# BOOK OF ABSTRACTS

### Fifth international symposium on Dynamic Energy Budget theory

May 31 - June 02 2017, Tromsø, Norway

We welcome you to the 5<sup>th</sup> international DEB symposium:

### Metabolic Organization Plays a Role in Planetary Stewardship

Brought to you by Akvaplan-niva, the IRD (French Research Institute for Development), IST (Instituto Superio Técnico), University of Melbourne, University of Crete, NIOZ (Netherlands Institute for Sea Research), MIO/ university of Aix-Marseille (Mediterranean Institute of Oceanography).

This year's event includes includes 75 participants from 20 different countries (Australia, Belgium, Canada, Croatia, Denmark, France, Germany, Greece, Italy, Japan, Netherlands, Norway, Portugal, Spain, Sweden, Switzerland, Taiwan, Tunisia, UK, USA). The programme includes five keynotes speakers, 30 contributed talks and 14 posters.

The symposium is linked to the international research project FREE: "FRamework for integrating Eco-physiological and Ecotoxicological data into marine ecosystembased management tools." The FREE project is a natural follow-up to the aquaDEB projects (http://www.ifremer.fr/aquadeb/). AquaDEB was formed after the 2001 edition of the DEB course, resulted in 3 special issues, and initialised the very first international DEB symposium in 2009, Brest. Scientists involved in these earlier initiatives coalesced over time into nodes of an international network of expertise, known as the DEBnet. The network continuously develops and applies DEB theory for practical applications in fisheries, aquaculture, eco-toxicity, pharmacology, medicine, biotechnology, sewage water purification, sustainable development, and economics. The focus of the FREE project is on synergizing these areas of expertise with the aim to develop a scientific basis for "ecosystem-based management" approaches for biomes of system earth (oceans, forests, deserts etc.). The DEB courses and symposia occur every other year, hosted by different nodes of the DEBnet. These events are central to synergizing disciplines and knowledge.

Over 500 papers have been published on diverse applications in waste water management, environmental risk assessment, human health, and more. Moreover, there have been 5 special issues on Dynamic Energy Budget theory. We are now organising a 6<sup>th</sup> special issue in the context of the 2017 courses and symposia. This is a celebratory milestone in the development and application of DEB theory in helping to solve contemporary societal problems in system earth's biomes. We warmly welcome your innovative, cross-disciplinary research to this special issue for the Journal of Sea Research.

A note on the title of this symposium: why does metabolic organisation play a role in planetary stewardship? Planet earth constitutes our life-support system providing the very water, food and air that we breathe. Life, and so metabolic organization, plays a key role in these services. The dynamic energy budget (DEB) theory has undone continuous research and development over the last 38 years making it the best tested quantitative theory on metabolic organization with unprecedented breadth of scope. DEB theory gave birth in 1979 to a completely new, biology-based, approach to environmental risk assessment whose wider adoption is increasingly essential in the face of the rapidly growing number of new chemicals entering the environment coupled with rapid climate change.

The aims of the symposium are:

- 1. Mixing researchers in biology, mathematics, engineering, chemistry, and physics to solve biological/ecological problems;
- 2. Introducing the DEBnet to the arctic research community, bringing international expertise in modelling biological systems to Norway
- 3. Introducing new challenging problems where mathematical analysis is used for solving ecological questions.
- 4. Stimulating biological research in the framework of physics, using explicit mechanistic assumptions and thinking about the implications of these assumptions in a new context (possibly never studied before).
- 5. Creating a platform for following up on ideas presented in previous lectures given in DEB courses
- 6. Bringing fresh ideas into the DEB community by inviting keynote speakers outside the DEB community.
- 7. Maximizing the broadness of scope of DEB applications and offering this to participants of the DEB course by integrating the symposium into the course.

All organizational and logistical aspects of the event can be found online:

- Scientific committee : <u>http://deb.akvaplan.com/symcommittee.html</u>
- Practical information concerning accommodation and travel: <u>http://deb.akvaplan.com/accomodation.html</u> and <u>http://deb.akvaplan.com/travel.html</u>
- Program: <u>http://deb.akvaplan.com/symprogram.html</u>

This event is organised by Akvaplan-niva with support from the Research Council of Norway MARINFORSK programme (project # 268237), and in association with the project <u>"FRamework for integrating Eco-physiological and Ecotoxicological data into marine ecosystem-based management tools</u>" (project # 255295). Additional support is provided through ARCEx – The Research Centre for Arctic Petroleum Exploration (RCN project # 228107)









**Oral Presentations** 

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### Wednesday, 31st May

08:00 Registration opens

09:00 Introduction (Starrlight Augustine)

### Chair 1: Mike Kearney

- 09:15 Environmental sustainability challenges in the Arctic developing solutions with the help of DEB (Keynote 1 JoLynn Carroll)
- 10:00 Relating sub-organismal processes that occur at the molecular and cellular level to dynamic energy budgets (Cheryl Murphy)
- 10:20 Using Dynamic Energy Budget theory at the population scale to limit the risk of structural sensitivity (Clément Aldebert)
- 10:40 Decrease in food abundance in the non-breeding habitat may increase resilience of migratory populations (Catalina Chaparro-Pedraza)
- 11:00 Coffee, tea break
- 11:30 Modelling effects of environmental stressors on the population dynamics of the European sturgeon: first insight on downstream migration (Maxime Vaugeois)
- 11:50 Exploring the effect of temperature change on the spatial distribution of benthic species with a DEB-IBM model (Yoann Thomas)
- 12:10 Discussion / Questions
- 12:30 Lunch

### Chair 2: Tânia Sousa

- 14:00 Effects of mixtures explained (Keynote 2- Jan Baas)
- 14:50 Modelling individual and population dynamics in application to risk assessment of chemical mixtures (Gonçalo Marques)
- 15:10 Mechanistic model of Paralytic Shellfish Toxins (PSTs) accumulation in the Pacific oyster, Crassostrea gigas (Emilien Pousse)
- 15:30 Dynamic Energy Budget for modelling 'imprinting': insights from rainbow trout (Bastien Sadoul)
- 15:50 Tea & posters

### Chair 3: Nina Marn

- 16:20 A Dynamic Energy Budget model of fish bioenergetics under exposure to realistic PCB and PBDE mixtures: consequences for life-history traits (Khaled Horri)
- 16:40 Dynamics of lipid storage in marine copepods and its consequences for effects of oil pollution (Tjalling Jager)
- 17:00 DebX MOOC on modelling metabolism at the individual level using DEB theory (Tânia Sousa)
- 19:00 Dinner at Skirri

### Environmental sustainability challenges in the Arctic – developing solutions with the help of DEB

### JoLynn Carroll<sup>1</sup>

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Rich in natural resources, the Arctic is experiencing a significant increase in sea-based activities related to maritime transport, offshore energy, tourism, coastal development, fisheries and aquaculture. This northwards expansion of industrialization is partly due to new discoveries of natural resources but also to improved access routes and newly available infrastructure in the region. In 2006, Norway became the first nation to establish an ecosystem-based management (EBM) policy approach to reconcile their nation's maritime activities with environmental sustainability. The European Union followed in 2008 with the adoption of the Marine Strategy Framework Directive. Translating EBM policy into practice requires development of ecosystems monitoring methods and modeling tools to identify changes and assess impacts. The consistent application of mechanistic principles, provided by the DEB approach, is essential to achieving this aim. In this presentation, I will present, from the end-user perspective, example applications of the DEB approach for environmental sustainability in the Arctic setting.

### **Biography**:

Trained originally as a sedimentary biogeochemist, Professor Carroll is Assistant Director of <u>Akvaplan-niva</u>, a leading organization in Norway's <u>High North Research Centre for</u> <u>Climate and the Environment</u> (Fram Center). She holds an adjunct Professorship at the University of Tromsø. Professor Carroll's activities relate to the detection of ecosystem responses to multiple anthropogenic impact factors, such as climate, fisheries, and petroleum development. Her work involves integrated problem-solving fostered through collaboration across institutional boundaries and creating partnerships among government, industry, and academia. At present, Professor Carroll is leading a large multi-disciplinary R&D program jointly financed by government and industry to create a flexible modeling platform for scenario assessments that integrates state of the art models and scientific knowledge on the ecosystem of the Barents Sea. She is the lead environmental scientist in two Norwegian Research Council supported Centers of Excellence – <u>Center for Arctic Gas Hydrate</u>, Environment and Climate (CAGE) and <u>Research Center for Arctic Petroleum Exploration</u> (ARCEx), both based at UIT – The Arctic University of Norway.

### Relating sub-organismal processes that occur at the molecular and cellular level to dynamic energy budgets.

### Cheryl Murphy<sup>1</sup>, Roger Nisbet<sup>2</sup>

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Ecological Risk Assessment quantifies the likelihood of undesirable impacts of stressors, primarily at high levels of biological organization: populations to ecosystems. However, data for assessing the impact of stressors usually comes from tests on individual organisms and increasingly from suborganismal studies at the molecular and cellular level. These tests generally cost less, are more high-throughput and minimize the use of animals. Interpreting these suborganismal data at the population or ecosystem level is challenging. We know how to relate individual (whole organism) responses to population dynamics using individual-based models, and there are emerging ideas on how to make connections to ecosystem services. By contrast, there is no established methodology to connect individual performance to suborganismal dynamics, in spite of progress in identifying Adverse Outcome Pathways (AOPs) that link "molecular initiating events" to ecologically relevant "key events". We are co-PIs of a working group at the National Center for Mathematical and Biological Synthesis that is exploring the feasibility of using DEB models of individual organisms as a "pivot" connecting suborganismal processes to higher level ecological processes. AOP models quantify explicit molecular, cellular or organ-level processes, but do not offer a route to an integrated characterization of arowth, reproduction, and survival. DEB models do describe these processes, but use abstract variables with undetermined connections to suborganismal biology. We propose linking DEB and quantitative AOP models by interpreting AOP key events as measures of damageinducing processes in a DEB model. We will report on the type and structure of data that are generated for AOPs. We also report on our progress on two case studies based on Daphnia and rainbow trout that merge information collected for AOPs with DEB. For rainbow trout, we focused on endocrine disruption for which there are quantitative AOPs that integrate molecular, cellular and organ level responses to predict effects on reproduction. Connecting with a DEB representation required modifying the "standard" DEB model to include feedbacks that characterize the integrated effects of hormonal control mechanisms. With Daphnia, there is little organ level data, so we seek correlative connections with transcriptomic data. Daphnia were exposed to a gradient of food rations and contaminant concentrations over time with measurements of gene expression and contaminant body burdens along with routine measurements of size, survival and reproduction. Gene expression data (interpreted as key events), summarized using statistical analyses appear to exhibit some molecular responses that may correlate with parameters controlling relevant DFB fluxes.

### Using Dynamic Energy Budget theory at the population scale to limit the risk of structural sensitivity

Clement Aldebert<sup>1</sup>, Bob W Kooi<sup>2</sup>, David Nerini<sup>3</sup>, Jean-Christophe Poggiale<sup>3</sup>

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The success of DEB theory to explain empirical data comes mainly from its focus on one the best defined levels of organization, the individual level. The individual level allows us to easily create mass and energy budgets, and thus provides a basis for a mechanistic description of individual life. At the population level, the interplay between processes occuring at multiple scales (individual, group, population) prohibits an accurate and generic modelling of key processes like predation. Even functional responses that are considered mechanistic (e.g.~Holling functional response) neglect various processes and might not be the best statistical description of data. This would not be a problem if similar functional responses lead to the same model predictions. However, model predictions in term of stable states and system resilience can be strongly affected by a slight change of model formulation, a phenomenon coined structural sensitivity. However, structural sensitivity has mostly been explored in models built at the population level, without describing individual metabolism. The question I will address is: Is structural sensitivity a merely mathematical issue or might it be a widespread problem for predictions in ecology? First, in data sets ranging from bacteria to mammals, I will show that similar mathematical functions fit functional response (or uptake rate) data with the same accuracy. This indicates that structural sensitivity may affect the predicted population sizes for many predator-prey systems. Second, by studying predator-prey models that describe individual metabolism using DEB theory, I will show that model predictions (bifurcation analysis) are less affected by structural sensitivity in models that include explicit resource dynamics and individual maintenance. In simple words, neglecting these processes in an ecological model, for instance by using the well-known logistic growth equation, is not only an inappropriate approximation of the ecological system, but also a source of more uncertain predictions. As a summary, DEB theory provides a theoretical basis to describe individual metabolism, and this background allows one to build models that are less sensitive to the uncertain formulation of more complex processes. This conclusion provides strong guidance to ecologists in their modelling choices, and supports the use of population models based on a metabolic theory for individuals.

### Decrease in food abundance in the non-breeding habitat may increase resilience of migratory populations

### Catalina Chaparro Pedraza<sup>1</sup>, André de Roos<sup>1</sup>

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Migratory species undergo a habitat switch between a breeding and a non-breeding habitat. The habitat switch has enormous consequences for the individual life history. In particular, we focus on the effects of two factors that affect the individual energetics: the change in food abundance between habitats and the energetic cost of the breeding travel. In spite of the well-known effects of these factors on the individual life history, in particular on fecundity, and that life history affects population dynamics, the role that the life history of individuals experiencing a habitat switch has on the ecology of a migratory population has not been studied. To do so, we formulate a structured population model for a population with a habitat switch. We base this population model on a Dynamic Energy Budget DEB model to describe the individual life history and parameterize the model with data of Atlantic salmon (Salmo salar). High energetic cost of the breeding travel causes extinction of a population. Surprisingly, the population is less likely to be extinct when food availability and hence the somatic growth potential in the non-breeding habitat is lower. During the habitat switch (smolting) from the breeding to the non-breeding habitat, individuals experience a discrete increase in food abundance that affects their energy allocation: the growth rate increases but the energy density decreases. Thus, individuals allocate more energy to structural mass and less to energy reserves. This change in energy allocation is large when individuals experience a large change in food abundance, which occurs when food abundance is high in the non-breeding habitat. These individuals grow larger and have a leaner body mass. During the breeding season, individuals depend on energy reserves for both traveling and reproducing. Larger individuals experience a stronger decline in energy reserves during the breeding travel, that added to a leaner body mass results in a depletion to a very low level of their energy reserves when the cost of the breeding travel is high. As a consequence, a small amount of energy is remaining to reproduce. In contrast, individuals migrating to a non-breeding habitat with low food abundance results in smaller individuals with higher energy density, that after the breeding travel count with a larger amount of energy to invest in reproduction. Thus, low food conditions in the non-breeding habitat causes the individuals to reproduce more efficiently and the population less vulnerable to extinction.

### Modeling effects of environmental stressors on the population dynamics of the European sturgeon: first insight on downstream migration

#### Maxime Vaugeois<sup>1</sup>, Patrick Lambert<sup>2</sup>

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European sturgeon (Acipenser sturio) is an anadromous fish that was previously found on most coasts of Europe, and that is nowadays a critically endangered species (IUCN 2010). Over-fishing, installation of impassable dams and gravel extraction are, among others, reasons for its limited geographical distribution and its small population size. Actually, the last population is reproducing in the Garonne basin near Bordeaux, southwest of France, and the last known natural reproduction event occurred in 1994. In order to avoid extinction, the applied strategy since 1985 has been to release young fish into the natural environment. Nevertheless, recently recorded data in the Garonne basin reveals hypoxic and high-temperature events, and also significantly high levels of pollution in estuary zone where juveniles are likely to grow. Therefore, the combined influence of these factors on the early developmental stages of this species needs to be assessed.

The long-term goal of our project is to provide key information for improving the management of young fish releases, especially age at release and release sites that maximize fish survival. In this purpose, we first calibrated a standard Dynamic Energy Budget (DEB) model that represent the whole life cycle of this species. The calibration is based on the large dataset provided by the long-term breeding of the ex-situ broodstock in Irstea facilities. This model was then integrated into a spatially defined Individual-Based Model (IBM) simulating the European sturgeon population dynamics in the Garonne basin. We firstly used this DEB-IBM model to better understand the mechanisms responsible for the downstream migration and secondly to estimate the impacts of external stressors on this phenomenon. To infer these impacts, we used data from the STURTOP project which partly focused on assessing habitat quality for first development stages and the vulnerability of embryos and larvae to different stressors. Results show differences in downstream migration pattern regarding the main mechanism involved, the food dependent or the maturity dependent one. Environmental stressors influence migration pattern depending on the impacted DEB parameter(s) and the migration mechanism.

### Exploring the effect of temperature change on the spatial distribution of benthic species with an IBM-DEB model

Yoann Thomas<sup>1</sup>, Alain Menesguen<sup>1</sup>, Cédric Bacher<sup>1</sup>

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Projecting scenarios for the evolution of species distribution is a major challenge in ecology, especially in the context of global changes. The distribution of species is controlled by a combination of physical and biological constraints, which determine the establishment and sustainability of populations. Most of the benthic species display a pelagic larval phase, thus hydrodynamics may be one of the main driver of the connectivity between populations. Moreover, species-specific biological traits linked to environmental factors will determine physiological performances. It is therefore necessary to evaluate the contribution of each factor in order to implement realistic evolution scenarios in species distribution modelling approaches. Here, we explore the effect of global warming on the dynamics and connectivity of several benthic species in the Northeast Atlantic. We combine (i) a statistical modelling approach defining potential habitats, and (ii) a mechanistic individual-based modelling approach of population dynamics, taking into account the species biological traits through the Dynamic Energy Budget theory and the spatial connectivity process. The effect of temperature changes over the XXIst century is explored based on climate models projections from the Intergovernmental Panel on Climate Change (IPCC) scenarios. The effects of warming on populations' growth rate variation are quantified, compared between species and linked to the modification of their physiological performances and phenological patterns. Finally, our results allow exploring the influence of biological traits on patterns of species spatial distribution.

### Effects of mixtures explained

#### Jan Baas<sup>1</sup>

#### <sup>1</sup>Centre for Ecology and Hydrology, UK, <u>janbaa@ceh.ac.uk</u>

In my presentation, I will give some background on the line of reasoning in ecotoxicology and how regulation has influenced this line of reasoning. I will explain how the use of DEB-based approaches can help our understanding of effects of toxicants under real life conditions with examples of applications and a future perspective on the progress in this area of research.

### Biography:

After my graduation as a chemist, I worked for 9 years at a Dutch contract research organisation The Netherlands Institute for Applied Scientific Research in Delft on environmental exposures. This was the first time I was faced with effects of possible effects of simultaneous exposures to multiple compounds (or mixtures) and the general incapability to deal with mixture effects. This led to a PhD at Vrije Universiteit of Amsterdam with Prof. Kooijman as a promotor and Dr Jager as co-promotor in understanding and predicting effects of mixtures. I am now based at the UK Centre for Ecology and Hydrology, where I still work on effects of mixtures.

### Modelling individual and population dynamics in applications to risk assessment of chemical mixtures

Gonçalo Marques<sup>1</sup>, Starrlight Augustine<sup>2</sup>, Jean-Lou Dorne<sup>3</sup>, Jan Baas<sup>4</sup>

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In ecological risk assessment of chemicals, hazard identification and hazard characterisation are most often based on ecotoxicological endpoints expressed as summary statistics such as Effect Observed Concentrations or Lethal Concentration values and No-Effect-Concentrations. Considerable research is currently ongoing to further improve methodologies to take into account toxicokinetic aspects in toxiclogical assessments, extrapolations of toxic effects observed on individuals to population effects and combined effects of multiple chemicals effects. In this context, the principles of the Dynamic Energy Budgets (DEB), namely the conservation and allocation of energy to different life-supporting processes in a wide variety of different species, have been applied successfully to the development of a number of DEB models. DEB models allow the incorporation of effects on growth, reproduction and survival within one consistent framework.

The European Food Safety Authority (EFSA) lead a call for a project with the overall objectives being to model population dynamics of aquatic and terrestrial organisms using DEB models and explore their potential applications for the ecological risk assessment of combined exposure to multiple chemicals "chemical mixtures".

DEB theory and models are very useful tools for extrapolations in risk assessment since many aspects of energy budgets are not species-specific but apply to many different organisms. The DEB framework provides a natural physiological interpretation of its parameters, has a high extrapolation potential since it allows for the straightforward use of body-size scaling relationships (co-variation of parameter values among species). These rules are useful for extrapolations of model predictions from one species to another and from one chemical compound to another. The most important extrapolations that can be envisaged using DEB models are from:

- Individual to population;
- Species to species;
- Chemical to chemical (particularly for structurally related compounds).

Finally, DEB models allow incorporating effects of stressors other than chemicals, like food availability, temperature, salinity, parasites, etc. DEB theory provides the proper context to capture how individuals progress their way through life and how stressors affect specific parameter values.

In this talk we will present some preliminary results of the project and future directions. We will discuss population model approaches as well as approaches for modelling the effects of chemical mixtures and present some DEBecotox products.

### Mechanistic model of Paralytic Shellfish Toxins (PSTs) accumulation in the Pacific oyster (Crassostrea gigas)

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The oyster Crassostrea gigas is one of the most commercialized molluscs in the world that can be affected by various agents such as pathogens (bacteria, viruses), parasites, xenobiotics and/or toxic algae. This filter-feeder can accumulate phycotoxins while feeding on harmful algal blooms (HAB), including paralytic shellfish toxins (PST). To protect human health, closures of shellfish harvesting are declared during HAB that impact the aquaculture industry.

Different mathematical models were developed to simulate the kinetics of accumulation/detoxification of paralytic shellfish toxins (PSTs) in C. gigas. None of them, however, allowed to describe accurately the interactions between oyster physiology and toxins. Dynamic energy budget (DEB) models (1) were demonstrated as powerful tools to quantify energy flows in molluscs and particularly in C. gigas (2). Coupling bio-accumulation to DEB models has allowed to simulate properly the dynamics of contaminants in marine organisms (3, 4) by taking into account contaminant uptake from the environment, food quantity and quality and excretion due to decontamination and spawning, and by assessing the influence of physiological variables (e.g. body size, tissue composition) on the contaminants kinetics.

In order to calibrate a mechanistic model of accumulation and detoxification of PST in *C. gigas* based on DEB theory, two experiments were performed, consisting in exposing *C. gigas* to the toxic dinoflagellate *Alexandrium minutum*. In a first experiment, the toxin accumulation in oysters was monitored over 2 days at the individual scale. A significant linear relationship between PST concentrations in oyster tissues and their individual ingestion rate was observed. Moreover, individual respiration rates were also linked to toxin accumulation after 2 days of exposure. Damages caused by the toxins may account for increasing the oyster respiration rate, i.e. in their maintenance costs. The second experiment consisted in exposing juvenile *C. gigas* to *A. minutum* for 2 months. Oyster growth, gametogenesis and toxin contents were estimated weekly to quantify the effects of PSTs on oyster maintenance costs. From these two experiments, impacts caused by the toxin on the oyster bioenergetics were studied. A DEB model was produced to simulate the evolution of toxin concentration through processes of ingestion, accumulation and detoxification and the effects of toxins on oysters.

(1) Kooijman 2000. DEB theory for metabolic organisation, Cambridge Univ. Press. (2) Alunno-Bruscia et al. 2011. J Sea Res 66, 340-348. (3) Casas & Bacher 2006. J Sea Res 56, 168-181. (4) Eichinger et al. 2010. J Sea Res 64, 373-385.

### Dynamic Energy Budget for modeling 'imprinting': insights from rainbow trout

Bastien Sadoul<sup>1</sup>, Starrlight Augustine<sup>2</sup>, Mathilakth M. Vijayan<sup>3</sup>

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Exposure to stressors at sensitive periods during early development can lead to long lasting effects on growth, reproduction and stress coping capacities. This phenomenon also called 'imprinting' has been demonstrated to be the consequence of diverse type of environmental stressors, including social modifications, physical disturbances and toxicant exposures. Previous work demonstrated that deposition of environmentally relevant concentrations of the endocrine disruptor bisphenol A (BPA) in eggs disrupted the growth trajectory over a 2-year period in rainbow trout. This long lasting effect was observable in terms of growth, but may also be related to the lasting disruption of maintenance mechanisms, which are up-regulated during the first months of life and then downregulated in BPA exposed fish. The use of Dynamic Energy Budget (DEB) modelling can help bridge the data observed at the individual and the molecular levels, and create a framework for making biological sense at the population level. Nevertheless, parameters of classic DEB models, commonly set to be fixed over given periods of time, need to be modified to take into account the temporal patterns, similar to the imprinting effects observed in our study. As a consequence, DEB has to allow effects to be carried over time, similarly to the longterm effects we saw in trout raised from eggs exposed to BPA. We present here a precise DEB model for a non-exposed control rainbow trout using data gathered from the literature, as well as our insights into a theoretical approach, which take into account the physiological imprinting in a DEB model.

### A Dynamic Energy Budget model of fish bioenergetics under exposure to realistic PCB and PBDE mixtures: consequences for life-history traits

<u>Khaled Horri</u><sup>1</sup>, Sébastien Alfonso<sup>2</sup>, Xavier Cousin<sup>3</sup>, Catherine Munschy<sup>4</sup>, Véronique Loizeau<sup>5</sup>, Lucette Joassard<sup>2</sup>, Didier Leguay<sup>2</sup>, Salima Aroua<sup>6</sup>, Marie-Laure Bégout<sup>2</sup>, Bruno Ernande<sup>1</sup>

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Persistent organic pollutants (POPs) gather a wide number of chemicals which are of great concern because of their persistence, bioaccumulation and toxicity. Among POPs, polychlorinated biphenyls (PCBs) and polybrominated diphenyl ethers (PBDEs) were shown to affect fish physiological traits. Their toxicity and underlying physiological modes of action (PMOA), at the individual level, have been studied through experimental exposure. However, experimental studies approaching environmental situations are scarce, i.e., in most cases, exposure conditions are quite different from environmental situations because of the use of single congeners and/or high concentrations. The effects of chemical stressors at the individual level are often used to infer population level effects using dynamical models. Among these, bioenergetic models are often employed to describe the effects of chemical stressors and their PMOA at the individual level and are particularly well suited for extrapolating these effects to the population level through coupling with population dynamical models. One of the besttested and most extensive bioenergetic approaches is the Dynamic Energy Budget theory (DEB). In the present study, we used DEB theory to study the PMOA of PCBs and PBDEs mixture using data on growth and reproductive life-history traits in experimental control and exposed zebrafish populations. Fish exposure to PCBs and PBDEs mixture was conducted through diet from the first meal and throughout the life cycle of the fish. The selected PCBs and PBDEs mixture was chosen to approach environmentally relevant conditions in terms of both congener relative concentrations and compositions. A DEB model was calibrated for each treatment and sex. Then, estimated parameters of the DEB models were compared between control and exposed fish and various PMOA were tested by patterns comparison. We found that the PMOA of the PCBs and PBDEs mixture was through an increase of the fraction k of energy allocated to somatic maintenance and growth at the expense of that dedicated to maturation and reproduction. This shift of the energetic trade-off between growth and reproductive function was confirmed by the observed increase in growth and a decrease in reproductive output, which are related to this parameter. No confounding effect was observed on the other DEB parameters in exposed fish. Given the strong dependency of population dynamics on lifehistory traits, such individual-level effects of PCBs and PBDEs could affect fish population recruitment and dynamics and associated fisheries productivity for commercial species. This research was founded by the French National Research Agency, project Fish'N'POPs (ANR-13-CESA-020).

### Dynamics of lipid storage in marine copepods and its consequences for effects of oil pollution

### Tjalling Jager<sup>1</sup>, Bjørn Henrik Hansen<sup>2</sup>

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Mechanistic models are essential tools for interpreting and predicting the consequences of a changing environment on the life histories of marine organisms. The ENERGYBAR project (funded by the Research Council of Norway) has focussed on the effects of pollution related to offshore petroleum activities on the calanoid copepod Calanus finmarchicus. Within this project, we applied toxicokinetic models to analyse body-residue data, GUTS models to analyse effects on survival, and DEB-based (DEBkiss) models to understand the life history of the copepods, including the determinate growth and the dynamics of lipid storage.

Nauplius larvae do not have a lipid storage; this feature starts to build up in the early copepodite stages and finally fills up a large fraction of the body just before the moult to adulthood. As the relative size of the lipid sac increases over the copepodite life stages, this body-mass component should not be seen as a DEB-style reserve but as a reproduction buffer in the  $1-\kappa$  branch. The lipid sac is used to pay maintenance costs during diapause, but most of it is used in gonad maturation and in support of egg production. However, the exact implementation into the DEBkiss allocation scheme requires further study. For example, it remains unclear whether the switch from maturation to storage at puberty is complete, and it is unclear how adult females use food and the remaining storage to fuel egg production and maintenance needs. The lipids in the storage (mainly wax esters) have a very high affinity for hydrophobic chemicals, thereby influencing toxicokinetics and toxicity. With regards to the toxicokinetics, we have to consider the lipid sac and the structural part of the biomass as separate compartment. The influence of lipid content on toxicokinetics thus depends on the partition coefficients and rate constants associated with these two biomass compartments. Toxicokinetic knowledge is essential to predict exposure of predators feeding on copepods, and to assess maternal transfer of toxicants with the eggs. Furthermore, we can assume that only the concentration in the structural part is directly related to toxicity in the copepods themselves. Although our model predicts that a high lipid content provides limited protection for the copepods from toxicity of hydrophobic compounds, the results from acute toxicity studies show contrasting results.

In this contribution, we provide some of the highlights of the ENERGYBAR project, focussing on the dynamics of lipid storage and its consequences for body residues and toxicity.

### DebX - A Massive Online Open Course on Modelling Metabolism at the individual level using DEB theory

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Instituto Superior Técnico in collaboration with Akvaplan-niva are developing a 5week Massive Online Open Course (MOOC) to teach the basics for modeling metabolism at the individual level using DEB theory (https://courses.mooc.tecnico.ulisboa.pt/courses/course-v1:IST+debX+2017/about).

The course will be used (1) for flipped classrooms in IST for undergraduates in Environmental Engineering and Microbiology, (2) as a stand-alone course for PhD students and (3) as part of the International DEB courses.

The MOOC will have videos that will guide students through the topics explored in this course. Some of the videos will be tutorials that guide and show the students how to use Matlab files (that are freely available) to run a DEB model and estimate DEB parameters (the DEBtool package). Quizzes and open-ended questions will provide feedback allowing students to assess their knowledge while Matlab exercises will test and develop intuition about the dynamics of metabolism and the effect of each parameter on metabolism.

At the end of the course the students will be able to: (1) understand the organization of metabolism, (2) quantify metabolic rates such as growth and assimilation as a function of temperature and amount of food, (3) discuss important concepts for metabolic organization such as weak and strong homeostasis, (4) understand the impact of the area-volume relationship on metabolism, (5) explain general empirical patterns such as Kleiber's law and von Bertallanfy growth, (6) make mass, energy and entropy balances for organisms and (7) model the metabolism of an organism through its life cycle.

In this presentation, we will talk about the structure, the main goals, the contents and the assessment of the debX MOOC and will show some of the material already available. The aim is to obtain feedback from the audience in order to improve the debX MOOC.

### Thursday, 1st June

09:00 Arrival & Coffee

### **Chair 4: Roger Nisbet**

- 09:15 A simple application of a complex ecosystem model (Keynote 3 Sofia Saraiva)
- 10:00 Using modelling to investigate effects of climate warming on the reproduction of the Pacific oyster Crassostrea gigas in the bay of Brest: from 1960 to 2100 (Mélaine Gourault)
- 10:20 Modelling the growth of the gilthead seabream (Sparus auratus) for aquaculture using the Dynamic Energy Budget (Inês Lopes)
- 10:40 Effects of plastic ingestions on the life cycle of an endangered sea turtle (Nina Marn)
- 11:00 Coffee, tea break
- 11:30 DeBInfer: Bayesian inference for dynamic models in R (Leah Johnson)
- 11:50 Comparison between two Derivative-Free Optimization Methods for DEB parameter estimation of different species (Jéssica Morais)
- 12:10 Discussion / Questions
- 12:30 Lunch

#### Chair 5: Jaap van der Meer

- 14:00 General Ecosystem Models: virtual tools for the living world (Keynote 4 -Mike Harfoot)
- 14:50 Unexpected dynamics (including canard explosion) of fast-slow bitrophic food chains (Bob Kooi)
- 15:10 Population dynamics with multiple limiting nutrients: Life history mediated effects (Romain Richard)
- 15:30 Dynamic energy budgets in individual based population models: cross species test and application (André Gergs)
- 15:50 A multi-agent approach to couple physiological and foraging models: Optimization of vulture foraging strategies (Dorra Louati)
- 16:10 Tea & posters
- 19:00 Networking Dinner at Polaria Aquarium

### A simple application of a complex ecosystem model

#### <u>Sofia Saraiva</u>1

### <sup>1</sup>Swedish Meteorological and Hydrological Institute, Oceanography Unit <u>sofia.saraiva@smhi.se</u>

In this talk I will describe a process oriented model that integrates physical, biogeochemical, ecological and physiological factors governing bivalve populated marine ecosystems. This modelling tool is the result of the coupling between an individual-based population model for bivalves (based on the DEB theory) and a hydrodynamic/biogeochemical model (MOHID). The model was implemented in the Balgzand area (Wadden Sea, The Netherlands) in a fine resolution domain to study mussel population dynamics and to quantify the influence of mussel communities on the pelagic system. I will describe some of the main results and achievements of this work but also the main uncertainties on the data, on the model setup and on the processes description as a step into the possible future applications.

### **Biography**:

I graduated on Environmental Engineering in 2001, by Instituto Superior Tecnico (IST), University of Lisbon (UL). In the same year, I started a junior position at MARETEC (IST) where I worked for several years, on several different projects and topics, always related with ecosystem modelling and biogeochemical cycles of nutrients. In 2005, I concluded my MSc project on modelling macroalgae in Ria de Aveiro (Portugal). Two years ago I defended my PhD project: 'Modelling bivalves in estuaries and coastal areas', which was a joint project between the University of Lisbon (Portugal), Vrije Universiteit Amsterdam (NL) and the Royal Netherlands Institute for Sea Research (NIOZ, NL). During the PhD I explored in detail the metabolic processes of bivalves, their growth and population dynamics, but also their effect on the pelagic system. I developed and coupled an individual-based population model (using the Dynamic Energy Budget theory) to a hydrodynamic and biogeochemical model (MOHID Water Modelling System) and applied it to a region of the Wadden Sea (The Netherlands). I am now based at the Swedish Meteorological and Hydrological Institute, Oceanography Unit, Research Department. In my current project we aim to build future climate projections on the water quality and lower trophic levels in the Baltic Sea. These scenarios are performed with the coupled physical-biogeochemical RCO 3D numerical model different meteo-oceanographic forcing that is the result of the downscale of Global Climate Models.

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### Using modelling to investigate effects of climate warming on the reproduction of the Pacific oyster Crassostrea gigas in the bay of Brest: from 1960 to 2100.

<u>Mélaine Gourault</u><sup>1</sup>, Sébastien Petton<sup>2</sup>, Yoann Thomas<sup>3</sup>, Laure Pecquerie<sup>4</sup>, Gonçalo Marques<sup>5</sup>, Christophe Cassou<sup>6</sup>, Elodie Fleury<sup>2</sup>, Yves-Marie Paulet<sup>1</sup>, Stéphane Pouvreau<sup>2</sup>

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One of the potential ecological consequences of a changing climate on marine species result in gradual or sudden changes in physiology, species distribution, species assemblages and/or phenology. In that context, the aim of this paper was to analyze the effects of the past, present and future climate variability on the reproduction of a key species, the Pacific oyster Crassostrea gigas, in the Bay of Brest, at the northern limits in France where its reproduction is still efficient. Using a biological and environmental dataset of 6 years (2009-2014) and the Dynamic Energy Budget (DEB) model previously developed, tested and proven for C. gigas, we first analyzed the actual variability of C. gigas reproductive cycle (spawning events, synchronicity and fecundity) according to environmental forcing parameters (temperature and phytoplankton). In a second step, the model was used to explore the reproductive strategy of this species through (1) a historical reconstruction exercise since 1960 and (2) a set of predictive simulations from 2040 to 2100, using two contrasted IPCC climate scenarios (RCP2.6, the "drastic decrease of CO2 emissions scenario" and RCP8.5 the "business as usual" scenario). In addition to these three temperature evolution scenarios, six potential phytoplankton dynamics were used in each case.

Altogether, these simulations highlighted three major results. First, due to recent warming, spawning events are more frequent nowadays than before the 90s. According to RCP8.5, these no-spawning summers will progressively disappear at the horizon 2060 but will remain within the same proportion under RCP2.6 scenario. Secondly, simulations show that the spawning date but also the synchronicity between individuals rely mainly on phytoplankton abundances and seasonal dynamics through an unexpected and complex coupling effect of phytoplankton dynamics and temperature cycle. Generally, earlier spawning takes places during August and nothing will change under the RCP2.6 scenario. Nevertheless, under RCP8.5 scenario, we show the emergence of a progressive phenological advance in spawning date around the 1st July according to phytoplankton profiles. Thirdly, in terms of fecundity variability, our results show no particular tendency whatever the climatic scenarios or phytoplankton profiles.

This thorough simulation exercise brings new insights into the invasive strategy of *C*. *gigas* in this northern region of France. Nevertheless, unknown fates for phytoplankton dynamics can temperate those results and this should be take into account in further studies.

### Modelling the growth of the gilthead seabream (Sparus aurata) for aquaculture using the Dynamic Energy Budget

#### Inês Lopes<sup>1</sup>

#### <sup>1</sup>MARETEC - Instituto Superior Técnico, Portugal, <u>ines.estalagem.lopes@tecnico.ulisboa.pt</u>

DEB theory aims to quantify the metabolism at the individual level, so it focuses on describing the energy budget in an individual organism based on fundamental principles. Four state variables are defined: structure, reserves, maturity and the reproduction buffer. It quantifies metabolism through the interaction of metabolic processes, such as feeding, maintenance, development, growth, reproduction, and aging. These processes are conditioned by environmental factors, such as ambient temperature and food availability. As of now, the DEB parameters for more than five hundred species have been estimated.

The DEB model was successfully applied to several research fields, such as microbial biology, climate change impact, aquaculture, with different fish species with economic value, namely, *Mallotus villosus, Diplodus sargus and Sparus aurata*. This study will focus on the potential use of *Sparus aurata* in aquaculture near Sines, a site on the west coast of Portugal.

MOHID is an hydrodynamical model used to simulate the dynamics of water masses, it has been used to explain different types of processes, physical chemical and ecological at different scales and marine systems. In recent years, this model was coupled with a DEB model, based on the studies by Dabrowski et al. (2013), to enable the study of the potential growth of the *Mytilus edulis* in the Tagus estuary (Pinto et al. 2013) and can now be used in many different studies. In this particular case, the aim is to improve this model, by amending some assumptions, rectifying oxygen consumption, and also apply it to a new case study, namely to identify the zones with the highest growth potential for Gilthead seabream (*Sparus aurata*) in the coast of Sines, in Portugal. The DEB models predictions were compared to observed length and dry weight of individual sea bream.

The model presented can also be used to evaluate environmental sustainability and productivity of a system and it is, therefore, a very important tool to aid in decision making and support the sustainable management of aquaculture.

Dabrowski, T., K. Lyons, M. Curé, A. Berry and G. Nolan (2013). "Numerical modelling of spatio-temporal variability of growth of Mytilus edulis (L.) and influence of its cultivation on ecosystem functioning." Journal of Sea Research **76**: 5-21.

Pinto, L., M. Mateus, I. Ascione, G. Franz and R. Neves (2013). Modelling mussel growth in the Tagus estuary: A preliminary approach. Ocean modelling for coastal management – Case studies with MOHID. I. Press: 175-183.

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### Effects of plastic ingestion on the life cycle of an endangered sea turtle

Nina Marn<sup>1</sup>, Marko Jusup<sup>2</sup>, Tarzan Legovic<sup>1</sup>, S.A.L.M. Kooijman<sup>3</sup>, Tin Klanjscek<sup>1</sup>

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The framework of the Dynamic Energy Budget (DEB) theory and the concept of Synthesizing Units (SUs) were combined to study the effects of plastic ingestion on the energy budget and life cycle of the loggerhead turtle (*Caretta caretta*). The loggerhead turtle is one of several hundred marine species which reportedly ingest plastic. Plastic ingestion has been observed to impact individual fitness, probably the best known example being tragically starved to death albatrosses. The long-term effects of plastic ingestion in a long-lived, slow-maturing species such as the loggerhead turtle are, however, still unknown, and are difficult to elucidate merely through experiments or from currently available data. This is where well-designed mechanistic models (such as DEB models) become extremely valuable.

In the context of enzyme kinetics (or SUs), the plastic was treated as an inhibitor: both food and plastic particles compete for available Assimilation Units(AUs). AUs can either be available, or busy with plastic/food particles. Ingested plastic was considered to be chemically inert and to contain no digestible energy. In this setup, an increase in the density of plastic particles in the environment, and thus in the gut, resulted in a reduction of the scaled functional response - which is analogous to food dilution. The severity of the effect, of course, depends on the relative amount of ingested plastic, and on the residence time of plastic particles in the gut. Guided by values reported in the literature, we simulated a range of ingested plastic amounts, and the same, or longer than that of food plastic gut residence time. Life history traits such as age and size at puberty, reproduction, and maximum size were predicted using a previously defined standard DEB model.

Results suggest that reproduction is impeded at 14% of ingested plastics, a value well within the empirically set range. When the plastic residence time is assumed to be three times longer than that of food, the predictions are even grimmer, with sea turtles not even reaching puberty at 3% of ingested plastics. While the results need to be discussed in the context of the simplifications used for the simulations (e.g. the percentage of ingested plastics was assumed constant throughout life), they do point to alarmingly serious consequences that our irresponsible management of plastic waste might have.

### DeBInfer: Bayesian inference for dynamic models in R

Leah Johnson<sup>1</sup>, Sadie Ryan<sup>2</sup>, Philipp Boersch-Supan<sup>2</sup>

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Differential equations (DEs) are commonly used to model the temporal evolution of dynamic systems in science and engineering. However, statistical methods for comparing DE models to data and for parameter inference are relatively poorly developed. Further, traditional least-squares methods don't allow straight-forward incorporation of prior information, which is problematic when wanting to fit models with latent states or parameters, noisy observations, or sparse data. In contrast, Bayesian approaches offer a coherent inference framework that can make use of prior information and account for multiple sources of uncertainty. This approach further offers a rigorous methodology modeling the link between unobservable model states and parameters, and observable quantities. We present deBInfer, an R package implementing parameter inference for DEs in a Bayesian framework. deBInfer provides templates for the DE model, the observation model, the data likelihood, and the prior distributions of the parameters, as well as a Markov chain Monte Carlo (MCMC) procedure to estimate the posterior distributions of the parameters and any derived quantities, including the model trajectories. Further functionality is provided to facilitate MCMC diagnostics, the visualization of the posterior distributions of model parameters and trajectories, and the use of compiled DE models for improved computational performance. The templating approach makes our code applicable to a wide range of DE models. We demonstrate the application of deBInfer to DE models of biological systems, including Dynamic Energy Budget models.

### Comparison between two Derivative-Free Optimization Methods for DEB parameter estimation of different species

### Jéssica Morais<sup>1</sup>

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Dynamic Energy Budget (DEB) theory aims to describe the acquisition of energy by an individual organism, and its utilization for maintenance, growth and reproduction, as a function of the state of the organism and of the environment. The construction of a DEB model is based on information obtained through the observation of natural populations and on experimental research. In this way, it is possible to identify the effects of controlled variables, as food availability or temperature, on feeding, growth and other metabolic rates. Using observational and experimental data, a number of parameters can be estimated. They define the model and help to describe the energy and mass fluxes of an organism throughout its life cycle.

For the estimation of DEB parameters, the covariation method has been widely used, linking predictions and experimental and field observations of distinct life stages of the individual, through the parameters. Presently the Add-my-pet procedure estimates the parameters using the Nelder-Mead Simplex algorithm (available in DEBtool). This numerical optimization method is used to minimize the difference between observed and predicted values based on a weighted least-squares criterion.

The Nelder-Mead Simplex algorithm is a popular direct search method which attempts to compute the minimum of a non-linear function, without any derivative information. However, it has been shown that this method could converge to a non-stationary point of the function. In fact, a family of strictly convex examples has been provided for which the algorithm applies consecutive shrinks towards a point that is not a minimizer. Moreover, the Nelder-Mead method was designed to be applied in unconstrained optimization. Presently, the algorithm has been improved substantially by setting boundary conditions that restrict the search to an area of the parameter space where the model makes mathematical sense. Nevertheless, convergence has not been systematically analyzed.

SID-PSM (A Pattern Search Method guided by Simplex Derivatives) is a numerical implementation of a directional direct search method which uses simplex derivatives to guide the search, and is suited for nonlinear derivative-free optimization. Convergence results were established for directional direct search, both for constrained or unconstrained problems, requiring only locally Lipschitz continuity of the function to be minimized.

The aim of this presentation is to show a numerical comparison between the results obtained using the Simplex of Nelder-Mead, that is already implemented, and SID-PSM, when estimating DEB model parameters of different species.

### General Ecosystem Models: virtual tools for the living world

#### Mike Harfoot<sup>1</sup>

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The ecosystems of planet earth are facing unprecedented pressures as a result of human action. At the same time, ecology as a discipline is increasingly demanding more mechanistic understanding of what causes observed ecological patterns, in part for the development of the science but also to help mitigate impacts. Here, I will present the Madingley Model, a General Ecosystem Model that aims to provide a mechanistic understanding of how ecosystems, on land and in the seas, are structured and how they function, and for how anthropogenic changes might alter that structure and function. Energy budgets are fundamental for organisms and so play a key part in the model, but questions remain to be explored about how metabolism interacts with other aspects ecology, for example organismal intelligence and behavioural responses.

### **Biography:**

Mike is an earth system scientist with a strong interest in the biological world and his work primarily involves developing mechanistic models to project biodiversity futures. In particular, Mike is working with colleagues at WCMC and Microsoft Research to develop the Madingley model, a novel model of ecosystems. In addition, Mike works with others in the Centre to construct and employ models that can provide insights and answers to specific conservation questions.

### Unexpected dynamics (including canard explosion) of fast-slow bitrophic food chains

### Bob Kooi<sup>1</sup>, Jean-Christophe Poggiale<sup>2</sup>

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Different modeling approaches and analysis techniques to study dynamics systems with slow/fast dynamics of a predator-prey system are considered. The predator-prey systems are modeled using ordinary differential equations, one for each trophic level. The slow-fast or time diversified system properties result from the assumption that the growth and loss rates of the predator are much smaller than the growth rate of the prey. Two model formulations are studied.

In the classical Rosenzweig-MacArthur (RM) model in absence of the predator the prey grows logistically. Consequently, no nutrient, resource for the prey, is modeled explicitly and the predator-prey model is described by a two-dimensional system. In this RM-model formulation the slow-fast assumption leads to an often-unrealistic assumption that the conversion efficiency needs to be small.

In a mass balance (MB) chemostat model the nutrient is explicitly modeled leading to a three-dimensional system. Then for the fast-slow case the unrealistic assumption having a small efficiency is avoided. Because this model is based on mass conservation laws, by perfect aggregation the dimension of the system can be reduced by one leading to again a two-dimensional system just as the RM-model.

We will show that the predicted long-term dynamics for the RM-model and the MBmodel differ significantly when in both models the time scales at the two population levels differ. For instance, in the RM-model a so-called canard explosion occurs and not in the MB-model.

B.W. Kooi, J.C. Poggiale, P.Auger, and S.A.L.M. Kooijman. Aggregation methods in food chains with nutrient recycling. Ecol Model, 157(1):69-86, 2002.

B.W. Kooi and J.C. Poggiale, Modelling, singular perturbation and bifurcation analyses of bitrophic food chains, submitted.

### Population dynamics with multiple limiting nutrients: Life history mediated effects.

### Romain Richard<sup>1</sup>, André M. de Roos<sup>1</sup>

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An organism may be limited by different nutrients in different stages of its life because of spatial and/or temporal variation in food quality. These patterns of multiple nutrient limitation translate to the individual level to affect the realized life history of the individual. Dynamic "energy" budgets can be used to account for these multiple nutrient limitations. A rather underappreciated, yet exciting, reason why it may be important to consider the possibility of multiple nutrient limitations is because stoichiometric requirements may vary throughout an individual's life. This may, for example, happen because the individual produces tissues with different compositions at different stages of its life (e.g. soma in juveniles, eggs in adults), or again, because it exhibits ontogenetic diet shifts or metamorphoses. In this presentation, I will discuss some of the implications of these ontogenetically-mediated patterns of nutrient limitation for the life history of individuals and for the dynamics of physiologically structured populations. This analysis is based on a simplified energy budget that incorporate different nutrient requirements for growth and reproduction in term of carbon and phosphorus.

### Dynamic energy budgets in individual based population models: cross species test and application

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In the ecological risk assessment of chemicals mechanistic effect models provide the possibility to extrapolate effects to untested scenarios. In particular, individual-based population models (IBMs) are able to make quantitative predictions on how populations perform under chemical stress based on organism level toxicity testing, thereby bringing more ecological realism into the effect assessment. In the past, IBMs have usually been designed for specific species and have been perceived as being too complex to understand mainly due to the variety of existing approaches. Therefore, the development of standard model designs has been suggested.

Here, we provide a test of a standardizable IBM using three different species, the pond snail *Lymnaea stagnalis*, the marine polychaete *Capitella teleta*, and the water flea Daphnia magna, where individual organisms are represented by formulations of the dynamic energy budget theory. In the model, the three species only differ in their parameter values while keeping the overall model implementation untouched. For testing, we confront model predictions with independent data of laboratory population dynamics which is available for the three species. Furthermore, using the example of D. magna exposed to Nonylphenol and Cadmium, we demonstrate how lethal and sublethal effects can be modelled using IBMs and again test model predictions with independent population dynamics for the three species and the two chemicals are well predicted by the IBM implying that the model be applicable as a risk assessment tool.

### A multi-agent approach to couple physiological and foraging models Optimization of vulture foraging strategies

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In a region where the resource distribution is spatio-temporally heterogeneous, animals faces the problem of finding a food spending a minimum of energy in- vestment. Depending on information quantity, animals use alternatively different searching strategies (i.e. Brownian or Lévy stochastic process). Optimal foraging strategy - as to maximize their net energy intake and minimize their invested energy.

Indeed, the choice of the foraging strategy depends on available information of food resource distribution on a foraging region. But, the physiological state of the individual, and the energetic cost of the chosen flight mode will determine how far vulture can travel. The potential travel distance and available time until the end of the day allow us to define the accessible foraging region.

These facts can be summarized as following: the size of the foraging region depends on the choice of flight mode, whereas foraging strategy depends on available information on the foraging.

Our goal is to study the impact of the distribution of resource on the strategy flight. Therefore, we develop a multi-level agent-based model, which is divided into four main parts: (1) Information transfer between individuals, (2) flight types choice (flapping or soaring) due to environmental condition, (3) foraging strategy choice and (4) eating and internal state dynamics processes.

In our model, we consider both flight strategies and physiological status of the animal. This requires a coupling between two different theories and models that result from, in our case, the theory of dynamic energy budget [1] and foraging theory [2].

[1] Kooijman, S. A. L. M. (2010). Dynamic energy budget theory for metabolic organisa- tion. *Cambridge university press*.

[2] Stephens, D. W., and Krebs, J. R. (1986). Foraging theory. Princeton University Press.

### Friday, 2<sup>nd</sup> June

#### 09:00 Arrival & coffee

### Chair 6: Jean-Christophe Poggiale

- 09:15 **Biodiversity in the context of DEB theory (**Keynote 5 Sebastiaan Kooijman)
- 10:00 The altricial-precocial spectrum of avian development according to DEB theory (Carlos Teixeira)
- 10:20 Physiological performances of Southern Ocean key species (Charlène Guillaumot)
- 10:40 Bayesian parameter estimation for Dynamic Energy Budget models of albatross growth (Philipp Boersch-Supan)
- 11:00 Coffee, tea break
- 11:30 Evolution and regulation of Symtrophic Symbiosis (Roger Nisbet)
- 11:50 Biologically mediated and abiotic mechanisms for light enhanced calcification and the cost of carbonates deposition in corals (Giovanni Galli)
- 12:10 Discussion / Questions
- 12:30 Lunch

### Chair 7: Bob Kooi

- 14:00 DEB for any species: making the most of existing knowledge (Jorn Bruggeman)
- 14:20 Demand driven reserve allocation: can the reproductive buffer modulate kappa ? (Erik Muller)
- 14:40 Energy-limited tolerance to multiple stressors in the purple-tipped sea urchin, *Psammechinus miliaris* (Rose Stainthorp)
- 15:00 Damage-related protein turnover explains inter-specific patterns of maintenance rate in the DEB theory (Olivier Maury)
- 15:20 Physics of metabolic organization (Marko Jusup)
- 15:40 Tea & Posters
- 16:10 Conclusions
- 16:40 END

### Biodiversity in the context of DEB theory

#### Sebastiaan Kooijman<sup>1</sup>

#### <sup>1</sup>VU University, Amsterdam, <u>bas.kooijman@vu.nl</u>

One of the key questions that grabbed me during the development of DEB theory was: How can a simple theory on the metabolism of organisms be that accurate despite the huge biodiversity that exists? In the context of DEB theory it is natural to look for answers in a table of parameters versus species. Ecophysiological literature is full of reports on life history strategies and on how properties depend on body size. Think of r-and-K strategies, altricial-precocial spectra, Kleiber's law, generalist versus specialist, evolution of parental care. We found several more, such as supply-demand spectra, metabolic acceleration, waste-to-hurry. My more detailed questions were: can we find these patterns back in the position of species in the parameter space and can we understand why this diversity could have been unfolded during evolution? Each strategy seems to have its own advantage and disadvantage. My lecture will try to share some of many wanderings and place it in the context of evolution of homeostasis and syntrophic interaction.

### **Biography:**

After my PhD on the statistical analysis of point processes on a surface at Leiden University, I worked for 9 years at TNO in Delft on environmental risk assessment. There I started to work on what I later called the Dynamic Energy Budget theory to quantify sublethal effects of toxicants on organisms and to evaluate their environmental significance. I continued development of this theory during my 30 years of service at VU University Amsterdam as professor in theoretical biology, and very much enjoyed working with 50 PhD students and many colleages in a variety of disciplines and many countries. My aim with the theory broadened over the years to become a foundation for quantitative eco-physiology in general, which combines nicely with my main hobby in field biology, where I like to hike in remote areas to enjoy the beauties of life.

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### The altricial-precocial spectrum of avian development according to DEB theory

Carlos Teixeira<sup>1</sup>, Tânia Sousa<sup>2</sup>, Tiago Domingos<sup>3</sup>

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Within the Neornithes, a broad spectrum of development patterns evolved and is known as the 'altricial-to-precocial' spectrum. The phenotypes exhibited by avian neonates, within this spectrum, have been characterized through anatomical, physiological and behavioural differences which can be visually assessed. It has been considered that these differences correspond to different relative degrees of maturation.

However, previous physiological studies raised questions. For instance, precocial birds hatch with very developed locomotion capacities but less matured digestive systems. Altricial birds hatch almost unable to move but with relatively more matured digestive systems. The relative maturity of each category is therefore difficult to assess.

We hypothesized that through the application of the Dynamic Energy Budget (DEB) theory, the relative maturity of avian neonates could be estimated in an explicit and quantified manner. For that purpose, we made use of previously estimated DEB parameter sets for bird species. Subsequently, we calculated and compared dry mass-specific maturity values at hatching, fledging and puberty as well as 'altriciality index' values, i.e., the ratios between the amounts of energy invested in maturation up to fledging or puberty and the corresponding amounts invested up to hatching. The ratios between the dry mass-specific maturity values at puberty or fledging and the corresponding value at hatching were also considered.

By comparing these different DEB compound parameters, it was possible to conclude that the selected ratios correlate significantly with the four main categories within the altricial-precocial spectrum. The fledging/hatching altriciality index is particularly accurate.

Significant differences between altricial and precocial species were also observed regarding core primary DEB parameters, such as the volume-specific somatic maintenance, or compound DEB parameters, such as the dioxygen use per gram of maximum dry weight.

Our results suggest the evolution from precocial to altricial strategies in birds, and particularly in the Neognathae. Based on our results it is also possible to discuss previous observations regarding the potential drivers, advantages and costs (such as in terms of parental care) of the different life strategies.

### Physiological performances of Southern Ocean key species

Charlène Guillaumot<sup>1</sup>, Antonio Aguera<sup>1</sup>, Bruno Danis<sup>1</sup>

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The Southern Ocean benthic ecosystems, characterized by a high level of biodiversity and isolation, are unique in term of specific adaptations to the challenging environment. However, there is a dearth of knowledge in these regions that urges the need to understand how global change may influence these ecosystems, in terms of structure and function. Among these systems, the ectotherm constituents are thought to be the most vulnerable.

In the framework of our study, we use Dynamic Energy Budget (DEB) theory to address these knowledge gaps, by focusing on the dynamics underlying the distribution and physiological performances of a range of key species. Parameters for some of these species already exist and others can be yielded using already available data.

Physiological properties of two echinoderms and two molluscs are described by means of DEB model parameters. These parameters are then used to compare the physiological strategies of these groups in the Southern Ocean and with members of the same group along different latitudes.

### Bayesian parameter estimation for Dynamic Energy Budget models of albatross growth

Philipp Boersch-Supan<sup>1</sup>, Sadie Ryan<sup>1</sup>, Richard Phillips<sup>2</sup>, Leah Johnson<sup>3</sup>

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Chick growth trajectories provide an integrated measure of physiological, behavioural, and environmental processes. In albatrosses and other seabirds, chicks exhibit non-monotonic growth trajectories that include a period of body mass decrease before fledging. Although most simple growth models, such as standard von Bertalanffy growth models, cannot account for this pattern, it can be captured mechanistically using Dynamic Energy Budget (DEB) models. We used a Bayesian inference framework to estimate DEB model parameters for four albatross species (Wandering, Black-browed, Grey-headed and Light-mantled Albatross), using growth and meal mass measurements collected primarily at Bird Island, South Georgia. The Bayesian approach offers a coherent framework for parameter inference that can account for multiple sources of uncertainty, while making use of prior information. This is highly relevant for DEB parameter estimation which often relies on disparate data sources. Bayesian inference furthermore offers a rigorous methodology for modelling the link between unobservable model states and parameters, and observable quantities. We provide the software used for model fitting as an open-source R package.

### **Evolution and Regulation of Syntrophic Symbiosis**

<u>Roger Nisbet</u><sup>1</sup>, Ross Cunning<sup>2</sup>, Glenn Ledder<sup>3</sup>, Erik Muller<sup>1</sup>, Sabrina Russo<sup>3</sup>

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DEB theory offers a natural framework for modeling mutualistic interactions (Kooijman 2010, Chapter 9). This was demonstrated in a model of coral, a "superorganism" whose growth involves interactions between a heterotrophic host and a photoautotroph (Muller et al. J. Theor Biol 259: 44-57, 2009). Balanced growth of the superorganism, defined as growth with a stable ratio of host to symbiont biomasses, does not require inter-organism communication (global control), but is an emergent property provided each species makes available to its partner any *surplus* resource (represented in the DEB model as the rejection flux from a synthesizing unit). The current authors and collaborators are currently extending this formalism to interactions among *organs* (root and shoot) in a terrestrial plant, as well as continuing with coral modeling.

We report work on a family of idealized models of interacting partners (organisms or organs) with carbon and nitrogen dynamics that include "sharing the surplus". We characterize biosynthesis using two synthesizing unit representations: Liebig's minimum rule (MRSU) and the Parallel Complementary SU (PCSU) widely used in DEB applications (Kooijman 2010, chapter 3). With the MRSU, stable balanced growth is achieved if at least one player needs a higher proportion than its partner of the element that it cannot obtain directly. The asymptotic balanced growth rate is equal to that previously shown using life history theory to be "optimal" for allocation of photosynthate between roots and shoots in a growing plant. During balanced growth, there is no unutilized carbon or nitrogen. When the condition for balanced growth is violated, growth dynamics are oscillatory, there is "wastage" of carbon and nitrogen, and the long run population growth rate is less than could be achieved with global control. With biosynthesis represented with the PCSU, there is always wasted carbon and nitrogen, but balanced growth is common, with oscillatory dynamics only occurring with extreme parameter values. The asymptotic rate of balanced growth is still optimal in the sense that no reallocation of elements by some global (e.g. hormonal) controller increases the growth rate. Adding additional feedbacks to the models may eventually cause breakdown of balanced growth. This is demonstrated with a model of coral bleaching that exhibits bistability and hysteresis, with balanced growth at both positive and negative rates being possible in the same environment.

In summary, our findings demonstrate that "sharing the surplus" leads to robust, evolutionarily plausible, dynamics, that may, nonetheless, be sensitive to environmental change.

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### Biologically mediated and abiotic mechanisms for light enhanced calcification and the cost of carbonates deposition in corals.

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Zooxanthellate corals are known to increase calcification rates under the light, a phenomenon called light enhanced calcification, that is believed to be mediated by symbionts photosynthetic activity. There is quite some controversy on the mechanism behind this phenomenon with hypotheses coarsely divided between abiotic and biologically mediated mechanisms. At the same time evidence is building up that calcification in corals relies on active ion transport to deliver the skeleton building blocks into the calcifying medium, hence it is a costly activity.

Here we build on generally accepted conceptual models of the coral calcification machinery and of the energetics of coral-zooxanthellae symbiosis to develop a model that can be used to separate the biologically mediated and abiotic effects of metabolic rates (respiration and photosynthesis), temperature and seawater chemistry on coral calcification rates and related metabolic costs. Our model is of mixed type, integrating elements of seawater carbonate chemistry and dynamic energy budget theory.

We tested this model on a dataset relative to the Mediterranean scleractinian Cladocora caespitosa (an acidification resistant species) and we conclude that most of the variation in calcification rates due to photosynthesis and temperature can be attributed to biologically mediated mechanisms, in particular to the metabolic energy supplied to the active ion transports. Abiotic effects are also present but of smaller magnitude, though they could be more relevant for acidification sensitive species. Based on these findings and on a literature-review we suggest that the energetic aspect of coral calcification has been so far overlooked.

### DEB for any species: making the most of existing knowledge

#### Jorn Bruggeman<sup>1</sup>

#### <sup>1</sup>Plymouth Marine Laboratory, UK, jbr@pml.ac.uk

The "add my pet" collection of DEB parameters is a veritable treasure trove of quantitative information on organism physiology across the animal kingdom. Crucially, it demonstrates that variation in DEB parameters is not random: as described in studies by Lika et al., there is evidence for covariation among parameters, and for similarity among species that share an ecological strategy, and often, evolutionary descent. This has implications for the way we estimate parameters for new species: these should incorporate prior knowledge about the species (e.g., maximum body length) while simultaneously accounting for its phylogenetic (or taxonomic) placement and for covariation among DEB parameters. Such an estimation approach is not only feasible - it can be automated. I demonstrate that by combining the "add my pet" dataset and the species taxonomy in an evolutionary random walk model, we quantify (co)variation among DEB parameters, and subsequently exploit this to infer DEB parameters for any species with known taxonomic placement. By integrating online taxonomic resources (http://www.catalogueoflife.org), we can automatically infer parameters for over 1.6M species. This work does not take away the need for experiments, but complements them: by presenting estimates as well as the associated uncertainty, it can guide the design of further experiments and support Bayesian analysis of new information.

### Demand driven reserve allocation: can the reproductive buffer modulate kappa?

<u>Erik Muller</u><sup>1</sup>, Konstadia Lika<sup>2</sup>, Cheryl Murphy<sup>3</sup>, Diane Nacci<sup>4</sup>, Roger Nisbet<sup>1</sup>, Christopher Remien<sup>5</sup>, Irvin Schultz<sup>6</sup>, Karen Watanabe<sup>7</sup>

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The kappa rule in DEB theory states that growing adults commit a fixed fraction of the catabolic flux to reproduction and maturity maintenance. This means that an adult with sufficient somatic reserves starts to accumulate reproductive reserves immediately upon maturation or following a spawning event. However, in species as diverse as marine mussels, annually spawning corals, rainbow trout and orchard fruit trees, most of the gonadal matter may not become recognizable until much later in the reproductive cycle. This reproductive behavior doesn't necessarily contradict the kappa rule, since somatic reserves may be earmarked for reproduction without becoming recognizable as such, in which case a complementary 'egg-load' modeling module may suffice to describe the conversion of 'invisible' reproductive reserves into gonadal matter. The question then arises where those 'invisible' reserves are located and, as a corollary, how the organism manages to distinguish somatic reserves, whose dynamics are considered to obey the weak homeostasis assumption, from those earmarked for reproduction, whose dynamics are not.

Alternatively, one could argue that kappa is not (approximately) constant, but may vary over time. Indeed, early on in the development of DEB theory, it was shown that pond snails kept under a long day light regime allocated more reserves to reproduction than conspecifics growing with less day light hours. This observation indicates that kappa is subject to the control of environmental drivers, which is further corroborated by the impact of endocrine disruptors, in particular compounds mimicking steroid hormones, on the partitioning of somatic reserves for somatic and reproductive or developmental processes. We extend this line of reasoning and explore how kappa may depend on the internal state of an organism while maintaining all other assumptions of the standard DEB model.

Motivated by the observation that reproductive organs and fruiting bodies can produce hormones regulating the accumulation of gonadal matter, we investigate the proposition that reproductive matter exerts negative and positive feedback control on the allocation of somatic reserves to reproduction. In particular, with published data on rainbow trout, we evaluate a model in which 1-kappa is proportional to the density of reproductive matter in structural biomass (positive feedback) and to the difference between a theoretical maximum and actual density of reproductive matter (negative feedback). We compare the predictions of this model to those of the standard DEB model with an additional module describing the conversion of reproductive reserves into gonadal matter following analogue feedback rules.

### Energy-limited tolerance to multiple stressors in the purple-tipped sea urchin, Psammechinus miliaris

### R. E. Stainthorp<sup>1</sup>, S. A. Morley<sup>2</sup>, A. E. Bates<sup>1</sup>

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In light of global climate change, it is important to understand the mechanisms underlying species' distributions in order to be able to predict future patterns of biodiversity. Shifts in species' biogeographic ranges have already been documented and are set to continue as temperature and other key environmental drivers interact with biological processes. Dynamic Energy Budget (DEB) theory offers a mechanistic basis to understand how the dynamics of individuals link to molecular processes, population dynamics and ecosystem-level consequences in a potentially variable environment. Here we apply DEB theory to investigate the interactive effects of multiple stressors on the energy budget of the purple-tipped sea urchin, Psammechinus miliaris. We present the results of a series of long-term (3 month) experiments investigating the combined effects of temperature, hypoxia and food availability on urchin metabolism, and estimate a set of DEB parameters to model growth and reproduction of P. miliaris based on realistic future climate scenarios. This model will be validated using an external data set to assure consistency, and used to predict population dynamics of wild populations at the species' range edges under varying environmental conditions.

### Damage-related protein turnover explains inter-specific patterns of maintenance rate in the DEB theory.

<u>Olivier Maury</u><sup>1</sup>, Olivier Aumont<sup>1</sup>, Jean-Christophe Poggiale<sup>2</sup>

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Maintenance is the energy that living organisms are bound to use to maintain their structure in a viable state. It includes all the metabolic and physiological costs that are not directly associated to the production of biomass (growth and reproduction) or to development (maturation). In the framework of the DEB theory, somatic maintenance rate can either be proportional to organism structural volume V or to structural surface V<sup>2/3</sup>. Being mostly associated to similar metabolic processes, volume-specific maintenance costs have no obvious reason to vary substantially at the interspecific level. In the DEB theory, the volume-specific maintenance rate is therefore supposed to remain approximately constant between species. However, a recent meta-analysis of DEB parameters using the add-my-pet database (Kooijman, 2014) reveals troubling patterns apparently violating these inter-specific scaling rules and challenging the DEB theory. It is indeed shown in this study that empirically-derived volume-specific maintenance rates scale approximately with Lm<sup>-0,4</sup>. We propose a simple physiological mechanism for the apparent decrease of volume-specific maintenance rate with ultimate size. It rests on the idea that protein turnover rate constitutes an important component of maintenance, which varies with metabolism, and hence decreases with size. We show that this implies that the actual volume specific maintenance rate varies both at the intra- and inter-specific levels in a range very similar to what is observed in the add-my-pet data estimations. If true, this implies that the apparent decrease of volume-specific maintenance rate with ultimate size is an artefact and it requires slight modifications to the standard DEB theory in order to capture empirical inter-specific scaling patterns of DEB-parameters while keeping the consistency of the theory at both intra- and inter-specific levels.

### Physics of metabolic organization

Marko Jusup<sup>1</sup>, Tiago Domingos<sup>2</sup>, Tânia Sousa<sup>2</sup>, Velimir Labinac<sup>3</sup>

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Dynamic Energy Budget (DEB) theory is deeply rooted in thermodynamics. Hitherto, these thermodynamic roots were more accessible to physicists and mathematicians, while applications were better suited to biologists, causing a dichotomy in what had originally been constructed as a single body of work. To bridge the gap between the two aspects of DEB theory, we overview key developments leading to the formulation of the standard DEB model. In particular, we: (i) adhere to the theoretical formalism, (ii) minimize the amount of information that needs to be processed, but also (iii) invoke examples from biology to motivate new concepts and to justify the assumptions made, and (iv) show how a general theory enables modular, self-consistent extensions that capture important features of the species and the problem in question.

Perhaps the most difficult among the concepts of the standard DEB model, the utilization (or mobilization) energy flow, is given particular attention in the form of an original and considerably simplified derivation. We make a step forward from the existing literature by proving that the concept of energy (weak) homeostasis can be mathematically formulated and derived from the common assumptions of DEB theory. Aside from the utilization energy flow, another mathematically challenging part of the standard DEB model is formulating the initial conditions. To resolve this problem in a novel manner, we find an explicit expression for scaled structural length as a function of the scaled reserve density during the embryonic development. This explicit expression provides a conceptually and practically simple way to calculate scaled length at birth, and finally the initial energy reserve. We outline the corresponding derivations and discuss the practical implications thereof. Finally, we present a particularly simple algorithm for resolving the initial conditions in the standard DEB model using Mathematica programming language.

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**Poster Presentations** 

### Trait distributions of key marine species from the Western Antarctic Peninsula

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Marine organisms in Antarctica are adapted to an extreme ecosystem including extremely stable temperatures and strong seasonality due to changes in day length. It is now largely accepted that Southern Ocean organisms are particularly vulnerable to global warming with some regions already being challenged by a rapid increase of temperature. Climate change affects both the physical and biotic components of marine ecosystems and will have an impact on the distribution and population dynamics of Antarctic marine organisms. To predict and assess the effect of climate change on marine ecosystems a more comprehensive knowledge of the life history and physiology of key species is urgently needed.

Dynamic Energy Budget (DEB) theory is a compelling method to better understand the functioning and properties of these benthic communities. In this study, we estimate the Dynamic Energy Budget (DEB) model parameters for key benthic Antarctic species (Odontaster validus and Laternula elliptica) using available information from literature and experiments.

Based on this DEB models we will project environmentally-determined life history traits, creating trait distribution maps, which will brought further information about species and communities performances in the area of the Western Antarctic Peninsula. By projecting the DEB outputs to other contrasted environments along different latitudes, the sensitivity of the species to environmental changes will be simulated and will address the need of understanding the impact of future potential shifts on these communities.

### Quantifying the effects of pathogen agents on the bio-energetics and the ecophysiology of the bivalve Crassostrea gigas

Marianne Alunno-Bruscia<sup>1</sup>, Bruno Petton<sup>1</sup>, Sébastien Petton<sup>1</sup>, Dominique Ratiskol<sup>1</sup>, Jacqueline Le Grand<sup>1</sup>, <u>Emilien Pousse<sup>1</sup></u>, Yannick Labreuche<sup>2</sup>, Frédérique Le Roux<sup>1</sup>

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Recent studies on mortality outbreaks of juvenile oysters (<1---yr old) Crassostrea gigas have focused on the causative agents (and on their pathogenicity), *i.e.* the herpes virus OsHV---1 µVar and Vibrio spp., as well as on the factors that influence the disease transmission. But physiological changes of the host during infection remain poorly documented. Here we propose to study the eco---physiology of C. gigas during infectious diseases in order to provide non---invasive indicators of the health status of oysters before, during and after a disease event and to test for any disruption of the host energy balance due to diseases. Two main questions will be addressed: i) Are ecophysiological indicators of C. gigas (filtration, respiration, assimilation, cardiac activity) relevant to monitor and describe at short term the host susceptibility during an infectious event associated with a polymicrobial disease? ii) What are the physiological sequelae of an early infection by a polymicrobial disease on the growth and the reproduction of survivors at later stages? Two complementary surveys will be set up in the field and in the laboratory at different temporal scales. On the one hand, a reciprocal transplant field survey will be conducted over 2 years in two geographic areas contrasted in terms of disease severity, bay of Brest (B, France) and Sylt (S, Germany) to monitor the growth, reproduction and survival of specific--pathogen---free (SPF) juveniles produced with genitors originating from B and S; environmental parameters (e.g. temperature, chlorophyll a) will be monitored in each site. On the other hand, the bioenergetics budget of B and S SPF juveniles will be estimated in the laboratory by means of ecophysiological measurements (filtration, respiration, assimilation rates and heart beat activity) in individual chambers before, during and after a polymicrobial infection. Based on (short---term) individual eco--physiological measurements and (mid---term) field growth and survival surveys of B and S oysters, the Dynamic Energy Budget (DEB) developed for C. gigas will be used to identify any physiological anomalies of SPF oysters during infection and to quantify effects of the polymicrobial disease on the host bio---energetics and physiology.

### **Optimization of cancer treatment**

### Slimane Ben Miled<sup>1</sup>, Ghassen Haddad<sup>2</sup>

#### University Tunis El Manar, LAMSIN, email TUNISIA Institut de recherche pour le développement IRD email

Personalized medicine is one of the challenges of tomorrow's medicine. By personalized we mean to take into account, the patient's biological profile and the molecular characteristics of the disease (cancer in our case), before prescribing treatment. The goal of our work is to develop a decision support tool for doctors, so they can simulate and monitor the effect of treatment prior to administration. To achieve our goal, we have to better understand the role of the interactions between the host, the tumor and the treatment. Thus, this project will allow the oncologist to have a systemic approach by enabling the prescription of a controlled, optimized and personalized treatment, which takes into account all the biological factors. Our modelling approach is based on modelling the energetic behavior of an organ hosting a tumor using Dynamical Energetic Budget theory (DEB theory) to model the tumor growth within the host, which is called tumor in host model based on the works of Vanleeuwen[1] and then we have integrated treatment as a control with the optimal control theory.

[1] Van Leeuwen, IMM and Zonneveld, C and Kooijman, SALM, British journal of cancer. The embedded tumour: host physiology is important for the evaluation of tumour growth, 2003.

### Mathematical modeling of the behavior of mussels Mytilus galloprovincialis in function of the spatio-temporal variations: Application of the Dynamic Energy Budget DEB theory

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Bizerte lagoon (located in the northern coast of Tunisia) is the most important mussel farming in Tunisia. The production and the behavior of *Mytilus galloprovincialis* are very influenced by the environmental factors. In order to understand the behavior of this mussel, the standard Dynamic Energy Budget (DEB) model is used to simulate growth and reproduction of the mussels according to food availability and water temperature in the Bizerte lagoon.

In the present study, we first proposed a biological life cycle of the mussels *Mytilus galloprovincialis* that corresponds to the life cycle of the DEB model (bioenergetics model). We observed that embryonic stage and the trochophore larva of the biological life cycle correspond to the embryonic stage of the DEB model when no food is ingested (The digestive system is not functional). Pediveliger larva, metamorphosis (plantigrade larva) and juvenile stage of the biological life cycle correspond to the ipvenile stage one, in which food is taken but resources are not yet allocated to the reproductive process. However, the adult stage is the same for both life cycles (biological life cycle and life cycle of the DEB model). This observation will be exploited next to construct a new DEB model for *Mytilus galloprovincialis*.

Second, we simulated the effect of food availability and water temperature (the environmental forcing data). For the DEB simulations of mussel growth (structural body volume (V) and volumetric structural length (L)), the dynamics of reserve energy and the dynamics of energy allocated to the reproductive buffer (ER), we used three approaches (considering the temperature and food variations specific to the lagoon, considering only the effect of food density X (t), considering only the effect of the temperature T (t)).

The results showed that a decreasing of 60% on food density implies a decreasing of 49.36% on energy allocated to reproduction and 28% on volume length. We, also, proved that temperature has a large effect on energy allocated to reproduction. Indeed, the effect of difference between maximum and minimum temperature on energy allocated to reproduction buffer is a decreasing rate of 78.48%.

### Energy dynamics may be mechanistically linking movement behaviour and life history traits.

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The space-use patterns of home range (HR) behaving fish is emerging as a cornerstone for a number of ecological processes. Recent studies have suggested the existence of consistent individual differences in HR behaviour (i.e., behavioural types), which may be maintained within a population as an adaptive solution to complex environments. Differences in the explored area and/or in the exploration rate may lead to differences in the feeding rate, which in turn imply differences in growth rate, reproductive output and even vulnerability to predators or fishing. Several correlation patterns support such an intuitive link. Here, we propose a link between a standard DEB model and a general movement model that leads the formation of a HR area through the assimilation rate and the way the energy needs are fulfilled. Specifically, we assess the responsiveness of the model to inter-individual variability of the activity level and the energy conductance parameter in three environments with different levels of resources. First, it is predicted that the more the area is covered the faster the growth is and the earlier the maturity is. Second, higher mobilization rates of the reserve energy leads to the establishment of bigger HR areas. Third, lower resource densities imply bigger HR and environmental variability leads to more variability in the dynamics of the HR size. Both, physiological and movement-related parameters may be under selection, since they determine the expected reproductive life of individuals. The scaled version of the model proposed here provides an outline for the exhaustive analysis of interactions between spatial occupation patterns, metabolic major fluxes and life-history traits in fish, in mechanistic way. This generic version of the model (with no current species application) is proposed as a general framework to better understand the ecological and evolutionary processes in which spatial behaviour directly connects the internal operating rules of the individual with the environment.

### Understanding the Environmental Factors Controlling the Host-Symbiont Relationship in Zooxanthellate Jellyfishes.

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In tropical and sub-tropical coastal ecosystems, numerous jellyfish species harbour symbiotic zooxanthellae (photosynthetic dinoflagellates). Those zooxanthellate jellyfishes can reach very high biomass especially in enclosed systems such as lagoons and marine lakes. They can be invasive as it is the case of *Phyllorhiza punctata* in the Mediterranean Sea and the Western Atlantic. They can also exhibit dramatic variation of populations density linked to climatic events like *Mastigias sp.* in Palau's marine lakes. In spite of those concerns, it is still unclear how the symbiotic relationship reacts to environmental changes and how it affects the jellyfish life-cycle. For instance, most studies agree that strobilation, formation of medusae from polyps, cannot be achieved without zooxanthellae. However, individuals or even populations of aposymbiotic adult jellyfishes do exist. This plasticity of the symbiosis could be a critical point to understand how the jellyfish populations respond to changes in their environment.

This poster is presenting the objectives of a three-year PhD project started in November 2016. This project aims to understand, based on a combined experimental and modelling approach, how jellyfishes and their symbionts would react to environmental changes. We will study the whole life-cycle of a zooxanthellate jellyfish in various conditions of temperature, food availability and light intensity. Biological parameters will be measured on both jellyfish and their symbionts. For jellyfish measurements will include growth rates, respiration and excretion rates, density of zooxanthellae, budding rates, gametes production or activity. For symbionts parameters such as growth rates or photosynthetic performance will be measured.

In this context, we believe that DEB theory is a suitable conceptual and quantitative framework for our experiments. By its ability to describe energetic flows along the lifecycle in various environmental conditions DEB theory could help us answer questions such as: Why do symbiont appear to be obligate most of the time? How environmental conditions could rule the necessity of symbiosis? Within the course of this PhD project, we hope to provide useful information regarding the ability of zooxanthellate jellyfishes to be invasive or why do they display populations variations linked with climatic events.

### Harpacticoid copepods in a DEB framework: Investigating pharmaceutical effects on Nitocra spinipes

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Over the past few decades, copepods have gained considerable popularity as test organisms in ecotoxicological studies. This is mainly due to their key role in freshwater and marine ecosystems. Harpacticoid copepods like the euryhaline brackish water species Nitocra spinipes, for instance, form an important link between the microphytobenthos and organisms of higher trophic levels. N. spinipes has been extensively used in ecotoxicity testing since the 1970s. An acute toxicity test and a larval development test with N. spinipes have been established under ISO. Furthermore, the OECD released a guidance document for a development and reproduction test with the harpacticoid copepod Amphiascus tenuiremis for which it recommends N. spinipes as an alternative test species. To date, there is a wealth of available life history data on this species under controlled conditions in the presence and absence of chemical stressors. However, while thus far adverse effects on different history traits have mostly been evaluated independently, it is our aim to investigate the underlying modes of action (MoAs), which lead to specific combinations of effects in N. spinipes. To investigate such MoAs on the level of energy uptake and allocation within N. spinipes, we made use of the dynamic energy budget theory (DEB) framework. In an individual based modelling approach (IBM) the DEBkiss ('keep it simple, stupid') model structure was used to build a mechanistic population model for N. spinipes. Small modifications to the generic model structure were made to account for specific peculiarities in the copepod life cycle. These include a change in shape in the course of an individual copepod's development, as well as an abrupt stop in growth after reaching the adult stage. We used the selective serotonin reuptake inhibitor citalopram as a model anthropogenic stressor to assess. Effects on the development time, adult body length, brood size, brood-to-brood development time, mortality and sex ratio of N. spinipes were measured experimentally and evaluated in terms of their MoAs.

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### Improving ecological models for a sustainable development of bivalve culture in eutrophic estuarine complexes, a DEB model for macroalgae

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Carrying capacity of coastal systems for bivalve culture has typically been investigated using mathematical models restricted to a Nutrient-Phytoplankton-Zooplankton-Detritus- cultured Bivalve representation. The present project aims at a more detailed understanding of nutrient dynamics in order to accurately gauge the influence exerted by cultured bivalves. Specifically, the impact of blooming macroalgae, a primary producer whose contribution can be significant, especially in eutrophic systems, will be integrated to an existing ecosystem carrying capacity model applied in Malpeque Bay (Prince Edward Island, Canada).

For the first time we developed a DEB model for a macroalgae species, *Ulva lactuca*, using the concept of Synthesizing Units to implement the assimilation of nutrients and energy through photosynthesis. Model development is supported by experimental work to characterize key parameters such as the volume-specific maintenance costs.

Later work will include the development of DEB models for wild bivalve populations of *Mytilus edulis*, *Crassostrea virginica*, *Mya arenaria* and *Mercenaria mercenaria* (parameters already available for the first three species). Adding these new modules will increase model veracity and provide new insights into aquaculture-coastal ecosystem interactions, especially in quantifying the influence on species with commercial, recreational and aboriginal value.

### Importance of protein on reproductive success of a large mammal

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All living organisms transfer energy and matter from their environment to themselves in order to live and reproduce. Energy is the fuel for all chemical reactions, while proteins are part of the structural body mass and the enzymatic activity of animals. Energy budget studies focus on the acquisition and allocation of energy and its implications on survival, growth and reproduction. For large mammals, energy and protein requirements are high, since they must build and maintain a large structural body mass and support lactation. Therefore, interactions between the transfer and allocation of protein and energy has a key role in their survival and reproduction. Brown bears exhibit a variety of reproductive life history traits linked with the diversity of their diet. Bear diets range from largely carnivorous to largely herbivorous. Energy and protein intake can therefore differ substantially among animals and populations. Previous studies have shown that energy storage plays a central role in the reproductive success of female bears, and most recently showing the importance of protein storage on reproduction in bears. Interactions between the allocation of energy and proteins might be especially significant because female bears give birth and begin nursing during hibernation. Using a dynamic systems approach to modeling, we built a simulation model that assesses the daily transfer of energy and protein from the environment to individuals considering the cost of maintenance, growth and reproduction. We used the model to assess how differences in food availability influence annual body mass storage. Results revealed that lean storage and high protein foods play a fundamental role in reproductive success of bears. The relationship between protein available early in the season and energy available late in the season determines the allocation of nutrients in growth and reproduction and thus influences life history traits. This work suggests that the energy budget alone is insufficient to comprehending the diversity in life history traits and to estimate the reproductive success of female brown bears. The inclusion of a protein budget allowed a better understanding and assessment of the effects of environmental variability on reproduction in bears. Since large mammals all have in common high protein demands, we suggest that nutritional and energetic budget studies take into account the acquisition and requirements of proteins.

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### The metabolic roots of sleep and the difference between herbivorous and carnivorous animals.

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Sleep is pervasive amongst animals. It has been observed from small invertebrates such as nematodes, insects or crustaceans to larger and more complex vertebrates such as reptiles, fishes, birds and mammals. Sleep is an obligatory phenomenon and sleep deprivation has dramatic consequences that rapidly lead to death. Such a universality of sleep amongst animals, despite the obvious costs of sleep, suggests a universal physiological function across all species. There is however no consensus as to what that function might be and sleep remains one of the biggest mysteries of modern science.

We propose a DEB-based model of animal sleep. We model human sleep changes from birth to adulthood and estimate the parameters by fitting predicted SWS and REM sleep time to data for humans. We distinguish carnivorous and omnivorous animals from herbivorous animals. Using the parameters estimated for humans, we show that our DEB-based sleep model explains sleep time and sleep rebound for nematodes, insects, fish, birds and mammals. It furthermore enables to understand the very different sleep patterns observed for carnivorous, omnivorous and herbivorous animals. It reveals that herbivorous animals have a fundamentally different metabolism from carnivorous animals. We discuss this surprising finding and some of its many life-history and evolutionary implications.

## Sex-specific decontamination and transfer of polychlorinated biphenyls (PCBs) to next generation in common sole (Solea solea): a coupled experimental and modelling approach.

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In environmental risk assessment, predicting body burdens and transfer of persistent organic pollutants to the next generation is necessary to assess ecological adverse effects. In the field, large variability of contamination levels is often observed. Disentangling and quantifying the chemical factors, the environmental factors and the different physiological states and processes underlying this observed variability remains a major challenge.

In order to better understand the variability of polychlorinated biphenyls (PCBs) concentration in juvenile and adult common soles (*Solea solea*) in the field, we developed a coupled experimental and modeling approach based on a unique laboratory experiment of chronic exposure of common soles to PCBs, which lasted six years (FishNPops project, Ifremer). The bioaccumulation model was developed within the conceptual framework of DEB theory to easily deal with temperature and food availability impacts on organism metabolism. A step-by-step modelling approach was carried out to disentangle the other processes at play: contaminant-specific assimilation efficiencies from food and individual-specific transfer to gametes.

First, we calibrated a full life cycle DEB model for the common sole, following the AmP procedure and using data from the literature. Second, to evaluate assimilation efficiencies of the four congeners studied in the experiment, we focused on juveniles as their contamination levels would only result from food uptake, since these congeners are poorly biotransformable. Despite limited genetic variability and identical experimental conditions, we observed a high variability of growth and contamination levels among individuals. Thanks to the model, food uptake trajectories were reconstructed for each individual using their respective growth curves, making possible to take into account behavioral differences in ingestion to compute theoretical contamination (i.e., with full transfer of contaminant from the assimilated food). These predicted contaminations were compared with observations to estimate assimilation efficiencies. The small variation in estimates among individuals validated our approach. Then, to generalize our results, we looked for relationships between congener specificities (e.g., hydrophobicity, spatial structure) and assimilation efficiencies. Third, to better understand and quantify egg contamination and decontamination processes in females through spawning, we focused on the four years of reproduction in which contamination levels were measured in mothers as well as in their gonads and oocytes. We were able to explain the larger proportion of female burden found in gonads in the field, compared to experimental data, by taking into account that females reared in experimental conditions had a much higher condition index; contaminants tend to remain in the fatter mothers.

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### Project ModelMeat - A model for the optimization of product environmental and nutritional performance as a decision support service for the extensive animal production sector

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The main goal of Project ModelMeat is to develop a decision support service (DSS) for integrated sustainability management in the extensive livestock production sector, starting with a sample of 1,000 farmers in Portugal. The project began in November 2016 and runs until October 2019. The project has three components:

(1) The animal species comprising the typical livestock populations in extensive regimes, mostly bovines (Bos taurus) of several breeds (e.g., Charolais, Limousin or Alentejana), and ovines (Ovis aries), will be modelled through the Dynamic Energy Budget (DEB) theory, allowing us to simulate the dynamics of feed, growth, maintenance and reproduction. This will provide farmers with estimates of the animal characteristics, the ensuing products (meat and milk) and the greenhouse gas (GHG) emissions resulting from the biology involved. In order to support the modelling procedure, grazing feed will be quantified using field measurements and correlating observations with remote sensing instruments such as aerial pictures from drone flights and satellite data;

(2) The feeding and management practices occurring *uptstream* from the farm will be environmentally and economically characterized, depending on the consumption of raw materials and energy, including concentrate feeds and others produced away from the farm, using parametric Life Cycle Assessment (LCA). LCA will also determine the indirect GHG emissions from these inputs;

(3) The third component regards processes occurring *downstream* from the farm, including the determination of nutritional, quality, health and sensory features of the products, as well as their economic valuation by consumers.

In this poster we present the activities and methods of the project, as well as how DEB theory will help us achieve our goal. The model will initially be calibrated using data from the Alentejo region, but the project will establish methods for data collection, modelling and analysis that can be replicated elsewhere.

The DEB model is currently being built. At the end of the project a software tool will be developed with the integrated implementation of ModelMeat.

Project ModelMeat is an innovative approach to surveying that will produce relevant methods (e.g. parametric LCA, correlation between remote sensing of grasslands and yield) and a DSS for future use by farmers and other actors in the agri-food sector. The DSS will allow farmers to estimate the environmental, economic and nutritional consequences of management decisions (e.g., selection of production systems such as conventional or organic) using the integrated on- and off-farm framework of ModelMeat.

### Modeling effects of Contaminants of Emerging Concern (CECs) exposures on fish populations

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Nowadays, environmental stressors such as invasive species, climate change and chemical pollution threaten ecosystems and their services. CECs are increasingly being detected in surface water impacting aquatic life. For instance, wastewater treatment plants discharge effluent containing estrogens, which have caused dramatic ecological effects such as fish feminization and fish population collapses. In addition, different types of chemical mixtures of CECs are released in urban and agricultural areas, with significant impacts on fish populations.

The effects of many CECs in organisms have been assessed via laboratory and field experiments that provide essential information about hazardousness of CEC and biological mechanisms involved in the effects of exposed organisms. However, these experiments tend to focus on a single chemical at the sub-population scale, which limits their applicability in wild setting because (i) fishes actually experience mixtures of CECs and (ii) these mixtures have unknown population-level consequences. Actually, chemicals in a mixture may interact and have the same mechanisms and same molecular target sites. Depending on the situation, the action of CECs can be independent, additive, or more complex and thus require specific investigation. Moreover, there is a need of scaling-up because ecological management and protection generally occur at population, community and ecosystem levels. Nevertheless, the linkages between the responses to chemicals at different scales are difficult to predict from environmental experiments since processes at higher levels of organization act at a high time scale. Modeling offers a tool to study impacts of chemicals and predict their impacts at different ecological scales.

Here we introduce and present early results of two research projects that both incorporate data on individual and sub-individual effects of contaminants into population models to infer the population-level effects. Both projects use DEB theory to model organisms at individual scale. Then, Individual-Based-Models are specifically developed for each project and/or species of interest. The first one is focused on the impacts of estrogens on abundances of fathead minnow (*Pimephales promelas*) and bluegill sunfish (*Lepomis macrochirus*) in a Minnesota pristine river. The main goal of this project is to identify the best wastewater treatment strategy for the protection of Minnesota's natural resources. The second project investigates the effects of two types of CECs mixtures on multiple fish species populations within the Great Lakes Basin. The goals are here to characterize and evaluate the extent to which CECs threaten fish population in the U.S. Great Lakes Basin.

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### A general modelling framework for intelligent environmental risk assessment - sublethal effects and starvation

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In current environmental risk assessment (ERA), plant protection products (PPPs) are tested on a diversity of standard test species for harmful effects. Recent developments in mechanistic effect modelling provide the possibility to extrapolate results from standard studies to untested species and untested ecological scenarios or exposure situations, which will improve the quality of ERA as well as saving time and resources. For lethal effects, toxicokinetic-toxicodynamic (TKTD) models have already proven the ability to identify patterns in effects across compounds and species. One crucial milestone of this development was the identification of a common modelling framework, the General Unified Threshold model for Survival (GUTS). This framework allows for using the same model for all species using different assumptions for death, which had previously believed to be conflicting.

The Dynamic Energy Budget (DEB) theory may have the potential to provide such framework for sublethal effects. Models based on DEB theory allow for mechanistic interpretation of effects on feeding, energy expenditure, growth and reproduction. The same modelling framework can be used for all organisms, which is crucial for across -species extrapolation of effects. Models based on DEB theory have been used in ecotoxicology for decades, however, one major problem so far has been the ability of the models to predict the effects of starvation. Since many compounds act on the ability of the organisms to feed or assimilate energy, predicting starvation responses is a crucial characteristic for a TKTD model for sublethal effects to be used in ERA.

We present here the first results of the i-ERA project (intelligent ERA). The aim of this subproject is to calibrate the DEB standard animal model in control conditions for a suite of vertebrate species, and to develop the starvation module for these species. In total, we are working on the standard DEB model plus starvation module for 11 species: two bird species (mallard duck, bobwhitequail), five mammal species (rat, mouse, rabbit, vole and woodmouse) and four fish species (rainbow trout, fathead minnow, zebrafish and medaka).

We present a meta-analysis of the standard models of the fish, birds and mammals. We further discuss the potential impact using this general modelling framework in ERA.