DEB2023 - 8th International Symposium and Thematic School on Dynamic Energy Budget Theory for Metabolic Organization

School: 4-13 June 2023   Symposium: 14-16 June 2023

Louisiana State University, Baton Rouge, Louisiana, United States

Book of Abstracts

About DEB2023

Welcome to DEB2023, the eighth edition of a prestigious series of tele-courses, schools, and symposia on DEB theory for metabolic organization. This year marks an exciting milestone as we gather in person for the first time in North America.

DEB theory serves as a unifying framework for understanding the metabolic organization shared by organisms across the entire tree of life, encompassing animals, plants, bacteria, and beyond. Based on a concise set of assumptions expressed as mathematical formulas, this theory enables the quantitative assessment of growth, development, and reproduction throughout an individual's life cycle, considering variables such as available food and temperature. Moreover, the process-based framework provides a means to model the impacts of multiple stressors such as contaminants, pathogens, oxygen levels, pH, and more.

The applications of DEB theory are vast and far-reaching. It empowers us to predict the effects of global change and environmental stressors, comprehend the geographical patterns of species, optimize bio-production, manage exploited resources, and control invasive species. Quantitative characterizations of metabolism in diverse biological contexts play a pivotal role in these endeavors, making DEB theory an invaluable tool.

With over 1100 publications to date incorporating DEB theory in various forms, it stands as a cornerstone in the era of abundant data. In our current scientific landscape, collaboration and synergy across disciplines and biomes are crucial. DEB theory provides a common ground for experts to unite and construct quantitative frameworks for problem-solving. Therefore, the thematic school that took place ahead of this Symposium not only equips new scientists with essential tools, mentorship, and training but also offers experienced researchers a platform to refine their skills, explore new avenues, and shape their research questions.

The theme of DEB2023 is "Metabolic Organization Across Scales of Space and Time." As we venture into the Anthropocene era and confront the challenges of breaching planetary boundaries, numerical modeling emerges as an increasingly vital tool for scientists, managers, and stakeholders alike. DEB theory facilitates the construction of related models rooted in a mechanistic understanding of individual metabolic processes. This mechanistic foundation enables the linkage of functional traits to predictive variables, ensuring the adaptability of models to changing conditions. Assessing parameter values is a critical aspect of model applications, and DEB theory has demonstrated its capacity to extract meaningful parameters from data, serving as a valuable resource for informed decision-making.

The symposium will showcase the latest advancements in this dynamic field of research and contribute to cutting-edge, cross-disciplinary developments. After the virtual edition in 2021 due to the COVID-19 pandemic, we eagerly anticipate reuniting for an in-person symposium. We encourage you to embrace the diverse range of presentations on the schedule, engage with fellow attendees, and forge connections centered around DEB theory and beyond.

We hope you thoroughly enjoy this brilliant series of presentations and find inspiration as we embark on this collective journey of knowledge and discovery.

The DEB2023 Organizers

Organization

Organizing Committee:

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

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Supporting organizations:

A not-so balanced diet: Merging DEB and Ecological Stoichiometry theories to understand non-static nutrient dynamics

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Abstract

Fluctuations at multiple time scales in resource quantity and quality can alter consumer population dynamics with profound effects on ecosystem health. Consumers face significant obstacles in maintaining their metabolic homeostasis within these dynamic nutrient environments: nutrient limitation/enrichment alters the trajectory of individual-level life history traits, culminating in altered population dynamics with critical feedbacks to ecosystem-level nutrient cycling. Moreover, distinct life history traits may have differential nutrient needs (e.g., somatic tissue may be nitrogen-rich compared to eggs), compounding population and environmental feedbacks. Despite this widespread ecological phenomenon, we currently lack a framework to (1) predict how population and nutrient cycling dynamics change under fluctuating nutrient input and (2) understand the multi-scale consequences of stoichiometric mismatch between resource and consumer biomass.

Here, I present a nutrient-explicit DEB model that incorporates concepts from Ecological Stoichiometry Theory to quantify resource nutrient quality and connect it to individual consumer growth, reproduction, egestion, and excretion. This multi-reserve, single-structure model tracks important elementally-rich pools, such as carbon-, nitrogen-, and phosphorus-rich compounds through a consumer. Consumed resources are assimilated into separate reserve pools, which are re-coupled to stoichiometrically fixed somatic and reproductive tissue using synthesizing units. Somatic maintenance has both energy and elemental building block requirements-and only certain compounds can substitute for others under nutrient limitation. Excretion stoichiometry therefore is driven by food quality, multi-reserve dynamics, and the stoichiometric mismatch between consumer biomass and resources.

This model overview will be presented along with the derived connections between food quality, consumer life history trajectories, and nutrient cycling.

Keywords: resource quality, ecological stoichiometry, resource fluctuations, nutrient cycling, multi, scale modeling

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Timescale separation and models of symbiosis: state space reduction, multiple attractors and initialization

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Abstract

DEB theory can be used to model interactions of different players, such as interacting symbionts or organelles within an organism. While insightful, such models can easily become complex and parameter rich.
One approach for simplifying such models (and models in general) is to assume that some processes act on a faster time scale than others. Those processes equilibrate immediately, allowing to substitute differential equations with algebraic equations and to reduce the number of parameters.

In simple models, this approach is straightforward and changes model dynamics little. However, in more complex models the fast variables can form closed feedback loops – meaning the algebraic equations can have multiple solutions. Additional information is needed to define such models.

We explore this topic using two examples: a simple DEB model for the nutrient exchange between a plant's root and shoot (Ledder et al, 2020) and a more complex DEB model for the symbiosis between corals and their endosymbiotic algae (Cunning et al, 2017).

We (1) identify whether auxiliary algebraic equations have a unique solution, (2) complete incomplete models with artificial fast state variables, (3) relate this approach to an older (discrete time) method, (4) interpret the method as a limiting case of reserve dynamics, (5) investigate how initialization of the fast system can affect long-term outcomes, and (6) show a new method for finding the lowest dimensional representation of such systems.

Related reading: "Timescale separation and models of symbiosis: state space reduction, multiple attractors and initialization" by Pfab et al. (2022).

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A novel dynamic Energy Budget model for a deep-sea bivalve and its symbionts: the abj-farming model

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Abstract

First Dynamic Energy Budget (DEB) model for a symbiotic deep-sea species has been developed successfully for *Christineconcha regab* (Mollusca, Bivalvia, Vesicomyidae) and its sulphur oxidizing bacterial symbionts. The biology and ecology of the host have been studied in reducing habitats (3000-5000 m depth) in the Gulf of Guinea during several cruises. As all adult vesicomyid clams, *C. regab* has a reduced gut, and is supposed to digest thiotrophic bacteria housed in its gills as a food source. A novel abj-farming model to capture the host farming strategy was built. This is an interconnected model with an abj model for the host and a V1-morph model for the symbionts, which demands twelve additional symbiont-related core parameters. New data were used and predicted, such as symbiont sulphide consumption and volume of the bacterial symbionts within the gills. The model gave unexpected results on host and symbiont dynamics, suggesting a trade-off strategy between the host and its symbionts: the host is willing to forgo maximum ingestion for stable ingestion. We also compared this novel model with a classical typified abj model, which does not have explicit data and parameters related to the symbionts. Both models gave good and comparable estimations for the host clam. This novel abj-farming model could be applied to similar symbiotrophic species from reducing habitats (cold seeps, hydrothermal vents, organic falls...) and used as a basis to develop more complex symbiotic models to give insight on the dynamic of symbionts.

Keywords: Deep sea, bivalve, symbiosis, cold seeps, farming, abj

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Dynamic Energy Budget approach for modeling growth and reproduction of Neotropical stink bugs

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Abstract

Global warming and other climate change drivers have a significant impact on the life cycle of insects which in turn affect their population dynamics and geographic distribution. Stink bugs (Hemiptera: Pentanomidae) are hemimetabolous agricultural pests that cause major damage on crops across many countries. Their life cycle consists of egg, nymph, and adult. The nymph grows and molts through a small number of instars and reach puberty, after which it ceases growth. For two species of the Pentanomidae family, we parametrized and compared two types of DEB models: the sbp-model that assumes isomorphic nymphal growth which ceases at puberty and the abp-model that assumes metabolic acceleration (V1-morph) between hatching and puberty, with no growth after acceleration. Two hypotheses were formulated for the allocation of the mobilized energy in adults: (H1) follows the -rule and (H2) deviates from -rule. Overall, both models capture well data on instar duration, adult longevity, fecundity, and survival, but the sbp-model captures better the nymphal evolution of length and wet mass. Both hypotheses result in good fits with slightly better fits for the H2 hypothesis. However, with the available data we cannot conclude which hypothesis is more likely the energy allocation in adults. Simulations show that temperature has a higher impact on stage durations and survival while food availability on the size and lifetime fecundity. Among the five instars, instars one and two are the most sensitive in temperature changes. The models can be used to simulate individual and population traits under different environmental conditions.

Keywords: Dynamic Energy Budget theory, modeling, nymphal growth, Pentatomidae, insect energetics

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[*]Speaker

ASSESSING BETWEEN-INDIVIDUAL VARIABILITY IN BIOENERGETICS MODELLING: OPPORTUNITIES, CHALLENGES, AND POTENTIAL APPLICATIONS.

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Abstract

Biological variability and, specifically, inter-individual variability are cornerstone for the resilience of wild populations. Populations with heterogenous life history traits are expected to be more resilient against environmental changes and/or human-related impacts. The outcomes of those impacts and possible solutions can be assessed considering between-individual variability through individual-based models (IBMs) coupled with bioenergetics models. However, the reliability of the population trends predicted by those IBMs depends on how inter-individual variability is considered. Dynamic Energy Budget (DEB) theory is an especially appealing bioenergetic framework for coupling with IBMs. However, despite many recent improvements, between-individual variability in DEB parameters estimates and their uncertainty are not usually considered. The use of a Bayesian inference framework and hierarchical modelling have shown promise for facing these two challenges. Here, a STAN (a software for Bayesian inference) routine was developed for estimating between-fish variability in two key DEB parameters (pAm, maximum assimilation rate per surface unit, J/day/cm2; and v , energy conductance, cm/day) from 69 cultured Gilt-head bream (*Sparus aurata*) for which up to 11 repeated measures (made at between 236 and 738 days) of length and wet weight were available per fish. In spite of some limitations of the approach presented here, between-fish differences in the two DEB parameters considered were remarkable. Such a parameter variability agrees with the large differences in length- and weight-at-age typically displayed by both, wild populations and cultured fish.

Keywords: DEB, between, individual variability, Bayesian, STAN

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Energetics of bird reproduction and egg-laying: case study of bobwhite quail

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Abstract

Bobwhite quail (*Colinus virginianus*) is an intensely studied bird species due to commercial and conservation interest, as well as its use as a test organism for higher tier risk-assessment. Quails produce 1-2 clutches of eggs per reproductive season in nature, but can produce eggs continuously when reared. Prior to and during reproduction, both wild and reared females drastically increase their feed uptake. We focus on elucidating the fate of the extra assimilates, in the context of egg-laying but also of birds building up the reproductive system and undergoing tissue remodelling prior to each reproductive season.

We expand the standard Dynamic Energy Budget (DEB) model with an explicit egg-laying module, and formulate and test two hypotheses for energy allocation of the extra assimilates: (H1)the energy and nutrients are used directly for egg production; and (H2)the energy is mostly spent on increased metabolic costs incurred by building up and maintaining the reproductive system and, subsequently, on egg-laying itself. Further, we explore potential sources of interindividual variability observed in data.

Results suggest that H2 is the more likely energy allocation pathway. Model predictions capture well the ontogeny of a northern bobwhite quail and can reproduce most of data variability by introducing three sources of variability: (i) egg size, (ii) egg-laying rate and (iii) assimilation potential. Reliable models with capacity to predict physiological responses of individuals are relevant not only for experimental setups studying effects of various natural and anthropogenic pressures on quail as model organisms, but also for wild quail management and conservation.

Keywords: energy allocation, Dynamic Energy Budget, interindividual variability, egg, laying module

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Combining process-based with data driven models for the minimisation of greenhouse gas emissions of beef cattle

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Abstract

Ruminant livestock production is now taken as a main culprit in environmental pressures. However, ruminants play a special role in a sustainable food system, due to their capacity to process human inedible (namely fiber-rich) feed transforming it into high-nutritional value milk and meat. Resource-wise, ruminants are especially effective when using fiber-rich feed, namely from grazing on pastures; this, however, leads to a trade-off with increased methane emissions, from lower digestibility of feed and from increased feed requirements from movement costs (the latter, however, being offset by decreased emissions from manure). Additionally, an adequate analysis of these systems requires the balancing between the life cycle emissions of feed and the direct methane emissions from the digestive process of cows, veals and heifers/young bulls. Strategies for optimising pasture-based systems include: reduction of direct methane emissions through feed additives and animal breeding; the promotion of carbon sequestration, on pasture soils and on associated agro-forestry systems. The analysis of all these strategies benefits from the combination of the use of process-based models, respecting mass and energy conservation, with data-based approaches, namely based on the techniques of machine learning, capturing, namely in DEB models, individual variability.

Keywords: Livestock, greenhouse gas emissions, animal breeding, life cycle assessment, machine learning

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[*]Speaker

Explaining individual variability in Mertolenga cattle with dynamic energy budget theory

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Abstract

The parameters of the DEB model are usually assumed constant for the whole species or breed, typically due to insufficient data, even though the consensus is that the parameters vary from individual to individual. Moreover, when individual data is available, it is often not sufficient to characterize its full life cycle.

For this reason, we developed a methodology that assumes two types of parameters: group parameters, that are constant for the species, and individual parameters, that are specific for each individual. We describe a new two-step procedure for the estimation of individual parameters. The first step consists of the calibration of a DEB model for the species using all available data. In the second step, we estimate the parameters of each individual using the individual's data and introduce the previously estimated group parameters as pseudo data to ground the estimation.

As a use case, we apply our methodology to a dataset of growth and food intake curves for 52 individuals of the Mertolenga cattle breed. Results show at least two parameters for each individual are needed to explain the variability in the data. From a mechanistic perspective, zoom factor and digestion efficiency are the most reasonable parameters to be chosen as individual for the data in question, and goodness-of-fit supports this choice when compared to all options of two individual parameters.

Leveraging the estimated individual parameters, we provide insight into metrics commonly used in livestock production to assess the efficiency of converting food to weight growth.

Keywords: individual variability, cattle metabolism, livestock production, efficiency metrics

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A generalized Dynamic Energy Budget model including 3D shape changes for modeling small pelagic fish growth

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Abstract

Understanding pelagic fish growth patterns is fundamental to predict larval survival and predator-prey dynamics, which are influenced by individual size. Dynamic Energy Budget (DEB) models constitute tools to predict these patterns in changing environments. In DEB models, individuals are assumed to grow either isomorphically, or to experience a metabolic acceleration phase between birth and metamorphosis, during which the shape coefficient changes and both the maximum surface-area specific assimilation rate and the energy conductance are multiplied by a metabolic acceleration coefficient function of structural length. Here we propose a different growth model based on a DEB model that captures deviations from isomorphy, allowing length and width to grow non-proportionally. Our model represents the fish's structural body as an ellipsoid and differentially allocates volumetric growth to length, height and width as a function of the distance between the current shape and characteristic stage-dependent shape attractors (expressed as aspect ratios). The resulting changes of the structural surface-to-volume ratios mechanistically explain the "metabolic acceleration" phenomenon invoked to interpret early life growth patterns. We estimated model parameters for the European anchovy *Engraulis encrasicolus*, using data covering growth at all life-stages, observed shapes at early life stages, transitions between life-stages, and reproduction. The calibrated model accurately reproduces the observed the exponential length-dominated growth until metamorphosis, its shift to height- and width-dominated growth (with a corresponding deceleration of growth in length) until the adult shape is reached, and finally isomorphic (characteristic von Bertalanffy) length growth, and could profoundly affect our understanding of larval survival, predator-prey and ecosystem-dynamics.

Keywords: generalized growth, structural ellipsoid, three dimensions

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Determining energy-limited tolerance to acute thermal stress in farmed finfish

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Abstract

Pinpointing thermal tolerance thresholds for commercially important species, such as aquaculture finfish, under acute and chronic thermal stress is becoming increasingly relevant in the context of climate change. While traditional experimental measures such as the Critical Thermal Maximum (CTmax), offers valuable insights, it is necessary to develop appropriate tools to predict thermal tolerance and unravel the underlying mechanisms. Here, we present a modelling approach based on the Dynamic Energy Budget (DEB) theory to describe the tolerance limits of fish under acute thermal stress in bioenergetics terms. It adopts the notion of energy-dependent tolerance to stress and defines acute tolerance limits at the intersection of fundamental energy fluxes, namely those of energy mobilization and maintenance costs. To showcase this approach, acute thermal stress was simulated using DEB models for two finfish, the European sea bass (*Dicentrarchus labrax*) and the meagre (*Argyrosomus regius*). The model could adequately capture the general tolerance patterns observed experimentally for the two species as well as pinpoint parameters that influence them. Specifically, tolerance correlated positively with the acclimation temperature, within the typical temperature range of the species, and the state of energy reserves, but negatively with the body size of the fish. Finally, the potential application of this method on higher taxonomic scales was evaluated, by running simulations on species belonging to major fish orders. The preliminary results indicate that the method can capture differences among groups that are consistent with literature, suggesting it may be a realistic mechanistic approach for studying thermal tolerance in ectotherms.

Keywords: climate change, aquaculture, thermal tolerance, DEB, modeling, acute stress

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Dynamic Energy Budget model for E. coli growth in carbon and nitrogen limitation conditions

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Abstract

Escherichia coli is a Gram-negative, rod-shaped bacteria, that is capable of conducting aerobic respiration in the presence of oxygen and fermentation when oxygen is absent. Its morphology, physiology, and genome are very well studied. Therefore it plays a huge role in modern biotechnology as a model organism. In terms of the Dynamic Energy Budget (DEB) theory, the bacteria culture in a liquid medium can be modeled as one organism. The such model organism grows by cell divisions, increasing its volume and area proportionally to the number of cells. Therefore it has to be considered as a V1-morph, an organism whose surface is proportional to its volume during growth. The carbon and nitrogen sources and assimilation pathways in *E. coli* are more or less independent. The strong homeostasis assumption in DEB theory implies that the chemical composition of the reserve or structure does not change in living organisms. Therefore, to model two or more independent assimilation pathways we need to consider the multi-reserve system, with a distinct reserve for each assimilation path. In the presented study we conducted the bioprocess of *E. coli* growth in carbon and nitrogen limitation conditions. The changes in bacterial biomass and C and N concentrations in the medium were monitored. The DEB model parameters were fitted to the full kinetic data set. DEB model fit was compared with the fit of standard Monod-like growth kinetic. The results were discussed regarding the future applicability of DEB models in biotechnological processes simulations, predictions, and optimization.

Keywords: bacteria, growth kinetics, bioreactor, biotechnology

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Nutritious vs. junk food in the Arctic Ocean: Predicting population impacts of environmental change in Arctic marine mammals

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Abstract

Conservation of target species and biodiversity requires understanding how individuals, populations, and communities interact and respond to environmental change. In the Arctic, the accelerated rate of warming and the loss of sea-ice has impacted several lipid-rich prey whose ecology is linked to sea-ice or cold temperatures. And it has led to the expansion of temperate and Subarctic species (of lower nutritious value) into higher latitudes and Arctic food webs. Such a shift in prey will likely result in the redistribution, behavioral change, and diet-switching of Arctic predators. Endemic Arctic species, including bowhead whales, beluga whales, and walruses, rely heavily on sea-ice algae-based food webs, and the seasonal formation of sea ice as protective and foraging habitat. Thus, these three Arctic predator species are expected to respond strongly to climate change. Furthermore, increasing stressors such as shipping, resource extraction activities, oil spills, and environmental pollution, coupled with the decrease in nutritious prey, will affect energy budgets and population health. We are developing a predictive modeling framework to compare the ecophysiology of bowhead, beluga, and walrus and assess their vulnerability to environmental stressors throughout the 21st century. The model uses Dynamic Energy Budget (DEB) Theory to simulate emergent population dynamics, incorporates environmental forcings, and includes new DEB modules to capture species-specific physiological processes and improve standard DEB assimilation approaches. These modules include stunted growth patterns during early developmental stages in bowhead whales, reproductive upregulation cycles, and periods of prolonged lactation where food supplements milk intake and reserve-mobilization drops.

Keywords: Ecophysiology, Arctic, Marine, Mammals, Assimilation, Sympagic, prey, Climate Change, Stressors

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[*]Speaker

Reconstructing the growth and feeding of the scallop Mimachlamys varia: a DEB inversion

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Abstract

For several years, toxic blooms of micro-algae of the *Pseudo-nitzschia* genus have been occurring regularly on the French coast. The domoic acid toxin produced by these algae is then bioaccumulated in the tissues of filter-feeding organisms such as bivalves, sometimes making them unfit for human consumption. *Pecten maximus*, or the King scallop, an important fishery resource in France has the particularity to be a slow depurator, and its fishing can therefore be prohibited for several months following each episode of toxic bloom. A shifting of fishing effort is then possible on another pectinid, the variegated scallop *Mimachlamys varia*, but its stocks are currently low. In this context, the present study developed for the first time a DEB model for this new species, with the aim to better understand its nutrition, growth and reproduction dynamics. The model development is based on a multi-site 3-year *in-situ* monitoring in the Bay of Brest (Régnier-Brisson *et al.*, submitted poster), used both for its parameterization and validation. In a second step, the trophic ecology of the variegated scallop was studied by inverting the DEB model, in order to reconstruct the feeding signal from the observed growth dynamics. Comparing to *in-situ* measurements (fluorimetry monitoring, stable isotope, flux cytometry and chlorophyll analysis), this approach helped us to better understand the trophic ecology of this species. We discuss future uses of this DEB model which could inform management strategies for the species to establish a sustainable fishery.

Keywords: Variegated scallop, Mimachlamys varia, Trophic ecology, DEB inversion, In, situ monitoring, Bay of Brest

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[*]Speaker

Understanding interspecific competition of native and invasive crayfish using Dynamic Energy Budgets

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Abstract

Crayfish are keystone species important for maintaining healthy freshwater ecosystems. Crayfish species native to Europe, such as *Astacus astacus* and *Austropotamobius torrentium*, are facing decline and are increasingly endangered by changing climate and invasions of non-native crayfish, such as *Pacifastacus leniusculus* and *Procambarus virginalis*. The success of these invasions largely depends on differences in ontogeny between the native species and the invaders and how changes in the environment will affect the ontogeny. Dynamic Energy Budget (DEB) models can be used to investigate such differences because the models capture dependence of metabolism, and therefore ontogeny, on environmental conditions. We develop DEB models for all four species and investigate key elements of ontogeny and metabolism affecting interspecific competition. We then use the DEB models to predict individual growth and reproduction in current and new conditions that are expected to arise from climate change. Although observations suggest that *P. leniusculus* poses the major threat to native species, our analysis identifies *P. virginalis*, in spite of its smaller size, as the superior competitor by a large margin-at least when considering metabolism and ontogeny. Our simulations show that climate change is set to increase the competitive edge of *P. virginalis* even further. Given the prospects of *P. virginalis* dominance, especially when considering that it is able to withstand and spread at least some crayfish plague strains that severely affect native species, additional research into *P. virginalis* is necessary.

Keywords: Decapoda, invasion potential, life history traits, ontogeny, standard DEB model, freshwater crayfish

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Integrating DEB models and NicheMapR to explore species coexistence in lacertid lizards

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Abstract

We focused on two lacertid lizards, *Podarcis muralis* and *Iberolacerta horvathi*, which exhibit an altitudinally segregated pattern of distribution but co-occur at mid-altitudes and compete for resources. The well-studied species pair offers an excellent opportunity to approach the topic of competition/coexistence from a niche modelling perspective. We first estimated DEB model parameters for *I. horvathi* and updated the existing add-my-pet entry for *P. muralis* using literature and our own field-collected data. Then, we used NicheMapR to simulate microclimatic conditions in 15 locations: five species-specific locations (5 for *P. muralis* and 5 for *I. horvathi*) and five syntopic locations. For each location we ran coupled biophysical and DEB model simulations for both species. Specifically, we simulated the whole life cycle of both species, including growth, development, energy allocation, and reproductive output, under modeled environmental conditions for each selected location. Our results showed differences among both slope and elevation of chosen locations, slope potentially being significant for co-occurrence. Models predict that both species mature faster and live shorter lives, have more offspring, more clutches, and more time available to forage in syntopic locations. Our study serves as a foundation for a novel methodological approach focusing on modeling multiple species systems while incorporating interspecific interactions. We strive to provide a fresh insight into how species, habitat and biotic interactions interact. Additionally, our results can inform future investigations into how changes in environmental conditions may affect species coexistence scenarios focusing on the intricacies of intraguild competition and the ecological factors that drive species interactions.

Keywords: DEB, NicheMapR, habitat, Lacertids, Slovenia, coexistence, competition

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Dynamic Energy Budget theory based invariants of life histories

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Abstract

AmP is an online creative commons animal database containing referenced eco-physiological data, Dynamic Energy Budget (DEB) parameters, and DEB implied traits for over 4000 species from all major animal phyla. Through the analysis of patterns in DEB traits from AmP, we found three noteworthy and perhaps even new invariants of animal life-history. The weight-specific respiration rate (mol/g/d)) was found to be inversely proportional to life span (d) with a factor of 0.1 mol/g. The ultimate neonate mass production rate (g/d) was found to be proportional to the respiration rate (mol/d) by a factor of 10 g/ mol. Thirdly, the accumulated mass of offspring produced per lifespan (g) was found to be equal to the maximum weight (g). We will show graphs with these three newly found life-history invariants and discuss how they hold with more or less scatter for different taxa. The third pattern could be an alternative to construing reproduction as being optimized over evolutionary time-spans to maximize fitness. The present finding builds on previous findings that observed reproductive output is substantially smaller than potential reproductive output given parameter values other than the allocation fraction of mobilized reserve to soma.

Keywords: life history, traits, biodiversity, respiration, life, time reproduction

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[*]Speaker

An application of DEB theory to understand the co-variation of life-history traits in freshwater populations

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Abstract

There has been an increased interest in the effects of global change on freshwater populations, because of their close dependence on environmental factors for survival. Changes in those factors, acting as selective pressures, could lead to differences in individuals' life-history. However, this adaptation might be restricted by evolutionary constraints due to the chemical and physical mechanisms at play and/or genetic correlation between traits.

According to the Pace-of-Life-Syndrom theory (i.e. POLS), the correlated expression of a set of life-history traits (LHTs), constrained by individual bioenergetic characteristics, defines "slow" or "fast" strategies. Thus, the expression of a set of specific genes related to energy processing will lead to specific values of LHTs (growth and reproductive traits). The resulting correlation between these traits could limit possible evolutionary pathways in response to environmental changes.

To understand how bioenergetic parameters could link different LHTs, we modelled energy allocation in two freshwater species (*Daphnia magna* and *Salmo trutta*) with the help of the Dynamic Energy Budget theory. We accounted for inter-individual differences by independently varying the value of primary parameters of the model under constant environmental conditions (optimal temperature and *ad libitum* food source). We then estimated the effect of this inter-individual variation on the correlations between several LHTs (Length, Lifespan, Age at Puberty, Reproductive Output and Respiration rate). This study of co-variation between traits provides clues to the actual evolutionary potential of LHTs in freshwater organisms.

Keywords: Survival, Reproductive output, Metabolism, Individual based modelling, Pace of life Syndrom

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Age-related changes in evolutionary potential can be predicted through DEB theory

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Abstract

Heritability, or the proportion of variance in a trait that is due to genetic variation, is a key parameter to estimate the ability of a population to adapt to new environmental conditions (i.e. evolutionary potential). It is thus of the utmost importance to provide reliable and consistent measures of heritability. However, empirical studies showed that heritability and genetic variance of life-history traits often increase with age. Various hypotheses have been put forward to explain these variations, such as a decrease in environmental or maternal effects with age, or the convergence of growth trajectories toward a genetically-determined maximal size. It is not currently possible to test them due to the lack of a theoretical null model describing the expected changes in traits during ontogeny. In particular, the physiological mechanisms that link genotype and phenotype are generally neglected. Therefore, we aimed to use a model based on DEB theory to predict the variation in evolutionary potential with age and thus find the origins of these variations. We simulated size and reproductive output of Daphnia magna under different regimes of variation in food, temperature and energy in the egg corresponding to the hypotheses above. We then compared the resulting age-dependence in the variance-covariance matrix of those traits, to conclude on the potential contribution of different hypothesized mechanisms.

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

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Using host nutrient limitation to model parasite production and link parasite-host life histories

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Abstract

The nutrients that limit growth and reproduction of an organism change based on their relative abundance in the food resources that are available. Parasites often have nutrient compositions that differ from their hosts, so a nutrient-limited host can have a parasite that is not limited by the same nutrient, which can lead to greater virulence and exacerbation of effects like parasite-induced mortality and reduced fecundity in the host. We examine *Daphnia magna* and two parasites, the bacterium *Pasteuria ramosa* and the microsporidian *Hamiltosporidium tvaerminnensis*, to see if modeling spore production of these parasites under different nutrient regimes creates stronger predictions of their effects upon individual hosts. Modeling the flow of the limiting nutrient in a given system may provide better insight than modeling other nutrients, as nutrient limitation can greatly affect how organisms consume and use resources. We hypothesize that, under P-limitation, models that use P as the resource currency will make more accurate predictions about virulence (and thus feedbacks on the host), whereas C will be the stronger predictor at higher P availabilities.

Keywords: Daphnia, Parasites, Nutrient limitation, Virulence

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[*]Speaker

Remarkable combinations of data types in the AmP collection

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Abstract

As is known, DEB parameters can only be estimated from combinations of several data types, rather than from a single data set. This poses strong constraints on what function of data, predictions and weight coefficients can be minimized to arrive at parameter estimates: the loss function. The classic regression loss function is of little use, due to differences in dimensions of the various data sets. It is not a distance measure between data and predictions, since they cannot be interchanged without affecting the value of this loss function. The symmetric bounded loss function is such a distance-measure: the mean relative error for some 15 data sets per species and over 4000 species is only 0.05. Many of the data set combinations in the AmP collection are simple, but some are remarkable in covering diverse aspects of metabolism, or showing how changes in food intake and temperature translate to changes in growth, reproduction or respiration.

This lecture discusses some of them briefly, to illustrate the challenges of estimating DEB parameters in practice and to show the predictive power of simple models. Take, for instance, the entry for Alburnus alburnus, with the data sets dry weight as function of time and respiration and feeding rate as functions of dry weight. One needs DEB theory to see why and how their combination determines the digestion and defecation efficiencies. They turn out to be much lower and higher, respectively, than the default values.

Keywords: AmP collection, Parameter estimation, Effects of environment

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[*]Speaker

Interpreting the toxicity of complex mixtures for ecological risk assessment using dynamic energy budgets

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Abstract

Standardized toxicity tests test the effects of chemicals on either growth or reproduction and/or mortality. Furthermore, these tests that can involve vertebrates are labor and time intensive and costly. The endpoints measured are too broad to attribute to specific mechanisms of toxicity and constrain the effect to a single process (ie. growth or reproduction, not both). But, within an organism, these processes are linked, and if one physiological process is affected by a contaminant, the others will also be affected through energetic tradeoffs. Single PFAS compounds also activate more than one toxicity pathway, and so the standardized toxicity tests as they are currently designed will not be able to detect competing energetic demands as an organism integrates its response to the toxic insult of just one compound. This is magnified if we consider mixtures of compounds. We propose to link data sets on the effect of a PFAS mixture across biological scales: computational chemistry to predict molecular initiating events and damage to protein structure, transcriptomics to determine toxicity pathways, analytical chemistry to determine bioaccumulation and toxicokinetic processes, Dynamic Energy Budget models to integrate toxicity pathways within an organism allowing for energetic tradeoffs between processes, and standardized tests that deliver endpoints such as growth and reproduction. We explore this for two model organisms, fathead minnows and Daphnia.This comprehensive approach will allow us to determine what subset of information is needed to determine toxicity of PFAS mixture in laboratory and field environments.

Keywords: PFAS, mixtures, DEB, Adverse Outcome Pathways

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[*]Speaker

The bobwhite quail exposed to fluopyram: analysis of standard sub-lethal bird OECD data with the DEB model

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Abstract

Dynamic Energy Budget (DEB) theory models can support assessing risks of chemicals to bird populations in terms of analysing risks linked to sub-lethal effects such as observing smaller chick sizes compared to untreated controls.We couple several dedicated toxicity and reproduction modules to a core DEB model in order to analyse data from multi-generational sublethal standardized tests for a model bird (bobwhite quail) exposed to a fungicide, Fluopyram. Our aims are (i) to predict the way F0 reproduction endpoints and F1 early chick development are impacted by increasing levels of Fluopyram in feed and (ii) to understand mechanisms underlying those effects. The model can capture the effects and predicts that effects recorded on the F1 generation (weights and hatch at 14 days) result from the offloading of toxic compounds from the mother to her eggs. We tested this hypothesis in detail via the implementation of a simplified effect module for the embryo and chick whereby the level of effect of the offspring is related to the level of contaminant in the mother (with no chemical offloading in eggs as baseline hypothesis). The modelling approach developed in this study provides tools for improving extrapolations of effects observed in the laboratory to quantifiable risks to wild bird populations.

Keywords: toxicity, DEB theory, OECD, quail, reproduction

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DEBlipid: A model allowing multiple life history choices in fluctuating environments

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Abstract

DEB models have the potential to predict individual and population responses to environmental change at many temporal scales. This is ecologically important because extreme events such as enhanced frequency of hurricanes, forest fires, or floods occur alongside slowly rising mean temperatures. Thus, ideally a DEB model must describe responses to arbitrary environmental change (slow/fast, small/large).

In Kooijman's "standard" DEB model, reserve regulation operates on the same time scale as other energy fluxes. This constrains its flexibility for investigating life history "decisions" in the face of rapid and/or extreme environmental change. We therefore formulated a modified version of the "DEBlipid" model (Martin et al. 2017), starting from a "stylized fact" (inferred from data on fishes) that storage density increases through ontogeny for juveniles but with little subsequent increase for adults. We assumed a simple dynamical mechanism (proportional feedback) for storage regulation, now implemented in a model with different architecture. Our study was theoretical, but computations used parameters appropriate for a zooplankter or a fish. Responses of individuals and populations to large environmental fluctuations were highly sensitive to the interplay of regulation strength and to the relative priority under stress of reproduction versus protecting storage (and thereby enhancing survival probability), a fundamental life history decision.

A "take-home" message for DEB researchers is that while focusing on specific ecological questions may lead to different choices of stylized facts and thereby to new models, rigorous analysis paralleling that previously used for standard DEB is required to tease out the implications of any "new" model.

Keywords: reserve regulation, DEBlipid, life history theory, variable environment, extreme events.

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[*]Speaker

Estimating methane emissions in fattening trials of crossbred Angus-Aberdeen young-bulls

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Abstract

Livestock is an important sector responsible for around 15% of global greenhouse gas emissions. The majority of these emissions come from methane produced directly or indirectly by ruminants, raised for meat or milk. Finding strategies to reduce these emissions is one of the main goals of agriculture policy.
One of the main strengths of DEB theory is the power of making predictions within a framework that is not only internally coherent, but also consistent with other fundamental knowledge, such as thermodynamics. This allows for the estimation of methane emissions of ruminants in a consistent manner.

In the GreenBeef project we performed a fattening trial with Angus-Aberdeen crossbred young-bulls, to estimate methane emissions. Four groups of five young-bulls each, were formed and put in side-by-side parks. For 10 weeks, two of the groups were fed with a standard combination of straw and concentrate, that is used widely in Portugal, and two other groups were fed with a Total Mixed Ration of silage and a feed using by-products available in the region, representing feed used by high-level beef producers in Portugal. Intake was measured for each group and the individual young-bulls were weighed biweekly. Moreover, one Greenfeed® equipment was circulated across the groups to measure individual methane emissions during that period.

Using data collected on the trial and an estimation of a DEB model for crossbred Angus-Aberdeen, we present the effect of different feed on methane emissions for this breed, and more robust insights on methane production parameters within this framework.

Keywords: methane emissions, cattle metabolism, livestock production

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DEB models of coral bleaching.

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Abstract

DEB theory describes the assimilation and utilization of energy and elemental matter by organisms. DEB also describes the synthesis of metabolic products, thereby offering an ideal framework for modeling "syntrophic" interactions between species where one species' metabolic products are a nutritional resource for the other - as with corals and their photosynthesizing symbionts. Muller et al (J. Theor. Biol. 2009, doi:10.1016/j.jtbi.2009.03.004) formulated a model of syntrophic symbiosis mediated by interchange of carbon and nitrogen compounds, and showed likely emergence of a stable equilibrium ratio of host and symbiont. Cunning et al (2017: J. Theor. Biol. 2017, http://dx.doi.org/10.1016/j.jtbi.2017.08.003) developed a simplified version of that model, but added a key new positive feedback through which surplus photosynthate is recycled by the host to fuel a carbon-concentrating mechanism in the symbiont. The proximate cause of bleaching is light-triggered production of reactive oxygen species (ROS) by the symbiont. There is hysteresis in the bleaching response: after bleaching, light levels must drop well below the bleaching threshold before coral growth resumes. The Cunning model underpinned subsequent studies of the effects of coral fertilization by nitrogen excreted by coral-dwelling fish and of the potential for bleaching resistance through symbiont substitutions. Current work focuses in detail on temperature effects, based on observed strong temperature dependence of photosynthetic efficiency, additional to uniform rate changes by an Arrhenius factor. Taken together, our studies enhance understanding of how different abiotic factors (e.g. light, nutrient, temperature) and biotic factors (e.g. host food, fish, competing symbionts) impact coral bleaching.

Keywords: Syntrophy, coral bleaching, mutualism, oxidative stress, photosynthesis

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Assessing Vulnerability of the U.S. Atlantic Sea Scallop to Ocean Acidification and Warming: A Dynamic Energy Budget Modeling Approach

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Abstract

The US Atlantic sea scallop (*Placopecten magellanicus*) fishery is valued at more than $500M US per year, making it the second highest valued fishery in the country and the largest wild scallop fishery in the world. While the fishery is currently considered to be well-managed, managers and industry stakeholders are concerned that changing ocean conditions driven by climate change will cause declines in scallop availability, harvest, and revenue. Sub-surface scallop habitats in the Northeast and Mid-Atlantic already experience suboptimal temperature and carbonate chemistry conditions episodically. Future projections indicate that conditions in the Gulf of Maine will begin to surpass suboptimal thresholds persistently by the year 2050. Here, we project the effects of ocean acidification (OA) and warming on sea scallop growth and reproduction historically and over the next century using a dynamic energy budget (DEB) model forced by a regional ocean model. Preliminary results suggest that end-of-century OA and warming, together, will cause sea scallops to grow faster but reach a smaller maximum size. Our future work will couple the DEB model to a larval transport model. This novel combination of approaches will allow us to quantitatively relate changing ocean conditions to changes in sea scallop population vulnerability and inform fisheries management by estimating changes in growth and identifying areas that are candidates for future fishing zones.

Keywords: Climate change, future projections, fisheries, management

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Energetic mechanisms of hypoxia impacts on early life stages of an estuarine fish

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Abstract

Ocean deoxygenation is intensifying worldwide due to warming and eutrophication, particularly in estuaries and coastal waters. Although the Atlantic silverside (*Menidia menidia*) has proven robust to the fluctuating environmental conditions in its estuarine environment, chronic hypoxia impairs hatching, growth, and survival in the early life stages. We used a DEBkiss model to test the hypothesis that experimentally observed changes in animal performance can be explained by one or more of the rate processes in the model. We sought to identify the DEBkiss parameters that, when adjusted with a correction factors, provided the best fit to hypoxia effects in the three state variables of total length, egg buffer mass, and survival over time. Because hypoxia reduces survival in embryos and newly hatched larvae, we added a survival state variable controlled by pre- and post-hatching mortality parameters. Increasing the maximum assimilation rate or the yield coefficient for conversion of assimilates to structure accounted for some of the hypoxia-related changes in all three state variables. However, simultaneously reducing the yield coefficient and increasing both mortality parameters provided the best fit. In contrast, increasing the parameter for maintenance rate with hypoxia had little impact on early life growth and egg buffer depletion, and no impact on survival rates. Reduced conversion efficiency under hypoxia would suggest that less of the energy invested by parents is converted into biomass in *M. menidia* offspring, while lower assimilation rates under hypoxia would have negative implications for the total energy available for growth, reproduction, and maintenance.

Keywords: hypoxia, marine fish, DEBkiss, estuarine, assimilation, stress

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The consequences of sea lamprey parasitism on lake trout energy budgets

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Abstract

Parasitism is an energetically costly event for hosts. Models derived from DEB theory specify how an organism converts food to reserves (maintenance-free energy available for metabolism) and allocates mobilized reserves to maintenance, growth (increase of structural body mass) and maturation or reproduction. DEB models thus provide a useful approach to describe the consequences of parasitism for host species. We developed a DEB model for siscowet lake trout and modeled the impact of sea lamprey parasitism on growth and reproduction using data collected from studies documenting the long-term effects following a non-lethal sea lamprey attack. The model was parameterized to reflect the changes in allocation of energy towards growth and reproduction observed in lake trout following sea lamprey parasitism and includes an estradiol module that describes the conversion of reproductive reserves to ovarian mass based on estradiol concentration. In our DEB model, parasitism increased somatic and maturity maintenance costs, reduced estradiol and decreased the estradiol-mediated conversion efficiency of reproductive reserves to ovarian mass. Muscle lipid composition of lake trout influenced energy mobilization from the reserve (efficiency of converting reserves allocated to reproduction into eggs) and reproductive efficiency. These model changes accurately reflect observed empirical changes to ovarian mass and growth. This model provides a plausible explanation of the energetic mechanisms that lead to skipped spawning following sea lamprey parasitism and could be used in population models to explore sublethal impacts of sea lamprey parasitism and other stressors on population dynamics.

Keywords: sea lamprey, lake trout, hormones, lipids, suborganismal processes

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DEB modeling of Dairy Sheep in Portugal: balancing welfare, ecology and quality

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Abstract

A key aspect of farming live-stock is balancing environmental impacts, animal welfare, economy and quality. In this study we develop modeling tools based Dynamic Energy Budget (DEB) theory in order to analyze data from ongoing experiments from the dairy sheep sector (the Lacaune breed). The experiments evaluate the impacts on mother's health, lamb size and numbers, and milk production of two distinct husbandry techniques: feeding in biodiverse sown permanent pastures *versus*
feeding with an industrial concentrate-based feed. Our aim is to predict the data from the experiment and then to compare the results of both experiments in terms of key parameters controlling processes related to feeding, growth, and reproduction. The insights from a DEB based analysis of the experimental data are intended to support the objectives of minimizing both the use of concentrate and emissions of greenhouse gases per liter of milk.
We here present the experimental design and an overview of the data followed by first results. DEB model parameters have been estimated for the Lacaune sheep breed. Size differences between males and females are captured as differences in their specific assimilation rate. This DEB model and associated parameters are used as a core from which two specific modules are coupled: a feeding module and a reproduction module. The latter includes fetal development of singles, twins and triplets, and their growth up to sale at one month of age. The model is fit to the lamb weights. We discuss these findings and highlight challenges linked to the feeding module.

Keywords: DEB theory, dairy sheep, welfare, milk, environmental impacts

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[*]Speaker

A not-so balanced diet: Merging DEB and Ecological Stoichiometry theories to understand non-static nutrient dynamics

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Abstract

Fluctuations at multiple time scales in resource quantity and quality can alter consumer population dynamics with profound effects on ecosystem health. Consumers face significant obstacles in maintaining their metabolic homeostasis within these dynamic nutrient environments: nutrient limitation/enrichment alters the trajectory of individual-level life history traits, culminating in altered population dynamics with critical feedbacks to ecosystem-level nutrient cycling. Moreover, distinct life history traits may have differential nutrient needs (e.g., somatic tissue may be nitrogen-rich compared to eggs), compounding population and environmental feedbacks. Despite this widespread ecological phenomenon, we currently lack a framework to (1) predict how population and nutrient cycling dynamics change under fluctuating nutrient input and (2) understand the multi-scale consequences of stoichiometric mismatch between resource and consumer biomass.

Here, I present a nutrient-explicit DEB model that incorporates concepts from Ecological Stoichiometry Theory to quantify resource nutrient quality and connect it to individual consumer growth, reproduction, egestion, and excretion. This multi-reserve, single-structure model tracks important elementally-rich pools, such as carbon-, nitrogen-, and phosphorus-rich compounds through a consumer. Consumed resources are assimilated into separate reserve pools, which are re-coupled to stoichiometrically fixed somatic and reproductive tissue using synthesizing units. Somatic maintenance has both energy and elemental building block requirements-and only certain compounds can substitute for others under nutrient limitation. Excretion stoichiometry therefore is driven by food quality, multi-reserve dynamics, and the stoichiometric mismatch between consumer biomass and resources.

This model overview will be presented along with the derived connections between food quality, consumer life history trajectories, and nutrient cycling.

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Application of an oyster DEB model to assess the impact of rearing density, environment variability and mortality on oyster production in Bourgneuf Bay (French Atlantic coast)

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Abstract

The natural productivity of ecosystems, farming practices and mortality events drive the rearing density and growth of oysters in shellfish farming areas. The variability of these drivers, which can be of natural or anthropic origin, is therefore an important source of variation in the growth performance and production of shellfish. Knowledge of these variabilities and their relative importance help producers to anticipate their effects and adapt aquaculture practices in order to limit negative impacts and guarantee a constant, or at least acceptable, level of production. In this study, we implement a 3D model coupling hydrodynamics and primary production (ECO-MARS3D) to an oyster DEB model to predict oyster growth and production in Bourgneuf Bay (French Atlantic coast). We set up numerous scenarios to compare and hierarchize the impacts of aquaculture practices, environmental variability and mortality events on shellfish production. In addition to better understand the growing conditions of oysters in the bay, the set of scenarios allowed us to propose a simplified management tool, in the form of response functions, to optimize shellfish farming practices interannually. This tool will help shellfish farmers quickly recover production levels in response to variations in mortality and/or environmental conditions.

Keywords: Oyster, Dynamic Energy Budget, Environment variability, Mortality, Scenarios, Management tool

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[*]Speaker

Reconstructing inter-individual variability of life history traits within small pelagic fish communities in high productivity ecosystems

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Abstract

Small pelagic fish (SPF) communities are a central link in marine food webs. Moreover, they account for 20% of the global catch. These populations are abundant in the boundary upwelling systems (Humboldt, California, Canary, Benguela Currents) where they are subject to strong variations in abundance. These changes are strongly linked to recruitment variations and environmental "bottom-up" forcing, which makes their dynamics difficult to predict. To better understand the mechanisms underlying these fluctuations, we propose to compare the life history traits of the most abundant species in these systems as well as the characteristics of their habitat that may underlie the observed dynamics. In this framework, the Ph.D. thesis I recently started proposes the development of a generic model of the life cycle of SPF based on DEB theory. Comparison of the same species in different habitats or close species in the same system is an approach that appears promising to limit the uncertainty around the estimated parameter sets. We also aim, in a second objective, to better reconstruct the inter-individual variability in these populations by linking otolith (fish ear bones) formation, to our SPF-DEB model. In this context, the mineral and organic fractions of the otolith are considered as metabolic products linked to the growth and dissipation transformations. This otolith growth module will be coupled with Lagrangian simulations to compare the observed and simulated variability of otolith patterns (size, opacity, and shape). This study will contribute to a better understanding of the variability of individual responses to environmental factors.

Keywords: Small pelagic fish, inter, individual variability, Dynamic Energy Budget, Upwelling systems, Otolith

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[*]Speaker

Acquisition of traits and experimental data for the development of host-symbiont bioenergetic models in two coastal mixotrophic bivalve species, Loripes orbiculatus and Lucinoma borealis.

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Abstract

The objectives of the LUNA project (2023-2024; EC2CO HYBIGE CNRS) are to get a range of zero-variate and uni-variate data from *in situ* sampling and laboratory experiments, in order to build a novel host-symbiont DEB bioenergetic model for the bivalves of the family Lucinidae. Lucinids are mixotrophic bivalves using two food sources: (i) symbionts with their sulfur-oxydizing symbionts hosted within their gills and (ii) organic matter from environmental photosynthesis. They are benthic intertidal and subtidal organisms living in reduced sediments (mangroves, seagrass-beds, pockmarks...). The future novel bioenergetic model will be based on the actual farming-DEB host-symbiont model developed for a strict symbiotrophic bivalve from the Vesicomyidae family (Vandenberghe et al. presented at this conference). However, in the mixotrophic lucinid bivalves, two food sources will be included instead of one (one linked to chemosynthesis from the symbionts – with a possible additional reserve of sulfur for the symbionts – and another food source linked to photosynthesis). The two species chosen are *Loripes orbiculatus* and *Lucinoma borealis* (Lucinidae) found around eelgrass beds at Roscoff on the Western English Channel (France). A series of laboratory

[*]Speaker

measurements (biometry, histology, *in situ* fluorescence microscopy, scanning electron microscopy, sulfur measurements...) as well as growth experiments and flux measurements (O2, H2S and NH4+) are planned to set parameters for the DEB bioenergetic models. Preliminary results on oxygen consumption following various temperatures, fecundity, size at first maturity, size at birth, growth experiments using calcein staining, biometry and C/S ratio will be presented, with preliminary results.

Keywords: Univariate data, zerovariate data, growth experiments, flux measurements, bivalves, symbiosis

Using spatial and process-based modelling for oyster aquaculture and restoration under current and predicted future water quality conditions

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Abstract

On-going and predicted changes in precipitation and river flow impact key coastal species. Among these, eastern oysters act as estuarine sentinels, serving as indicators of change, and as ecosystem engineers, altering their environment and providing ecosystem services. Given rapid past and predicted changes in estuarine conditions, identifying suitable locations to ensure resilient oyster populations and to support future production remains a challenge for managers. Here, we use an existing DEB model to assess oyster growth, reproduction and mortality across Louisiana and Texas estuaries under current and predicted future conditions of temperature, food availability, and salinity. Forcing variables for the oyster model are based on a combination of field monitoring data, remote sensing, and climatic model predictions. We present spatialized results of oyster performance in 3 Louisiana estuaries and 3 Texas estuaries under averaged current conditions, which constitute a baseline for comparison with future condition predictions. A set of outputs including oyster growth, reproduction and mortality are spatially displayed to enable site-specific decision making related to aquaculture siting, and production and restoration site selection. Under future conditions, suitable areas for oyster production and restoration are likely to expand and shift further south in Louisiana estuaries. Low resolution of future projections in coastal areas limits interpretation in Texas estuaries. Because of the mechanistic nature of the bioenergetic model used, applications for other key estuarine species will be developed for crab and shrimp species using the same framework.

Keywords: Aquaculture, Oysters, Remote sensing, Mapping, Salinity

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[*]Speaker

Fast and slow depurators of amnesic shellfish toxin: a bioenergetic modelling approach to compare two pectinid species

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Abstract

Microalgae species of the genus *Pseudo-nitzschia* may produce toxic domoic acid and form blooms. Domoic acid, the amnesic shellfish toxin, is a threat for Humans, thus its concentration is monitored within exploited shellfish species. Indeed, by their active filtration, bivalves may accumulate toxins in their tissues. When the sanitary threshold is exceeded, fishing is closed until decontamination. In France, the king scallop (*Pecten maximus*) is the second most economically important bivalve species. Over the last decade, fishing closures have led to a decrease in the fishing fleet in the Bay of Brest and a significant economic loss. Not all bivalve species respond in the same way to contamination, there exist "slow" depurators, such as *P. maximus*, and "rapid" ones like *Mimachlamys varia*, the variegated scallop. The French MaSCoET project aims to understand the ecology of this microalgae and the contamination and decontamination kinetics of the king scallop compared to other bivalves. The objectives of my PhD thesis are to compare these two pectinid species by developing a contamination/decontamination model of domoic acid, linked to the bioenergetics of the individual. The final goal should be to develop a tool to predict decontamination duration depending on environmental conditions and organism physiology, in order to help fishermen managing their fishing activity in case of a toxic algal bloom. The methodology used to develop the model and compare two pectinids species with their own toxin retention and how we could tackle the questions of depuration predictions will be presented.

Keywords: King scallop, Variegated scallop, Amnesic Shellfish Toxin, Contamination kinetic, Dynamic Energy Budget Theory

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The von Bertalanffy growth rate depends on food and relates to the specific body growth rate at maximum absolute growth

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Abstract

The length trajectory of the standard DEB model reduces to the von Bertalanffy (VB) growth curve at constant food density (f) and temperature. However, the VB growth rate (VBGR) is not a DEB parameter, but an emergent property which depends on f and integrates the underlying processes of assimilation, maintenance, reserve mobilization, and costs for growing.

For increasing f, the inverse VBGR increases linearly with ultimate length. The slope of this line relates to reserve mobilisation and the intercept to a ratio between maintenance costs and that for synthesis of structure. We compare growth curves of males and females from sexually dimorphic species where the difference between genders is interpreted as differences in assimilation capacities. This implies that the maximum reserve capacity is larger for the larger gender. The growth curves are initially similar and later diverge. As reserve capacity contributes to weight (which is proportional to cubed length) the larger gender is heavier for the same length. This gives support for a key assumption of DEB theory: weak homeostasis. The weight-specific GR decreases with time since birth. The absolute GR initially increases over time since birth, hits a maximum, after which it decreases. Recent findings show that the specific rate at maximum absolute GR is 1.5 times the VBGR for the std model.

Keywords: von Bertalanffy growth rate, Dynamic energy budget theory, weak homeostasis

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Structuring animal biodiversity according to five patterns

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Abstract

The AmP database contains model parameters and life-history traits based on Dynamic Energy Budget (DEB) theory for over 4000 animal species from all major phyla. A major bottleneck for obtaining reliable parameter values is data availability. The problem of data availability can be reduced by estimation in context: exploring parameter and trait patterns across and within taxa reveals how well a given species parameters fit in context. Over the ontogeny of the theory and its large-scale application to animal species, five major patterns were identified, that structure animal biodiversity.

First, co-variation of parameter values, based on the idea that species share extensive (scaled to size) parameter values, while appropriate ratios of extensive parameters are intensive. Second, metabolism is specified as a mix of supply and demand components, and species are ranked according to the supply-demand spectrum; the position on the spectrum is quantified by a corresponding DEB trait. Third, the altricial-precocial spectrum is quantified by another DEB trait, which enables placing all animals on the spectrum. Fourth, small bodied species have a metabolic route to handle temporary peaks in their food supply by boosting growth and reproduction, dubbed "waste to hurry" strategy. Last, metabolic acceleration structures the animal kingdom, implying the importance of life-cycles. These findings provide a basis for comparing animal taxa and shed light on metabolic constraints and interrelationships that together with environmental pressures structured animal biodiversity as we know it today. We present how these patterns work in practice and how adaptations modify the expectations.

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Development and growth of true soles (Solea spp) simulated under future climate change scenarios

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Abstract

True soles (*Solea* spp) undergo a drastic physical metamorphosis during their ontogeny. The metamorphosis usually coincides with the migration – a (mostly) passive journey that pelagic larvae undertake to reach the nurseries as young benthic juveniles. The timing of the migration will primarily depend on the spawning period, which largely depends on temperature. Temperature– in combination with food availability -will also affect the metabolic rates and life history traits of freshly spawned larvae and later juveniles: development (including metamorphosis and sexual maturation) and growth. Development and growth will affect recruitment -the process of small, young fish transitioning to an older, larger life stage –which will, ultimately, affect sole populations. Determining the combined effect of temperature rise and food reduction (two expected outcomes of climate change) on early-life history traits of fish larvae is valuable for anticipating and adjusting fishing pressure and policy, especially for commercial species like soles. We use a dynamic energy budget (DEB) model for the common (*S.solea*) and the Senegalese sole (*S.senegalensis*), to predict the effects of temperature and food availability on *Solea* spp. early life-history traits under seven simulation scenarios. Our results show that temperature and food availability both affect the age at metamorphosis, which is advanced in all scenarios that include a temperature rise, and delayed when food is limited. Age at puberty was also affected by the temperature increase, but portrayed a more complex response that is dependent on the spawning period. We discuss the implications of our results in a climate change context.

Keywords: recruitment, phenological adaptations, fish development

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Parameter estimation for the variegated scallop, Mimachlamys varia, an exploited bivalve, for a better understanding of its life cycle

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Abstract

The variegated scallop, *Mimachlamys varia*, is historically a fishing resource in some areas of the French Atlantic coast. Nevertheless, since the 1970s its stocks have declined, leading nowadays to fishing restrictions and/or interdictions, particularly in the Bay of Brest. In order to support *M. varia* sustainable fishing activities, it is important to understand its ecology and population dynamics. However, few information on this species is currently available. As part of the French MaSCoET project, a 2.5-years *in-situ* monitoring was realised in the Bay of Brest. It examined growth in length and weight of two cohorts, as well as their gonado-somatic index, coupled with environmental conditions. The present study aims to better understand the link between the environment and the organism's physiology. Using a Dynamic Energy Budget model, we further investigated the life cycle of *M. varia*. The parameters were estimated with the AmP procedure, using the Tinduff hatchery data as zero-variate data and the early stages' growth. The first cohort growth data from the *in-situ* monitoring was used as uni-variate data for adults. The originality of our study is that we were able to validate the model using the second cohort monitoring data. This model will be used for the investigation of (i) the trophic ecology of this species in three contrasted locations within the Bay of Brest using a model inversion approach (Régnier-Brisson *et al.* submitted oral communication) and (ii) the contamination and decontamination by domoic acid (phycotoxin) using a coupled kinetic model (Le Moan *et al.*, submitted poster).

Keywords: Variegated scallop, Mimachlamys varia, in, situ monitoring, parameter estimation, Add my Pet (AmP) procedure

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Applying a DEB model to simulate chronic polyethylene microplastic exposures in Daphnia magna

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Abstract

Daphnia are a well-established and fantastic model organism for both acute (48 hour) and chronic (21 day) environmental toxicity assessments. Due to their historic use, there is a wealth of data and understanding of their response to various toxicants. *Daphnia* have been used as a model to explore microplastic pollution effects in freshwater environments, in part due to their transparent bodies facilitating the visual quantification of particle uptake. We can apply DEB theory to further our understanding of the mechanistic toxicity driving Daphnids response to microplastics, and combine this with studies exploring the variability of mixture toxicity to understand the combined impacts of plastics and chemicals, for example, the addition of microplastics made the surfactant (SDS) more acutely toxic in Daphnia. Data from chronic reproduction tests with *D. magna* was used to explore potential changes to the daphniid's energy budget in response to different combination of toxicant exposures. Three exposure combination were explored in addition to a control;

a) Polyethylene particles 1-4 μm (25 mg/L) as a particle toxicant

b) Sodium Dodecyl Sulphate (SDS) (40 mg/L) as a chemical pollutant

c) Polyethylene and SDS in a combined exposure
The DEB models can then be further discussed in combination with other sublethal markers of stress, such as changes to excreted proteins, variations in concentration and distribution of lipid, and morphological defects in the daphnids over the 21-day testing period, to further explore the links between these sublethal markers and toxicant impacts on the energy deviations from the controls.

Keywords: Daphnia magna, microplastics, polyethylene, surfactant, combined toxicity

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Modeling Freshwater Mussels to Assess Risks to Threatened and Endangered Species

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Abstract

Freshwater mussels are one of the most endangered taxonomic groups in North America: 70% of the 296 species currently identified in the US are considered threatened, endangered, or of special concern. Many factors are identified as potential drivers of decline, such as physical habitat degradation, invasive species, complex life cycle, and chemical pollution. However, because of the prohibition on testing of endangered species and the difficulty of working with freshwater mussels in the laboratory, it is unclear how exposure to various stressors translates into long-term fitness consequences for distinct species with specific physiology and life history. Consequently, it is important to develop predictive methods to better assess the risks posed to threatened and endangered freshwater mussels by a multitude of stressors. We developed DEB models for 47 species belonging to three life-history categories, and we compared how exposure to stress of identical intensity impacted growth, reproduction, and development across species and life-history categories. We found that impacts on development and reproduction were more variable among species than impacts on growth and that intensity of simulated impacts was driven more by species-specific energetics than life-history categorization.

Because long-term population viability of these listed species is the focus of risk assessment, we plan to integrate the developed DEB models into agent-based models to evaluate how perturbations to listed mussel bioenergetics determine population-level outcomes. Ultimately, our approach will generate insights about the sensitivity of physiological processes, life-history traits, and populations from exposure to various stressors, including pesticides, of data-sparse threatened and endangered species.

Keywords: Trait, based approach, Freshwater mussels, endangered species

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