</em></td>
<td></td>
<td><em>Modelling effects of variability in feeding rate on growth a vital step for DEB-TKTD modelling</em></td>
<td><em>MultiCalib4DEB: a toolbox bringing multimodal optimization for DEB parameters calibration</em></td>
<td><em>Modelling nanoflagellates – bacteria interactions in the oligotrophic Eastern Mediterranean Sea</em></td>
<td><em>The larvae, which eat polystyrene: growth, development, and survival analysis</em></td>
</tr>
<tr>
<td>16:00</td>
<td>16:20</td>
<td>16:30</td>
<td>16:50</td>
<td>17:10</td>
<td>17:30</td>
<td>17:50</td>
<td></td>
</tr>
<tr>
<td><strong>Break</strong></td>
<td><strong>General Discussion</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Wednesday, May 26th, 2021**

<table>
<thead>
<tr>
<th>15:00</th>
<th>16:00</th>
<th>16:20</th>
<th>16:30</th>
<th>16:50</th>
<th>17:10</th>
<th>17:30</th>
<th>17:50</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Poster session</strong></td>
<td><strong>Break</strong></td>
<td><strong>Marko Jusup</strong>, Tokyo institute of Technology, Japan</td>
<td><strong>Tin Klanjšček</strong>, Ruđer Bošković Institute, Croatia</td>
<td><strong>Joaquim Tomàs-Ferrer</strong>, Laboratori d’Investigacions Marines i Aquicultura, Spain</td>
<td><strong>Gonçalo Marques</strong>, MARETEC Universidade de Lisboa, Portugal</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td><em>Let the concept of trait be theoretical</em></td>
<td><em>DEB theory should not be a dead Christmas tree</em></td>
<td><em>Bayesian estimation of DEB parameters using STAN</em></td>
<td><em>Direct greenhouse gas emissions in livestock production</em></td>
<td></td>
<td></td>
</tr>
<tr>
<td>16:30</td>
<td>16:50</td>
<td>17:10</td>
<td>17:30</td>
<td>17:50</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Break</strong></td>
<td><strong>General Discussion</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Thursday, May 27th, 2021

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

Benoit Goussen, ibacon GmbH, Germany
A DEB egg-laying module for birds exposed to pesticides

Break

Kim Rakel, Research institute gaiac, Germany
Alive and kicking? - Earthworm cocoon test for TKTD Modelling in soil risk assessment of chemicals

Sandrine Charles, Laboratoire de Biométrie et Biologie Evolutive (LBBE), France
Towards a facilitated use of Modelling in Environmental Risk Assessment

José Moreira, MARETEC Universidade de Lisboa, Portugal
Impacts of climate change in temperate and sub-tropical fish species

Tiago Domingos, MARETEC Universidade de Lisboa, Portugal
DEB modelling and IPCC accounting methods: a bridge between frameworks

General Discussion

Friday, May 28th, 2021

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

Sylvie Gaudron, Laboratoire Océanologie et Géosciences (LOG), France
Inferring functional traits in a deep-sea wood-boring bivalve using dynamic energy budget theory

Break

Emilien Pousse, NOAA NEFSC, United States
Projecting the effect of ocean acidification and warming on two Atlantic surfclam...

Isabel Smallegange, University of Amsterdam, Netherlands
Unusually paced life history strategies of marine megafauna drive atypical sensitivities to environmental change

Charlotte Récapet, Behavioural Ecology and Fish Population Biology Laboratory, France
Intra-specific variation of life-history traits in Atlantic salmon: environmental and genetic factors

Joany Mariño, Memorial University, Canada
Resource and seasonality drive interspecific variability in the Dynamic Energy Budget model

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

Benjamin Martin *

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.

*Corresponding author: tm604@york.ac.uk
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
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

1 UMR 8187 Laboratoire d'Océanologie et de Géosciences (LOG) – Univ. Lille, Univ. Littoral Côte d'Opale, CNRS – F-59000, France
2 Écologie et Modèles pour l’halieutique (EMH) – Institut français de Recherche pour l’Exploitation de la Mer – Ifremer, rue de l’Île d’Yeu, 44311 Nantes Cedex 03, France
3 UMR 8187 Laboratoire d'Océanologie et de Géosciences (LOG) – Univ. Lille, Univ. Littoral Côte d’Opale, CNRS – F-59000 Lille, France
4 UMR 8187 Laboratoire d'Océanologie et de Géosciences (LOG) – Univ. Lille, Univ. Littoral Côte d’Opale, CNRS – F-59000 Lille, France
5 UFR 918 UFR 927 – Sorbonne Univ. – 75005 Paris, France

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 ≥ 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 km² resolution : www.hermes.acri.fr) and daily values of SST (4 km² 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.

*Speaker
†Corresponding author: lola.decubber@gmail.com
Keywords: DEB, IBM, Arenicola marina, Arenicola defodiens, Population dynamics, Spatial distribution, Traits
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

*Speaker
†Corresponding author: wissam.barhdadi@ugent.be
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
2 University of Zadar (UNIZD) – Ul. Mihovila Pavlinovica, 23000 Zadar, Croatia

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

---

*Speaker

†Corresponding author: ihaberle@irb.hr

‡Corresponding author: tin@irb.hr
Predicting the effects of resource pulses on snail and human schistosome dynamics using a DEB-IBM

L. M. Bradley *† 1, David Civitello 1

1 Emory University – 1510 Clifton Rd 2006, Atlanta, GA 30322, United States

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

*Speaker  
†Corresponding author: lbradl8@emory.edu
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.

*Corresponding author: m.kearney@unimelb.edu.au
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

1 UMR 6282 Biogéosciences, Université de Bourgogne Franche-Comté – UMR 6282 Biogéosciences – 6 bd Gabriel F-21000 Dijon, France
2 Marine Biology Lab. (ULB) – Université Libre de Bruxelles (U.L.B.), Avenue F.D. Roosevelt, CP 160/15. B-1050 Bruxelles, Belgium
3 School of Zoology, George S. Wise Faculty of Life Sciences – Tel Aviv University, Tel Aviv, Israel
4 ESE, Ecology and Ecosystem Health, INRAE – ESE, Ecology and Ecosystem Health, INRAE – 35042, Rennes, France
5 Marine Biology Lab. (ULB) – Université Libre de Bruxelles (U.L.B.), Avenue F.D. Roosevelt, CP 160/15. B-1050 Bruxelles, Belgium
6 UMR 6282 Biogéosciences, Université de Bourgogne Franche-Comté – UMR 6282 Biogéosciences – 6 bd Gabriel F-21000 Dijon, France

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.

*Presenter
**Keywords:** Kerguelen Islands, sea urchin, integrated approaches, Bayesian inference, Species Distribution Modelling

**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

Tom Martin *,† 1, Roman Ashauer 1,2, Mark Hodson 1

1 University of York – Wentworth Way, Heslington, York, YO10 5NG, UK, United Kingdom
2 Syngenta Crop Protection AG – 4058, Basel, Switzerland, Switzerland

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

*Speaker
†Corresponding author: tm604@york.ac.uk
MultiCalib4DEB: a toolbox bringing multimodal optimization for DEB parameters calibration.

Juan Francisco Robles *, 1 Antonio Agüera 2, Manuel Chica 1, Sergio Damas 1

1 Universidad de Granada (UGR) – Avda. del Hospicio, s/n C.P. 18010 Granada, Spain
2 Flødevigen Research Station (IMR) – Institute of Marine Research (IMR) Nye Flødevigveien 204817 HIS, Norway

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

*Speaker
DEBtools limitations

- A single acceptable DEB model calibration in a run
- Understand parameters-model relationship while checking the specificity of the calibrated parameters
- Complete validation process with modeler

MultiCalib4DEB contribution

- Evolutionary multimodal optimization algorithms to return a set of alternative model calibration solutions in a single run
- Quantitative and visual sensitivity analysis and parameters’ exploration based on the solutions set
- An integral and interactive framework to enhance the validations and results acceptance
Modelling nanoflagellates – bacteria interactions in the oligotrophic Eastern Mediterranean Sea

Eleni Livanou *,† 1,2, Anna Lagaria 3, Andreas Oikonomou 2, Stella Psarra 2, Konstadia Lika 1

1 Department of Biology, University of Crete – Voutes University Campus, 70013, Heraklion, Greece
2 Institute of Oceanography, Hellenic Centre for Marine Research – Thalasocosmos, Former US Base at Gournes, 71003, Heraklion, Greece
3 Department of Biological Applications and Technology, University of Ioannina – 45110 Ioannina, Greece

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

*Speaker
†Corresponding author: livanou@hcmr.gr
A conceptual model of nanoflagellates – bacteria interactions in the Eastern Mediterranean Sea
The larvae, which eat polystyrene: growth, development, and survival analysis

Konrad Matyja * 1, Justyna Rybak 2

1 Wrocław University of Science and Technology, Faculty of Chemistry, Department of Micro, Nano, and Bioprocess Engineering, – 27 Wybrzeże Wyspiańskiego st. 50-370 Wrocław, Poland
2 Wrocław University of Science and Technology, Faculty of Environmental Engineering – 27 Wybrzeże Wyspiańskiego st. 50-370 Wrocław, Poland

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

*Speaker
Let the concept of trait be theoretical

Michael Kearney*, 1, Marko Jusup † 2, Melodie Mcgeoh 3, Sebastiaan Kooijman 4, Steven Chown 5

1 School of BioSciences, University of Melbourne – Royal Parade, Parkville VIC 3052, Australia
2 Tokyo Tech World Hub Research Initiative, Institute of Innovative Research, Tokyo Institute of Technology – 4259 Nagatsuta-cho, Midori-ku, Yokohama 226-8503, Japan
3 School of Life Sciences, La Trobe University – Plenty Rd. & Kingsbury Dr., Bundoora VIC 3086, Australia
4 VU University Amsterdam – De Boelelaan 1105, 1081 HV Amsterdam, Netherlands
5 School of Biological Sciences, Monash University – Wellington Rd., Clayton VIC 3800, Australia

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

*Corresponding author: m.kearney@unimelb.edu.au
†Speaker
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

Keywords: general DEB, quick reserve turnover, multicompartmental toxicokinetics, sublethal toxicant effects, Christmas tree and ornaments
Bayesian estimation of DEB parameters using STAN

Joaquim Tomàs-Ferrer * 1,2,3, Miquel Palmer 2, Andrea Campos-Candela *

1 Laboratori d’Investigacions Marines i Aqüicultura (LIMIA) – Port d’Andratx, Spain
2 Institut Mediterrani d’Estudis Avançats (IMEDEA-CSIC-UIB) – Esporles, Spain
3 Institut de Recerca i Formació Agrària i Pesquera (IRFAP) – Palma, Spain
4 Leibniz institute of freshwater ecology and inland fisheries (IGB) – Berlin, Germany

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 built-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


**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](image)

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

Gonçalo Marques *, Carlos Teixeira, Tânia Sousa, Tiago Morais, Ricardo Teixeira, Tiago Domingos

1 MARETEC / LARSyS, Instituto Superior Técnico, Universidade de Lisboa – Av. Rovisco Pais 1, 1049-001 Lisboa, Portugal
2 MARETEC / LARSyS, Instituto Superior Técnico, Universidade de Lisboa – Av. Rovisco Pais 1, 1049-001 Lisboa, Portugal
3 Instituto Superior Técnico - Universidade de Lisboa (IST) – Av. Rovisco Pais, 1, 1049-001 Lisboa, Portugal

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

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

Cheryl A. Murphy*

Professor, director of the Michigan State University Center for PFAS Research, East Lansing, MI, United States

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, subcellular 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.

*Corresponding author: camurphy@msu.edu
A DEB egg-laying module for birds exposed to pesticides

Benoit Goussen * 1, Starrlight Augustine 2, Markus Ebeling 3, David Heckman 3, Lika Konstadia 4, Nina Marn 5, André Gergs 3

1 ibacon GmbH – Arheilger Weg 17 64380 Robdorf, Germany
2 Akvaplan-Niva, Fram High North Research Centre for Climate and the Environment, – 9296 Tromsø, Norway
3 Bayer Cropscience – Monheim, Germany
4 Department of Biology, University of Crete – University of Crete, 71003, Heraklion, Greece
5 Ruđer Bošković Institute, Zagreb – Croatia

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

Kim Rakel * 1, Gregor Ernst 2, André Gergs 2

1 Research institute gaiac – Kackertstr 10, 52072 Aachen, Germany
2 Bayer AG – Monheim, Germany

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

*Speaker*
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

1 MARETEC - Marine, Environment & Technology Center, LARSys, Instituto Superior Técnico, Universidade de Lisboa – Av. Rovisco Pais 1, 1049-001 Lisboa, Portugal, Portugal
2 Interdisciplinary Centre of Marine and Environmental Research (CIIMAR), University of Porto – Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos, S/N, 4450-208, Matosinhos, Portugal, Portugal
3 MARE – Marine and Environmental Sciences Centre, Guia Marine Laboratory, Faculty of Sciences, University of Lisbon (FCUL) – Avenida Nossa Sra do Cabo 939, 2750-374 Cascais, Portugal
4 Division of Aquaculture and Seafood Upgrading (DivAV), Portuguese Institute for Sea and Atmosphere (IPMA, I.P.) – Rua Alfredo Magalhães Ramalho 6, 1495-165 Lisboa, Portugal, Portugal

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

*Speaker
†Corresponding author: j.miguel.moreira@tecnico.ulisboa.pt
DEB modelling and IPCC accounting methods: a bridge between frameworks

Gonçalo Marques ¹, Tiago Domingos * ²

¹ MARETEC / LARSyS, Instituto Superior Técnico, Universidade de Lisboa – Av. Rovisco Pais 1, 1049-001 Lisboa, Portugal, Portugal
² MARETEC / LARSyS, Instituto Superior Técnico, Universidade de Lisboa – Av. Rovisco Pais, 1, 1049-001 Lisboa, Portugal

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 IPCC accounting methods and DEB modelling.

Keywords: Climate change, Greenhouse gas emissions, Cattle metabolism

*Speaker
Towards a facilitated use of Modelling in Environmental Risk Assessment

Sandrine Charles *

1 Laboratoire de Biométrie et Biologie Evolutive (LBBE) – CNRS : UMR5558, Université Claude Bernard - Lyon I (UCBL), INRIA – 43 Bld du 11 Novembre 1918 69622 VILLEURBANNE CEDEX, France

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

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

Sabrina E. Russo*

Professor at the University of Nebraska-Lincoln, School of Biological Sciences, Lincoln, NE, USA

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.

*Corresponding author: srusso2@unl.edu
Inferring functional traits in a deep-sea wood-boring bivalve using dynamic energy budget theory

Sylvie Gaudron *, Sébastien Lefebvre 1, Gonçalo Marques 2

1 UMR 8187 Laboratoire Océanologie et Géosciences (LOG) – Univ. Littoral Côte d’Opale, CNRS, Univ. Lille, UMR 8187, LOG, Laboratoire d’Océanologie et de Géosciences – Station Marine de Wimereux, F-59 000 Lille, France
2 MARETEC - Marine, Environment & Technology Center, LARSys, Instituto Superior Técnico, Universidade de Lisboa – Lisboa, Portugal

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 ($E^p_H$), and the maximum reserve capacity [$E_m$]. $\dot{v}$ and $E^p_H$, 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

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

Isabel Smallegange *† 1, Marta Flotats Avilés 1, Kim Eustache 1

1 Institute for Biodiversity and Ecosystem Dynamics - IBED (NETHERLANDS) – University of Amsterdam, Netherlands

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

---

*Speaker
†Corresponding author: i.smallegange@uva.nl
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
Resource and seasonality drive interspecific variability in the Dynamic Energy Budget model

Joany Mariño *† 1, Suzanne Dufour 2, Amy Hurford 2, Charlotte Récapet 3

1 Memorial University of Newfoundland – 232 Elizabeth Ave., St John’s, NL, A1B 3X9, Canada
2 Memorial University of Newfoundland – 232 Elizabeth Ave., St John’s, NL, A1B 3X9, Canada
3 UMR ECOBIOP, INRA-Université Pau Pays de l’Adour – Université de Pau et Pays de l’Adour – 64310 St Pée sur Nivelle, France

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

---

*Speaker
†Corresponding author: jmarinocoron@mun.ca
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

Margot Arnould-Pétré *, Charlène Guillaumot †, Bruno Danis ‡, Jean-Pierre Féral §, Thomas Saucède

1 UMR 6282 Biogéosciences, Université de Bourgogne Franche-Comté – UMR 6282 Biogéosciences – 6 bd Gabriel F-21000 Dijon, France
2 Marine Biology Lab. (ULB) – Université Libre de Bruxelles (U.L.B.), Avenue F.D. Roosevelt, CP 160/15. B-1050 Bruxelles, Belgium
3 Aix Marseille Universite/CNRS/IRD/UAPV, IMBE-Institut Méditerranéen de Biologie et d’Ecologie marine et continentale, UMR 7263 – Aix Marseille Universite IMBE – Station Marine d’Endoume, Chemin de la Batterie des Lions, 13007 Marseille, France

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 deterministic 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.

*Presenter  †Corresponding author: charleneguillaumot21@gmail.com
(C) Forcing environmental variables

Inter-individual variability
Density-dependent regulation

(B) IBM

Background mortality
Temperature mortality

Temperature
Food resources

(A) DEB model

Reserve (E)

Somatic maintenance \( p_s \)
Maturity maintenance \( p_m \)
Structural volume (V)
Complexity (EH)
Reproduction buffer (Ep)

Ageing mortality
Starvation mortality

Temperature mortality
Backgound mortality

Keywords: Kerguelen Islands, climate change, model sensitivity, endemic echinoderm
Enchytraeus crypticus, a suitable soil species for DEB-TKTD modelling

Sylvain Bart∗1,2, Tjalling Jager3, Alex Robinson4, Elma Lahive2, David Spurgeon2, Roman Ashauer1,5

1 University of York – Wentworth Way, Heslington, York, YO10 5NG, UK, United Kingdom
2 UK Centre for Ecology & Hydrology (UK CEH) – MacLean Building, Benson Lane, Wallingford, Oxon, OX10 8BB, UK, United Kingdom
3 DEBtox Research (DEBtox Research) – De Bilt, Netherlands
4 UK Centre for Ecology & Hydrology (UK CEH) – MacLean Building, Benson Lane, Wallingford, Oxon, OX10 8BB, UK, United Kingdom
5 Syngenta Crop Protection AG – 4058, Basel, Switzerland, Switzerland

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.

∗Presenter
Conceptual DEB coupled agent-based model for ticks’ species.

Cyrine Chenaoui *† ¹, Dorra Louati ¹², Mohamed Gharbi ³, Mourad Rekik ⁴, Mohamed Darghouth ³, Slimane Ben Miled ¹

¹ Institut Pasteur de Tunis, Lab BIMS (Bio-Informatic, Mathematics, Statistic) (IPT-BIMS) – 13, place Pasteur, B.P. 74 1002 Tunis, Belvédère, Tunisia
² South Mediterranean University, Mediterranean Institute of Technology (SMU-MedTech) – Tunis, Tunisia
³ Ecole Nationale de Médecine Vétérinaire (ENMV) – Sidi Thabet, Tunisia
⁴ International Centre for Agricultural Research in the Dry Areas (ICARDA) – Tunis, Tunisia

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

*Presenter
†Corresponding author: cyrine.chenaoui@gmail.com
Std instead of abj type DEB model should be assumed when fitting freshwater crayfish ontogeny

Ana Dobrović *, Sandra Hudina 1, Tin Klanjšček 2, Nina Marn † 2

1 University of Zagreb, Faculty of Science, Department of Biology – Rooseveltov trg 6, 10000 Zagreb, Croatia
2 Ruđer Bošković Institute, Division for Marine and Environmental Research – Bijenička 54, 10000 Zagreb, Croatia

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 virginalis*). 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

*Presenter
†Corresponding author: Nina.Marn@irb.hr
Building a Dynamic Energy Budget for A. poculata: modeling and parameterizing facultative symbioses

Caroline Fleming ∗† 1, Erik Muller 2,3, Randi Rotjan 1, Justin Mcalister 4

1 Boston University [Boston] (BU) – One Silber Way, Boston, MA 02215, United States
2 Norwegian University of Science and Technology [Trondheim] (NTNU) – NO-7491 Trondheim, Norway
3 University of California [Santa Barbara] – Marine Science Institute, University of California, Santa Barbara, CA 93106, United States
4 College of the Holy Cross – 1 College St, Worcester, MA 01610, United States

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

∗ Presenter
† Corresponding author: cgflem@bu.edu
Can DEB models infer metabolic differences between intertidal and subtidal morphotypes of the Antarctic limpet *Nacella concinna* (Strebel, 1908)?

Charlène Guillaumot *1,2, Thomas Saucède 2, Simon A. Morley 3, Starrlight Augustine 4, Bruno Danis 1, Sebastiaan Kooijman 5

1 Marine Biology Lab. (ULB) – Université Libre de Bruxelles (U.L.B.), Avenue F.D. Roosevelt, CP 160/15. B-1050 Bruxelles, Belgium  
2 UMR 6282 Biogéosciences, Université de Bourgogne Franche-Comté – UMR 6282 Biogéosciences – 6 bd Gabriel F-21000 Dijon, France  
3 British Antarctic Survey, National Environment Research Council – Cambridge, CB30ET, United Kingdom  
4 Akvaplan-Niva, Fram High North Research Centre for Climate and the Environment, – 9296 Tromsø, Norway  
5 Department of Theoretical Biology, VU University Amsterdam – de Boelelaan 1087, 1081 HV Amsterdam, Netherlands

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

*Speaker  
†Corresponding author: charleneguillaumot21@gmail.com
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.

**Keywords:** Southern Ocean, marine benthic species, model relevance, model accuracy
A bioenergetic model to predict changes in evolutionary potential with age

Clélia Gauthier *, † 1, Charlotte Récapet ‡ 1

1 UMR ECOBIOP, INRA-Université Pau Pays de l’Adour – Université de Pau et Pays de l’Adour – 64310 St Pée sur Nivelle, France

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

*Presenter
†Corresponding author: cleliagauthier16@gmail.com
‡Corresponding author: charlotte.recapet@univ-pau.fr
Modelling growth and reproductive traits of green-lipped mussel under contrasting climate scenarios in 2100 and 2150

Jeffrey Ren *, † 1, Cliff Law 2, Vonda Cummings 2

1 National Institute of Water and Atmospheric Research – PO Box 8602, Christchurch 8440, New Zealand
2 National Institute of Water and Atmospheric Research – Private Bag 14901, Wellington, New Zealand

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 pCO₂ would cause significant increases of growth and reproduction, particularly in 2150. The model predicts that the flesh weight would increase from ∼30% to ∼150%, while the reproductive capacity would increase from ∼80% to ∼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

*Presenter
†Corresponding author: j.ren@niwa.co.nz
Parameterization of a DEB model for the Taiwanese smooth skink (Scincella formosensis): life history responses of a winter-active lizard to temperature

Hao-Chun Fan ¹, Shu-Ping Huang ¹, Romain Richard ² ³ ¹

¹ National Sun Yat-Sen University (NSYSU) – 70 Lienhai Rd. Kaohsiung 80424, Taiwan

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 CO₂ production, in order to parameterize a DEB model. Our data showed a decline of growth at temperatures ≥ 28 ℃, although CO₂ 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

²Presenter
³Corresponding author: romain.richard@mail.nsusu.edu.tw
The DEB theory as a framework to approach the mass mortalities of *Pinna Nobilis* in the Mediterranean sea

Konstantina Rizou *, John A Theodorou *, Konstantina Lika †, Basil Michaelidis ‡, Ioannis Karakassis ‡

1. University of Patras – Patra, Greece
2. University of Crete – Crete, Greece
3. Aristotle University of Thessaloniki – Thessaloniki, Greece

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

*Presenter
†Corresponding author: jtheo@upatras.gr
Integrating earthworm movement and life history through dynamic energy budgets

André Gergs 1, Kim Rakel 2, Dino Liesy 2, Yvan Capowiez 3, Gregor Ernst 1, Vanessa Roeben *† 1

1 Bayer AG – Alfred-Nobel-Str. 50, 40789 Monheim am Rhein, Germany
2 gaiac – Kackertstr. 10, 52072 Aachen, Germany
3 INRAE – Institut national de recherche pour l’agriculture, l’alimentation et l’environnement (INRAE)
   – 228 route de l’Aérodrome, 84914 Avignon Cedex 9, France

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:


*Speaker
†Corresponding author: vanessa.roeben@bayer.com
Keywords: soil, earthworms, movement, abiotic factors, life, history
Modeling the energetic implications of early life responses to ocean acidification in an estuarine fish

Teresa Schwemmer *, †1, Roger Nisbet 2, Janet Nye 3

1 School of Marine and Atmospheric Sciences, Stony Brook University – Stony Brook, NY 11794, United States
2 Department of Ecology, Evolution and Marine Biology, University of California, Santa Barbara (UCSB) – Santa Barbara, California 93106, United States
3 Institute of Marine Sciences, University of North Carolina at Chapel Hill – Morehead City, NC 28557, United States

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 CO₂ 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 CO₂ and hypoxia, we are also interested in testing the hypothesis that CO₂ 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 CO₂ 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

*Presenter
†Corresponding author: teresa.schwemmer@stonybrook.edu
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 Toxicokinetic – 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 eco-toxicology (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
List of participants

- **Antonio Agüera**  
  antonio.aguera@hi.no  
  Institute of Marine Research  
  Low Trophic Aquaculture

- **Peter Alsip**  
  peterals@umich.edu  
  University of Michigan Cooperative Institute for Great Lakes Research  
  NOAA Great Lakes Environmental Research Lab

- **Andre Felipe Andrade**  
  andrefaandrade@gmail.com  
  Universidade Federal de Goiás  
  TheMetaLand Lab

- **Margot Minju Arnould–Pétré**  
  m.arnould-petre@nhm.ac.uk  
  Natural History Museum, London. Lab: Algae, Fungi and Plant division

- **Starrlight Augustine**  
  starrlight.augustine@akvaplan.niva.no  
  Akvaplan Niva

- **Wissam Barhdadi**  
  wissam.barhdadi@ugent.be  
  Ghent University  
  Department of Data Analysis and Mathematical Modelling

- **Alpar Barsi**  
  alpar.barsi@ctgb.nl  
  Dutch Board for the Authorisation of Plant Protection Products and Biocides Ctgb

- **Sylvain Bart**  
  sylvain.bart@york.ac.uk  
  University of York and UK Centre for Ecology & Hydrology

- **Barbara Bauer**  
  barbara.bauer@rifcon.de  
  Rifcon GmbH

- **Amel Bejaoui**  
  bejaoui-amel@hotmail.fr  
  INAT

- **Imene Belgaid**  
  ibelgaid@usthb.dz  
  Université de Sciences et Technologies Houari

- **Slimane Ben Miled**  
  slimane.benniled@fst.utm.tn  
  University of Tunis el Manar  
  BIMS-Pasteur Institute of Tunis

- **Halle Berger**  
  halle.berger@uconn.edu  
  University of Connecticut

- **Konstanze Bergunder**  
  kobergunder@gmail.com  
  University of Greifswald, animal ecology
• Brandy Biggar
  bsbiggar@mun.ca
  Memorial University
  Bates

• Lynda Bradley
  lbradl8@emory.edu
  Emory University
  Civitello lab, Waller lab

• Alec Burslem
  acb35@st-andrews.ac.uk
  University of St Andrews
  Miller lab

• Maxim Buyck
  mailto:maxim.buyck@ugent.be
  Ghent University
  Department of Mathematical Modelling, Statistics and Bioinformatics

• Andrea Campos-Candela
  andreacamposcandela@gmail.com
  Leibniz-Institute of Freshwater Ecology and Inland Fisheries
  Dept. Biology and Ecology of Fishes

• Sandrine Charles
  sandrine.charles@univ-lyon1.fr
  Université de Lyon I
  Predictive Modelling and Ecotoxicology Group

• Cyrine Chenaoui
  mailto:cyrine.chenaoui@gmail.com
  Institut Pasteur de Tunis
  Lab BIMS, Bio-Informatic, Mathematics, Statistic

• Filipe Chichorro
  filipechichorro@gmail.com
  Finnish Museum of Natural History
  Laboratory for Integrative Biodiversity Research, LIBRe

• Natalie Dallmann
  natal12@gmx.de
  gaiac

• Anna Davis
  amdavis@umd.edu
  University of Maryland, College Park

• Lola De Cubber
  decubber@gmail.com
  Ifremer
  Department of Environment and Resources

• Jean-Pierre Desforges
  jean-pierre.desforges@mcgill.ca
  McGill University
  Natural Resource Sciences

• David Deslauriers
  david_deslauriers@uqar.ca
  Institut des sciences de la mer de Rimouski/Université du Québec à Rimouski
  Laboratory of Advanced Bioenergetics
• Tamara Djerdj
tamara.djerdj@biologija.unios.hr
Department of Biology, Josip Juraj Strossmayer University of Osijek
Laboratory for Ecological Modelling

• Ana Dobrovic
ana.dobrovic@biol.pmf.hr
University of Zagreb, Faculty of Science, Department of Biology
Division of Zoology

• Tiago Domingos
tdomingos@ist.utl.pt
Universidade de Lisboa, Instituto Superior Técnico
MARETEC

• Bass Dye
bass.dye@nioz.nl
Royal Netherlands Institute for Sea Research NIOZ, University of Groningen, Wageningen University & Research
Coastal Systems

• Markus Ebeling
markus.ebeling@bayer.com
Bayer AG

• Ashley Elgin
ashley.elgin@noaa.gov
National Oceanic and Atmospheric Administration
Great Lakes Environmental Research Laboratory

• Urtzi Enriquez Urzelai
urtzi.enriquez@gmail.com
Czech Academy of Sciences

• Bruno Ernande
Bruno.Ernande@ifremer.fr
Ifremer
UMR MARBEC

• Martina Fenske
fenske@bafg.de
Federal Institute of Hydrology - BfG
Biochemistry & Ecotoxicology

• Ramón Filgueira
ramon.filgueira@dal.ca
Dalhousie University
Marine Affairs Program

• Caroline Fleming
cgflem@bu.edu
Boston University
Rotjan Lab

• Jorge Arturo Flores Valiente
jorgefloresvaliente@gmail.com
Sorbonne Université
Unité de Modélisation Mathématique et Informatique des Systèmes Complexes, UMMISCO

• Jonathan Flye-Sainte-Marie
jonathan.flye@univ-brest.fr
Université de Bretagne Occidentale
Lemar
• Vânia Freitas
  vpfreitas@ciimar.up.pt
  CIIMAR

• Nika Galic
  nika.galic@syngenta.com
  Syngenta Crop Protection LLC

• Sylvie Gaudron
  sylvie.gaudron@sorbonne-universite.fr
  CNRS Université de Lille Université de la Côte d’Opale
  UMR8187 Laboratoire d’Océanologie et de Géosciences

• Clélia Gauthier
  cleliagauthier16@gmail.com
  INRAE
  Aquapole Saint-Pée-sur-Nivelle UMR Ecobiop

• Sunčana Geček
  suncana.gecek@gmail.com
  Ruder Bošković Institute
  Laboratory for Informatics and Environmental Modelling

• Andre Gergs
  andre.ergs@bayer.com
  Bayer AG

• Elena Gorokhova
  elena.gorokhova@su.se
  Stockholm University
  ACES

• Benoit Goussen
  benoit.goussen@gmail.com
  ibacon GmbH

• Charlène Guillaumot
  charleneguillaumot21@gmail.com
  Université Libre de Bruxelles
  Marine Biology Lab

• Thomas Guyondet
  thomas.guyondet@dfo-mpo.gc.ca
  Fisheries and Oceans Canada
  Aquaculture and coastal ecosystems

• Ines Haberle
  ihaberle@irb.hr
  Ruder Bošković Institute
  Laboratory for Informatics and Environmental Modelling, Division for Marine and Environmental Research

• Domagoj Hackenberger
  domagojhack@gmail.com
  Department of Biology, Josip Juraj Strossmayer University of Osijek
  Laboratory for quantitative ecology

• Simon Hansul
  simon.hansul@ugent.be
  Ghent University
  GhEnToxLab
• David Heckmann  
david.heckmann@bayer.com  
Bayer Crop Science

• Laura Hennigs  
laura.hennigs@uni-greifswald.de  
University of Greifswald  
Zoological Institute

• Vincent Hin  
Vincent.Hin@wur.nl  
Wageningen Marine Research

• Shu-Ping Huang  
sphuang0711@gmail.com  
National Sun-Yat sen University

• Audrey Huff  
huff0114@umn.edu  
University of Minnesota Duluth Large Lakes Observatory  
Ozersky

• Martin Huret  
martin.huret@ifremer.fr  
Ifremer  
STH/LBH

• Saana Isojunno  
sj66@st-andrews.ac.uk  
University of St Andrews  
Sea Mammal Research Unit

• Tjalling Jager  
tjalling@debtox.nl  
DEBtox Research

• Marko Jusup  
mjusup@gmail.com  
Tokyo Institute of Technology

• Michael Kearney  
m.kearney@unimelb.edu.au  
University of Melbourne  
Climatic and Metabolic Ecology Lab

• Thomas Kiffney  
thomas.kiffney@maine.edu  
University of Maine  
Brady Lab

• Tin Klanjšček  
tin@irb.hr  
University of Zagreb  
Ruder Bošković Institute

• Josef Koch  
koch@gaiac-eco.de  
gaiac

• Bob Kooi  
bob.kooi@vu.nl  
Faculty of Science  
VU Amsterdam
• Bas Kooijman
salm.kooijman@gmail.com
VU University
Retired

• Jordan Kroeker
kroj0001@uqar.ca
Université de Quebec à Rimouski, Institut des sciences de la mer de Rimouski
Dr. David Deslauriers

• Romain Lavaud
rlavaud@agcenter.lsu.edu
Louisiana State University Agricultural Center
School of Renewable Natural Resources

• Yen Le
yen.le@uni-due.de
University of Duisburg-Essen
Department of Aquatic Ecology, Faculty of Biology

• Sébastien Lefebvre
sebastien.lefebvre@univ-lille.fr
University of Lille
UMR 8187 LOG

• Dina Lika
lika@uoc.gr
University of Crete

• Eleni Livanou
livanou@hcmr.gr

• Annika Mangold-Döring
annika.mangold-doering@wur.nl
Wageningen Marine Research

• Joany Mariño
jmarinocoron@mun.ca
Memorial University of Newfoundland
Theoretical Biology Lab & Marine Symbiosis Lab

• Nina Marn
nmarn@irb.hr
Ruder Bošković Institute
Laboratory for Informatics and Environmental Modeling

• Gonçalo Marques
goncalo.marques@tecnico.ulisboa.pt
Universidade de Lisboa, Instituto Superior Técnico
MARETEC

• Olivier Maury
olivier.maury@ird.fr
IRD, MARBEC

• Ben Martin
b.t.martin@uva.nl
University of Amsterdam
Department of Theoretical and Computational Ecology
• **Lucas Martin**  
lucas.martin@uqar.ca  
Université du Québec à Rimouski  
Ismer

• **Thomas Martin**  
tm604@york.ac.uk  
University of York

• **Omera Matoo**  
omatoo2@unl.edu  
University of Nebraska-Lincoln

• **Konrad Matyja**  
konrad.matyja@pwr.edu.pl  
Wroclaw University of Science and Technology, Faculty of Chemistry  
Department of Bioprocess Engineering, Micro- and Nanoengineering

• **Katie McFarland**  
katherine.m.mcfarland@noaa.gov  
NOAA National Marine Fisheries  
Milford Lab

• **Clara Menu**  
clara.menu@ifremer.fr  
Ifremer  
LBH

• **Tahiri Mohamed**  
tamamed7@gmail.com  
Faculté des sciences et techniques  
Laboratoire de mécanique et génie civil

• **Cristian Monaco**  
cristian.monaco@ifremer.fr  
Ifremer  
Unité Ressources Marines en Polynésie, PDG-RBE-RMPF

• **Dillon Monroe**  
dillonjmonroe@gmail.com  
Texas State University  
GASP lab

• **Adrian Moore**  
moorea@umn.edu  
University of Minnesota, Twin Cities

• **José Moreira**  
j.miguel.moreira@tecnico.ulisboa.pt  
University of Lisbon, IST

• **Alaia Morell**  
amorell@ifremer.fr  
IFREMER  
Boulogne-sur-mer

• **Erik Muller**  
bbleus@yahoo.com  
UCSB  
MSI
• Cheryl Murphy  
camurphy@msu.edu  
Michigan State University  
Center for PFAS Research

• Vaskar Nepal  
vnepalkc@vims.edu  
Virginia Institute of Marine Sciences  
Fisheries Sciences

• Dirk Nickisch  
dirk.nickisch@rifcon.de  
Rifcon GmbH

• Sylvie Oddou-Muratorio  
sylvie.muratorio@inrae.fr  
INRAE  
ECOBIOP

• Carlos Oliveira  
carlosklein0@gmail.com  
Universidade Federal de Goiás  
Theory, Metacommunity and Landscape Lab

• Miquel Palmer  
palmer@imedea.uib-csic.es  
Institut Mediterrani d’Estudis Avancats  
IMEDEA

• Laure Pecquerie  
laure.pecquerie@ird.fr  
IRD  
Lemar

• Heidi Pethybridge  
Heidi.Pethybridge@csiro.au  
Oceans and Atmosphere  
Ecosystem modelling

• Jean-Christophe Poggiale  
jean-christophe.poggiale@univ-amu.fr  
Aix-Marseille University  
Mediterranean Institute of Oceanography

• Suzanne Poiesz  
suzanne.poiesz@nioz.nl  
Royal Netherlands Institute for Sea Research

• Emilien Pousse  
emilien.pousse@noaa.gov  
NOAA  
NEFSC Milford, CT

• Ilie Racotta  
iracotta@cibnor.mx  
Centro de Investigaciones Biologicas del Noroeste  
Metabolismo energetico

• Kim Rakel  
rakel@gaiac-eco.de  
Research institute gaiac
• Aude Ratier
  aude.ratier@univ-lyon1.fr
  University of Lyon, Lyon I
  LBBE

• Charlotte Récapet
  charlotte.recapet@normalesup.org
  Université Pan Pays de l’Adour
  UMR 1224 ECOBIOP

• Laure Regnier-Brisson
  laure.regnier.brisson@ifremer.fr
  Ifremer
  DYNECO/LEBCO

• Jeffrey Ren
  j.ren@niwa.co.nz
  NIWA

• Romain Richard
  romain.richard@mail.nsysu.edu.tw
  National Sun Yat-sen University
  Department of Biological Sciences

• Konstantina Rizou
  rikonstantina@gmail.com
  University of Patras
  Ecology of Aquatic systems

• Juan Francisco Robles
  jfrobes@ugr.es
  University of Granada
  Andalusian Research Institute in Data Science and Computational Intelligence, DaSCI Institute

• Vanessa Roeben
  vanessa.roeben@bayer.com
  Bayer Crop Science

• Mark Rowe
  mark.rowe@noaa.gov
  NOAA
  Great Lakes Environmental Research Laboratory

• Sabrina Russo
  srusso2@unl.edu
  University of Nebraska-Lincoln
  The Russo Laboratory

• Bastien Sadoul
  bastien.sadoul@agrocampus-ouest.fr
  Agro Campus Ouest
  Pôle halieutique, mer et littoral

• Trystan Sanders
  t.b.sanders@soton.ac.uk
  University of Southampton
  Marine Biology and Ecology

• Samantha Abreu Alves Santos
  samanthaabreualves@gmail.com
  Universidade Estadual Paulista
  mathematical modeling laboratory
• Sofia Saraiva  
saraivadasneves@hotmail.com  
University of Lisbon  
MARETEC

• Adriana Sardi  
adrianasardi@gmail.com  
Université de Bordeaux  
EPOC-LPTC

• Christoph Schür  
schuer@bio.uni-frankfurt.de  
Goethe University Frankfurt  
Aquatic Ecotoxicology

• Teresa Schwemmer  
teresa.schwemmer@stonybrook.edu  
Stony Brook University, School of Marine and Atmospheric Sciences

• Eleni Servou  
elenservou@gmail.com  
HCMR  
University of Creta

• Yu Shuangen  
yushuangen@163.com  
Ocean University of China

• Daniel Small  
daniel.small@dfo-mpo.gc.ca  
Institut Maurice-Lamontagne

• Isabel Smallegange  
i.smallegange@uva.nl  
Institute for Biodiversity and Ecosystem Dynamics  
University of Amsterdam

• Tânia Sousa  
taniasousa@tecnico.ulisboa.pt  
Instituto Superior Técnico

• Orestis Stavrakis-Zachou  
ostavrak@hcmr.gr  
University of Crete

• Brecht Stechele  
brecht.stechele@ugent.be  
Ghent University  
Department of Animal Sciences and Aquatic Ecology

• Laura Steeves  
laura.steeves@dal.ca  
Dalhousie University  
Marine Affairs Program

• Louise Stevenson  
stevensonlm@ornl.gov  
Oak Ridge National Laboratory  
Environmental Sciences Division
• Xin Sun
  307368070@qq.com
  Ocean university of China
  Laboratory for Marine Fisheries Science and Food Production Processes

• Hend Taboubi
  hend.bejaoui@hotmail.fr
  Isb
  Isst

• Liz Talbot
  sat@pml.ac.uk
  Plymouth Marine Laboratory

• Tjui Yeuw Tan
  tan.tjui-yeuw@unesp.br
  Universidade Estadual Paulista
  UNESP, Laboratório de Modelagem Matemática

• John A. Theodorou
  jtheo@upatras.gr
  Dept of Animal Production, Fisheries & Aquaculture
  Aquatic Ecology Systems

• Yoann Thomas
  yoann.thomas@ird.fr
  IRD
  LEMAR

• Joaquim Tomàs-Ferrer
  jtomas@imedea.uib-csic.es
  Consejo Superior de Investigaciones Científicas
  Institut Mediterrani d’Estudis Avançats

• Sara Tramontini
  sara.tramontini@efsaeuropa.eu
  European Food Safety Authority

• Marie Trijau
  marie.trijau@ibacon.com
  ibacon GmbH
  Ecological modelling section

• Marine Uguen
  marine.uguen@hotmail.fr
  Université de Lille
  Laboratoire d’Océanologie et de Géosciences, LOG

• Jahangir Vajedsamiei
  jahanvajed@gmail.com
  GEOMAR
  Benthic experimental ecology

• Jaap van der Meer
  jaap.vandermeer@wur.nl
  Wageningen Marine Research

• Anieke van Leeuwen
  anieke.van.leeuwen@nioz.nl
  Royal NIOZ
  Fish Ecology, COS
• **Marine Vandenberghe**  
marine26.vdb@orange.fr  
University of Lille / CNRS  
UMR 8187 LOG

• **Fabio Vannucchi**  
fs.vannucchi@unesp.br  
São Paulo State University  
Instituto de Biociências, Câmpus do Litoral Paulista

• **Karel Vlaeminck**  
karel.vlaeminck@ugent.be  
Ghent University  
Department of Animal Sciences and Aquatic Ecology

• **Neil Waters**  
nawaters3@gmail.com  
University of Tokyo  
Kimura Lab

• **Kristi Weighman**  
kristi.weighman@ugent.be  
Ghent University  
GhenToxLab

• **Mathieu Woillez**  
mathieu.woillez@ifremer.fr  
Ifremer  
Laboratoire de Biologie Halieutique

• **Yvonne Wolf**  
yvonne.wolf@bayer.com  
Bayer AG, CropScience Division

• **Barrett Wolfe**  
barrett.wolfe@utas.edu.au  
Institute for Marine and Antarctic Studies, University of Tasmania

• **Liyan Xie**  
liyan.xie@bios.au.dk  
Aarhus University  
Climatic Stress Lab