MODELING OF ANURAN METAMORPHOSIS IN THE DYNAMIC ENERGY BUDGET FRAMEWORK

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Abstract

The metamorphosis of anuran tadpoles into tetrapods is sensitive to natural and anthropogenic stressors, making it a key process in environmental risk assessment. Existing Dynamic Energy Budget (DEB) models lack a focus on the plasticity of the metamorphic climax, limiting their ability to evaluate such impacts. To address this, we developed two independent modeling modules that describe anuran metamorphosis and its plasticity, and integrated them into the standard DEB model.

Our model meets three essential criteria. First, adequately fed tadpoles emerge as viable froglets or toadlets. Second, it allows for the partial repurposing of structural mass, such as resources from the tail and gills. Third, it predicts that moderate temperature increases lead to earlier emergence at a smaller body size. The model effectively describes critical endpoints, including the onset and completion of metamorphosis, as well as the weight and length of tadpoles from hatching through metamorphosis as functions of food availability and temperature.

We validated the model using anuran species from four families: the common frog (*Rana temporaria*), the common toad (*Bufo bufo*), the African clawed frog (*Xenopus laevis*), and the gray tree frog (*Dryophytes versicolor*). The modules are expected to be applicable to other amphibians.

Outline of the energy flows in the standard DEB model for juveniles (solid arrows) with additional flow active only for tadpoles during metamorphosis (dotted arrow). During the climax of metamorphosis tadpoles do not feed (grey scale), while structure is recycled at a rate such that the reserve density remains constant.

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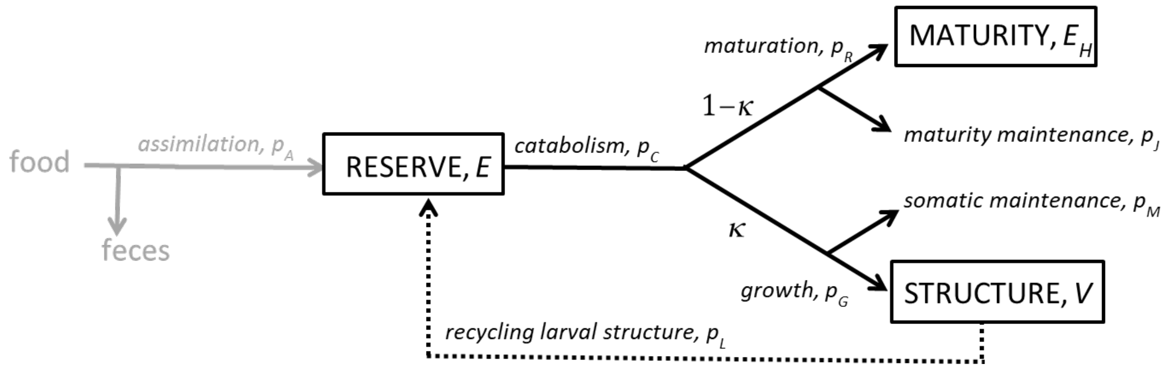
*Speaker



Outline of the energy flows in the standard DEB model for juveniles (solid arrows) with additional flow active only for tadpoles during metamorphosis (dotted arrow). During the climax of metamorphosis tadpoles do not feed (grey scale), while structure is recycled at a rate such that the reserve density remains constant.

Predicting Coral Bleaching in the Red Sea Using a Dynamic Energy Budget Model

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Abstract

The Red Sea's coral reefs are among the most biologically diverse ecosystems globally, providing essential food and income for coastal communities. However, they are increasingly threatened by climate change-induced coral bleaching, which has led to significant coral cover loss during recent mass bleaching events. Given the ecological and socio-economic importance of reef-building corals, advanced predictive models for coral bleaching are essential. Most existing models primarily focus on thermal stress, often overlooking essential factors such as water quality, heterotrophic feeding, and physiological processes. The Dynamic Energy Budget (DEB) theory provides a biologically coherent framework for multi-stressor analysis, allowing the integration of physiological traits with various environmental variables. In this study, we applied a pre-existing DEB symbiosis model to simulate coral bleaching in the Red Sea. The model was driven by outputs from an operational 3D hydrodynamic-biogeochemical model (MITgcm-NBLING) and satellite-derived Photosynthetically Active Radiation (PAR) data. Simulations were performed at the basin scale, and model performance was assessed against historical field observations of coral bleaching. The DEB symbiosis model effectively replicated observed spatiotemporal bleaching patterns, underscoring its potential as a valuable tool for investigating coral bleaching dynamics and enhancing predictive capabilities.

Keywords: symbiosis, corals, bleaching, Red Sea

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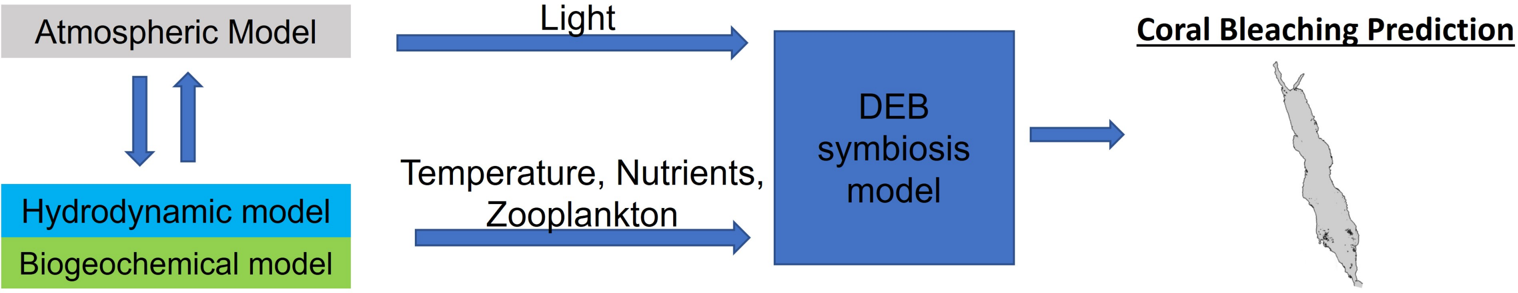
*Speaker


Atmospheric Model
Light
Coral Bleaching Prediction
DEB symbiosis model
Temperature, Nutrients, Zooplankton
Hydrodynamic model
Biogeochemical model

Inter-species comparison of life traits related to amnesic shellfish toxin kinetic in five scallop species

Eline Le Moan*[1], Laure Pecquerie[1], Laure Régnier-Brisson[2], Hélène Hégaret[1], Paulo Felipe Lagos[1], Léo Heyer[1], Salvador Emilio Lluch Cota[3], Fred Jean[1], and Jonathan Flye Sainte-Marie[1]

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Abstract

Pectinid species (scallops) hold significant economic value, but their filtration activity makes them vulnerable to harmful algal blooms, particularly *Pseudo-nitzschia* species producing domoic acid (DA). This neurotoxin, responsible for Amnesic Shellfish Poisonings (ASPs) in birds and mammals, leads to prolonged sales bans when concentrations exceed the regulatory threshold. However, DA retention is species-specific, and the underlying mechanisms remain poorly understood. This study aims to compare pectinid species to assess whether interspecific differences in energetic traits influence DA retention. Using Dynamic Energy Budget (DEB) theory and the AmP multi-species estimation procedure as a common conceptual framework, we compared five pectinid species: two slow depurators (*Pecten maximus* and *Placopecten magellanicus*), two fast depurators (*Argopecten purpuratus*, *Mimachlamys varia*) and *Nodipecten subnodosus*, hypothesised fast depurator. We collected and compared life-history traits, focusing on life cycle transitions and reproductive effort, to establish the multi-species DEB parameter estimation. Three key parameters were then examined to explain differences in DA retention: specific assimilation, somatic maintenance costs and energy conductance. Our results, in addition to refined individual parameter estimations for the five species, revealed differences among species in these three parameters. However, only energy conductance consistently increased along the "slow-to-fast'" depuration gradient. Furthermore, we identified a limitation in describing the bivalve life cycle due to inconsistencies between larval and adult growth data. This study lays the groundwork for DA kinetics modelling and highlights the potential of multispecies parameter estimation for species comparisons. The presentation will cover key hypotheses, challenges and insights from this multispecies parameter estimation approach.

Keywords: Multispecies parameter estimation, Dynamic Energy Budget, scallops, amnesic shellfish toxin

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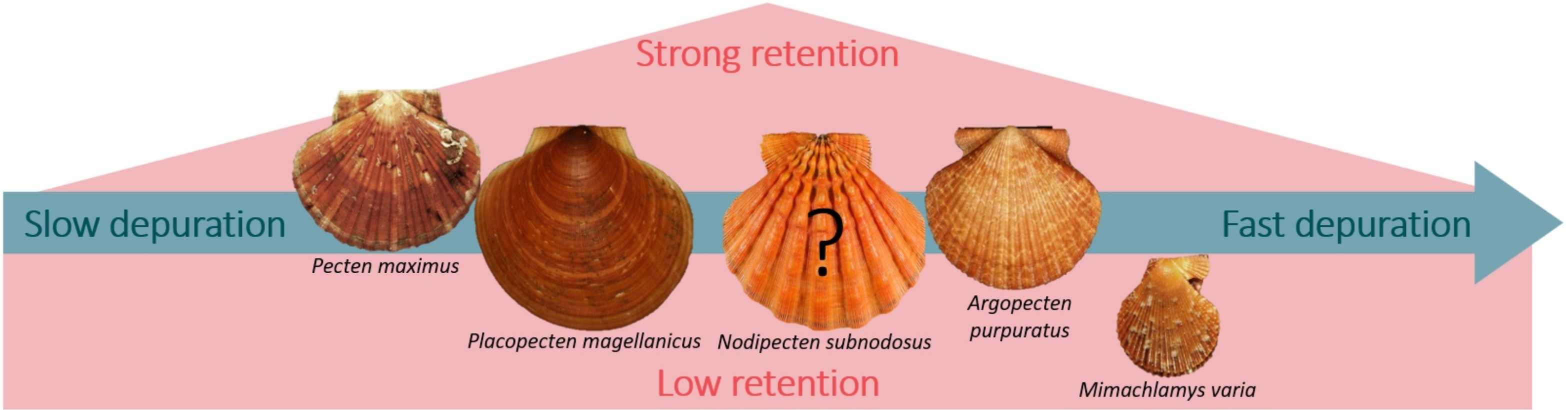
Strong retention
Slow depuration
Fast depuration
Pecten maximus
Placopecten magellanicus
Nodipecten subnodosus
?
Argopecten purpuratus
Mimachlamys varia
Low retention

Modelling the Bioenergetics and Life History Traits of Chironomus riparius – Consequences of Food Limitation and Toxicant Exposure

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Abstract

Chironomids have a number of characteristics that make them a useful group for investigating the impact of environmental and chemical stressors on their life cycle stages. It is crucial to first understand sensitivities to environmental factors, as this provides a foundation for interpreting toxicity test results. Moreover, the interactions of chemical stressors with environmental stressors (e.g., temperature increases and food reduction) are underexplored. We focused on *Chironomus riparius* – one of the most extensively studied species in aquatic toxicity tests – to examine larval-stage changes conditions of both food abundance and limitation. We developed a model based on Dynamic Energy Budget (DEB) theory, a framework to capture the entire life cycle of an individual under varying food and temperature conditions. Information from this study and the literature indicate that the first three larval instars are immature, while the fourth larval instar is mature, during which the organism stores energy in two phases to support essential processes occurring in the subsequent non-feeding stages. The model successfully predicts the observed prolonged duration of the fourth instar under food limitation, the timing of life history events (e.g., pupation and emergence), as well as growth and egg production. To enhance our understanding of the impact of insecticides and of their interactions with environmental stressors on chironomids, we further developed a DEB-based toxicokinetic-toxicodynamic (DEB-TKTD) model. The DEB-TKTD model was subsequently used to explore the combined effects of multiple stressors – specifically, imidacloprid exposure, temperature and food availability – under both constant and time-variable exposure scenarios.

Keywords: Dynamic Energy Budget theory, holometabolous insects, aquatic insects, Chironomus riparius, biphasic larval growth, DEB, TKTD

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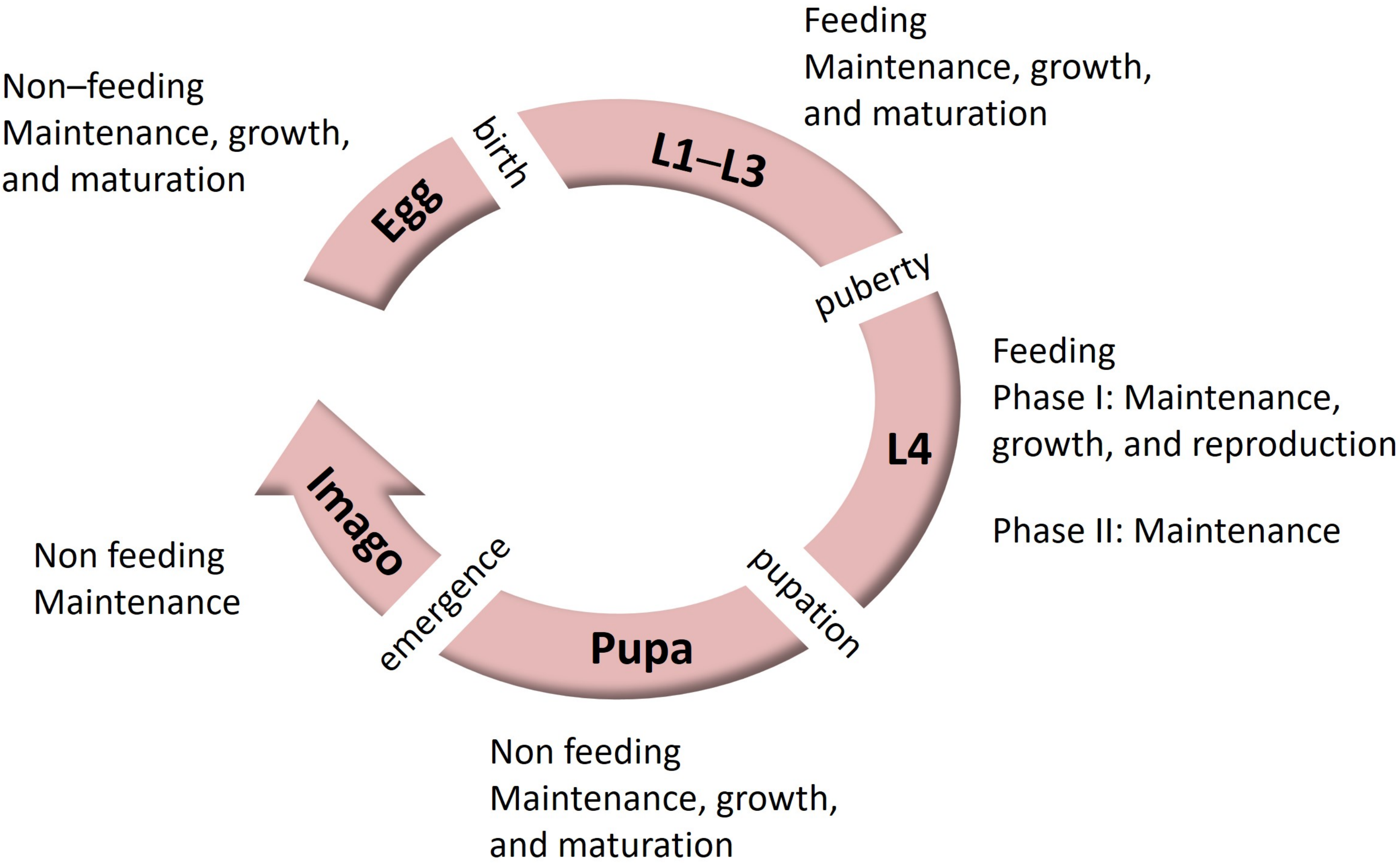
[*] Speaker


Non–feeding
Maintenance, growth,
and maturation
Egg
birth
L1–L3
Feeding
Maintenance, growth,
and maturation
puberty
L4
Feeding
Phase I: Maintenance,
growth, and reproduction
Phase II: Maintenance
pupation
Pupa
Non feeding
Maintenance, growth,
and maturation
emergence
Imago
Non feeding
Maintenance

Advancing DEB Model Accuracy for New Zealand Green-lipped Mussel: A Lab-Centric Approach

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Abstract

We present an enhanced DEB model for the New Zealand green-lipped mussel *Perna canaliculus* (GreenshellTM), calibrated using an extensive new suite of laboratory data (growth, reproduction, oxygen consumption, biometry, ingestion/assimilation, defaecation, starvation, and temperature response) alongside previously published values. This expanded dataset advances the DEB model's completeness score from 2.5 to 5.5, making *P. canaliculus* one of the most comprehensively parameterized organisms in the *Add-my-Pet* database. Our goal was to assess how much additional knowledge and predictive power could be gained by incorporating data from targeted laboratory experiments - specifically designed to meet DEB model requirements - into the calibration process.

Key findings include:

(i) Reliable temperature-response data are essential for accurately defining the thermal response curve; the presence or absence of such data should be considered when assessing DEB model completeness and its capacity to predict species' thermal responses;

(ii) Species-specific parameters, such as tissue organics and water content, improve accuracy compared to taxonomically generalized values;

(iii) Data from targeted laboratory trials as well as from diverse literature sources (spanning different environmental conditions, life stages, and populations) are essential for calibrating a robust species-level mechanistic model; and

(iv) Estimating energy requirements of bivalves would benefit from measuring routinely byproducts (pseudofaeces) and checking the experimental setup for potential feed residue.

These insights are highly relevant for predicting outcomes in commercial mussel aquaculture, particularly in the context of climate change adaptation, and emphasize the importance of robust parameterization in DEB-based analyses

Keywords: Targeted Experiments, Model Completeness, Thermal Response, Shellfish Aquaculture

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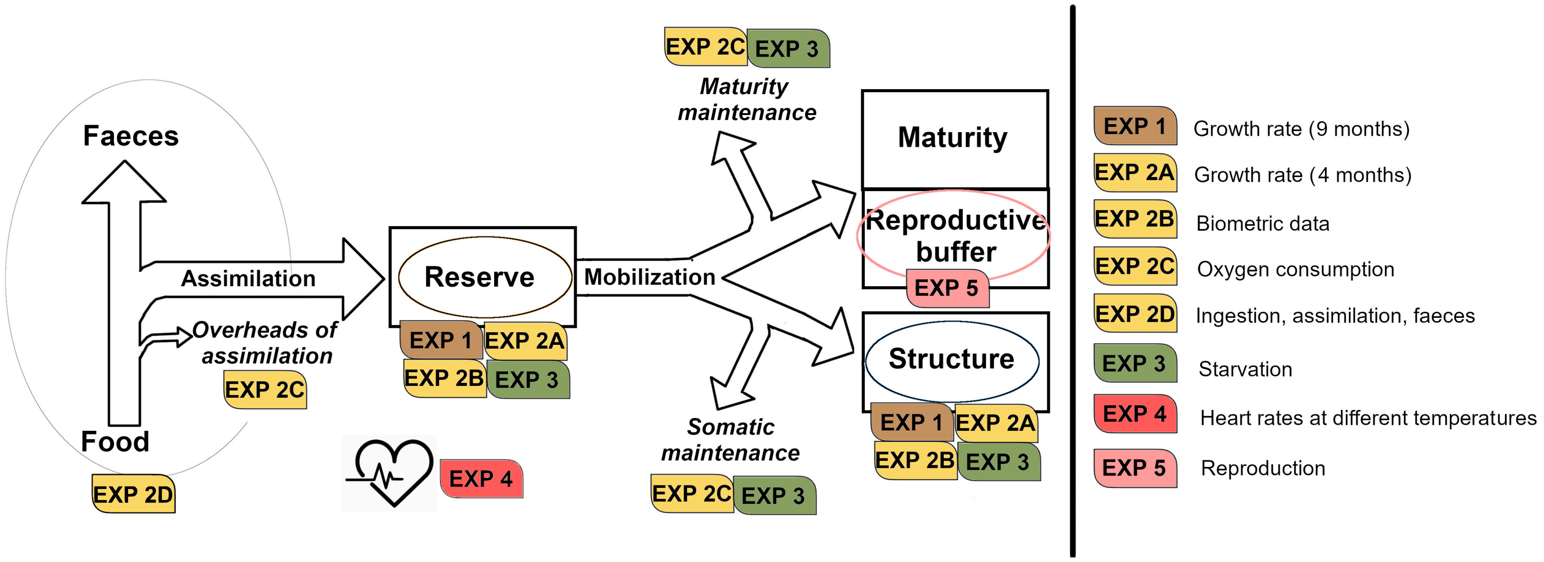
*Speaker

Perna canaliculus



A new-modeling framework to estimate environmental determinants and intra-specific variability in life history traits: an application to fish

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Abstract

Understanding and predicting rapid phenotypic changes critically rely on identifying the sources of variability among and within populations as well as their consequences on life-history traits. While the Dynamic Energy Budget (DEB) theory stands out as a powerful tool to describe life-history traits of various aquatic species in an environment where food and temperature fluctuate, it traditionally assumes homogeneous populations, where all individuals share the life history traits and DEB parameters of an "average" individual. This approach overlooks the inherent, partly genetic, variability between and within populations, often attributing it solely to environmental differences. Yet, accurately predicting dynamic environmental effects on life history traits requires accounting for inter-individual variability to better disentangle both effects. We introduce *OptMyDEB,* a new flexible modeling tool that addresses these shortcomings. This generic modeling platform implements an integrated DEB model that is sufficiently flexible to incorporate many types of data and to capture parameter variability across populations, sexes and individuals. *OptMyDEB* is an R package that has been designed to fit DEB models through maximum likelihood estimation using

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*Speaker

Template Model Builder (TMB). TMB is a statistical framework that combines automatic differentiation for efficient gradients computation and Laplace approximation for integrating random effects. This allows the optimization of high-dimensional parameter spaces, making TMB well-suited for fitting complex nonlinear dynamic systems. The ability of the framework to reliably estimate DEB parameters and their variability is first demonstrated using a simulation-estimation approach. Then, experimental data are used to infer individual variability in DEB parameters for two fish populations.

Keywords: Dynamic Energy Budget, life history traits, interindividual variability, Template Model Builder, R package

FishNess

FISH ROBUSTNESS

The use of Artificial Intelligence to facilitate the estimation of DEB parameters using the AmP procedure

Somaya Jabir*[1], Laure Pecquerie*[1,2], Hasna Elalaoui Elabdallaoui[1], Jihad Zahir[1], Abdelwahed El Hassan[1], Diogo Miguel Ferreira De Oliveira[3], and Gonçalo M Marques[3]

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Abstract

Dynamic Energy Budget (DEB) theory provides a rigorous mathematical framework for modeling the processes of energy acquisition, allocation and utilisation in living organisms. The Add-my-Pet (AmP) portal provides estimates of DEB parameters for nearly 6,000 entries together with the data and the Matlab codes used for the estimation procedure. However, the manual generation of the species-specific files (mydata, predict, pars_init, run) remains time-consuming and limits the expansion of DEB models to new species.
Artificial intelligence (AI) is being considered as a solution to partially automate this process. It is planned to use machine learning and natural language processing (NLP) to automatically extract and structure the data needed to generate the mydata file for new species. Additionally, by leveraging the nearly 6,000 entries in the AmP database, AI could:

Automatically generate the complementary files (run, predict, pars_init).

Identify which parameters could be fixed and which could be estimated based on the available data.

Suggest initial parameter values based on phylogeny and the AmP database.

Future work will include the development of a DEB chatbot based on a Large Language Model, capable of assisting users in refining species-specific AmP files, which could be particularly useful in a learning context. However, some challenges remain, particularly regarding data curation and the carbon footprint of AI models. Solutions such as using optimized AI models with lower environmental impact are being considered to ensure efficient automation while maintaining the scientific rigor of the AmP procedure.

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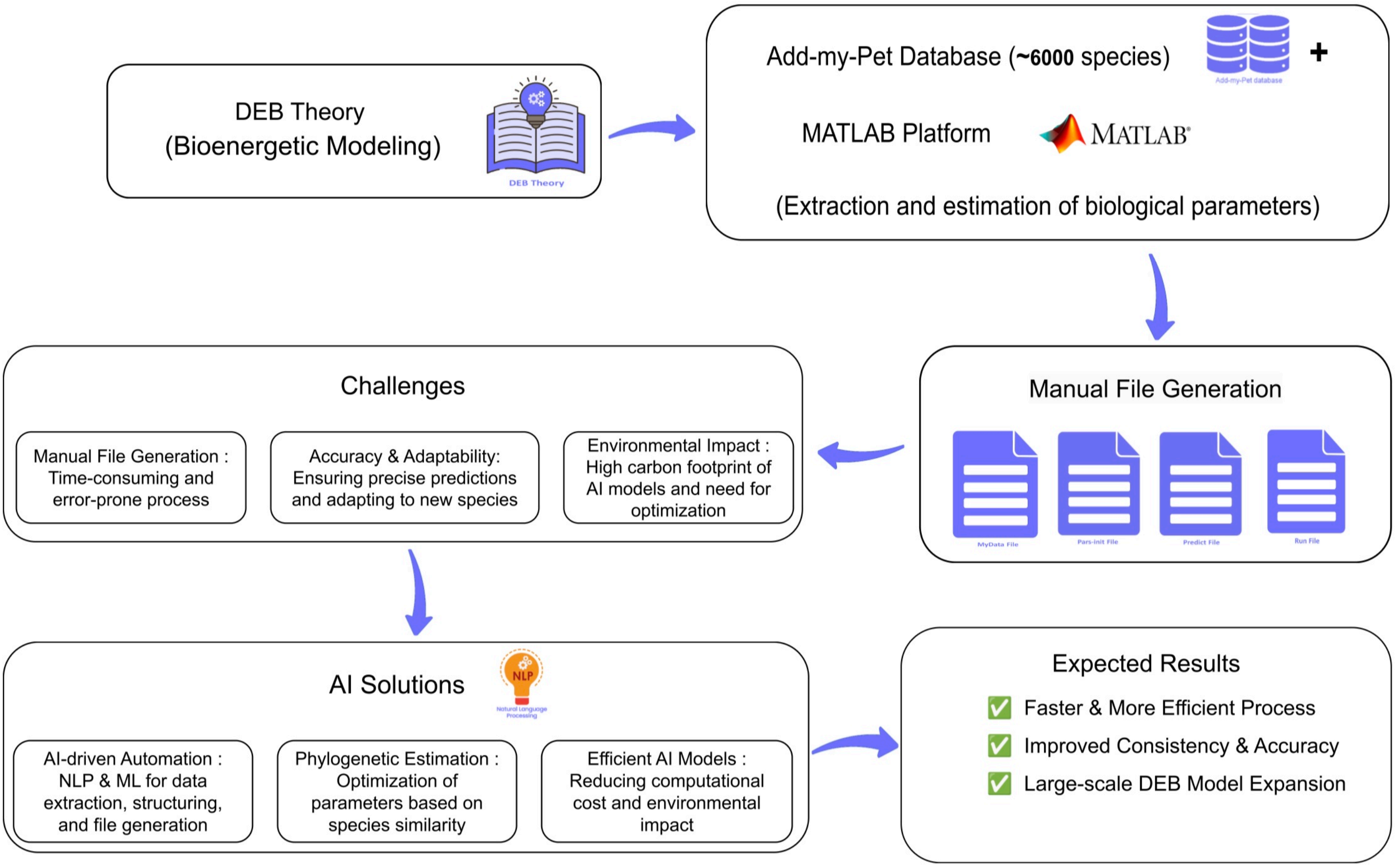
*Speaker

Keywords: Dynamic Energy Budget (DEB) theory, AmP Procedure, Natural Language Programming, Large Language Model

The use of Artificial Intelligence to facilitate the estimation of DEB parameters using the AmP procedure



DEB Theory
(Bioenergetic Modeling)

Add-my-Pet Database (**~6000** species)

MATLAB Platform

(Extraction and estimation of biological parameters)

Manual File Generation

Challenges

- Manual File Generation : Time-consuming and error-prone process
- Accuracy & Adaptability: Ensuring precise predictions and adapting to new species
- Environmental Impact : High carbon footprint of AI models and need for optimization

AI Solutions

- AI-driven Automation : NLP & ML for data extraction, structuring, and file generation
- Phylogenetic Estimation : Optimization of parameters based on species similarity
- Efficient AI Models : Reducing computational cost and environmental impact

Expected Results

✅ Faster & More Efficient Process
✅ Improved Consistency & Accuracy
✅ Large-scale DEB Model Expansion

Machine-learning initialization methods for the calibration of DEB models

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Abstract

The selection of initial parameters for the calibration of a DEB model is not trivial. The parameter set must be feasible so the estimation procedure can begin. Ideally, it should also be close to the true species parameters to ensure fast convergence. A poor initial choice may even lead to numerical instabilities that halt the estimation procedure.

Currently, the only automated initialization method is the bijection method, an exact algorithm that predicts core parameters from zero-variate data. Here, we propose using machine learning techniques to provide initial parameters for DEB model calibration, introducing two approaches: a nearest-neighbor model and a neural network.

The nearest-neighbor model automates the ad hoc practice of selecting parameters from a similar species. It chooses initial parameter values from a taxonomically close species with similar ultimate weight and then adjusts them with covariation scaling relationships.

The neural network is inspired by the structure of the bijection method. The model predicts parameters using ages and weights at multiple life stages complemented by taxonomic and eco-code information. By restricting the outputs of the model, the predicted parameter set is guaranteed to respect all constraints except reaching birth.

The models were trained and evaluated on 2363 species . Both proposed approaches produce feasible solutions for 99% of species, while the bijection method had a success rate of only 40%. In a paired comparison, the nearest-neighbor initialization achieved lower final loss values for 50% of species, whereas the neural network approach performed better in 34% of cases (with 16% ties).

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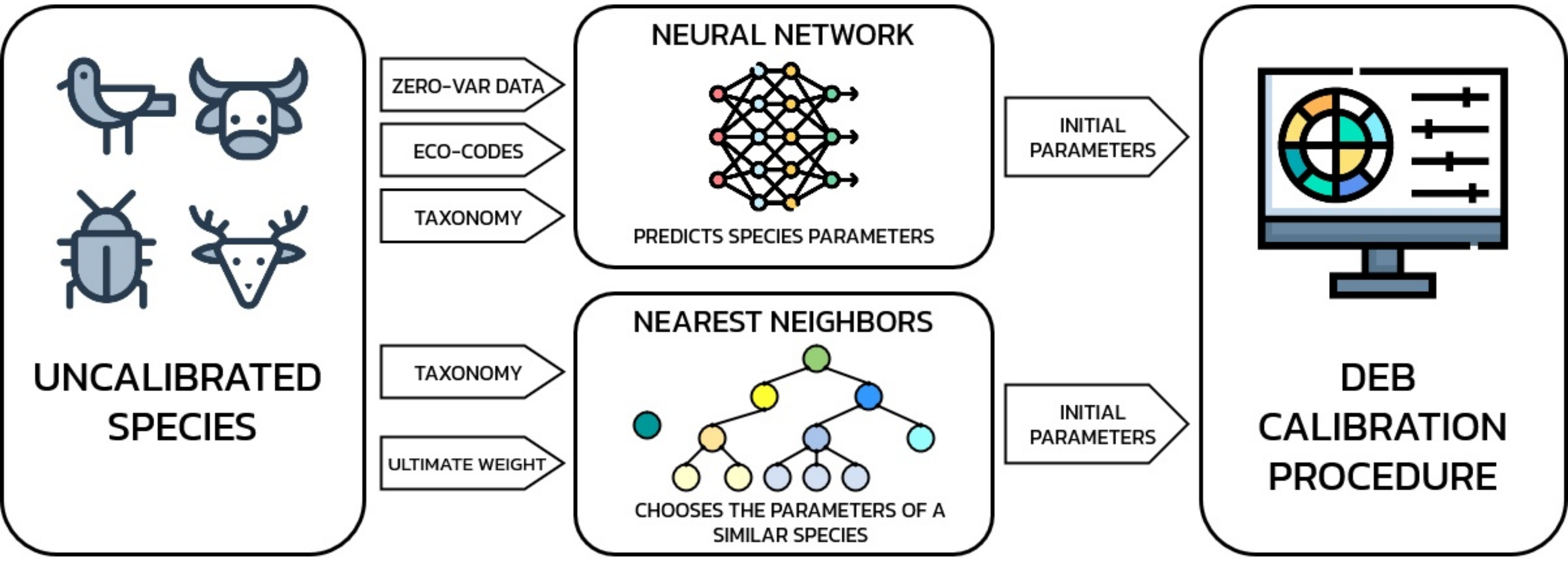
*Speaker

Keywords: parameter estimation, machine learning, initialization


UNCALIBRATED SPECIES
ZERO-VAR DATA
ECO-CODES
TAXONOMY
NEURAL NETWORK
PREDICTS SPECIES PARAMETERS
INITIAL PARAMETERS
TAXONOMY
ULTIMATE WEIGHT
NEAREST NEIGHBORS
CHOOSES THE PARAMETERS OF A SIMILAR SPECIES
INITIAL PARAMETERS
DEB CALIBRATION PROCEDURE

The control of Escherichia coli mass and energy budgets by specific biochemical pathways inhibition

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Abstract

Many industrial, agricultural, and medical products are currently obtained in biotechnological processes. Host organisms, often genetically modified, are used to produce amino acids, biopolymers, biosurfactants, and organic acids. One of the key and most widely used microorganisms is *Escherichia coli.* The optimization of metabolic pathways leading to bioproduct overexpression was achieved mainly through genetic engineering techniques like gene 'knock out', which has led to an increase in the number of genetically modified organisms (GMO) used in bioprocesses. However, unlike non-modified strains, genetically modified organisms require specialized cultivation, storage, and disposal conditions. Wild-type strain metabolism control and optimization have to be achieved by adjusting the physical and chemical conditions of the culture including temperature, pH, media composition, and inhibitors occurrence. Inhibition of specific enzymes and biochemical pathways can lead to mass-energy imbalance and shifts towards other pathways. Therefore in this study, we discuss metabolism regulation of naturally occurring *E. coli* by chemical inhibition of specific biochemical pathways. We ask the question of how the mass and energy fluxes described by the Dynamic Energy Budget (DEB) theory will be affected by particular inhibitors of biochemical pathways involved in cell growth and development, and how can we use this knowledge to prepare simulations, predictions, and optimization of industrial bioprocesses conducted by *E. coli.* To answer this question, the influence of four antibiotics with specific known modes of biochemical action on *E.coli* growth and metabolism was tested: ciprofloxacin, azithromycin, rifaximin, and trimethoprim. *E. coli* was cultivated in batch reactors in a controlled environment. DEB model parameters identifiability was analyzed and their values were estimated. The changes in specific parameter values were used to explain the influence of inhibitors on the energy budget and to show possibilities of controlling and optimizing the potential bioprocess.

Keywords: optimization, bioprocess, biotechnology, antibiotics, inhibition

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*Speaker

How can a multi-reserves DEB model help us design experiments to better understand brown holopelagic algae Sargassum spp. growth and survival.

Maria José Lagunes*[1,2], Laure Pecquerie[2], Evelyn Raquel Salas-Acosta[3,4], Román Vásquez-Elizondo[4], Gonçalo Marques[5], Thierry Thibaut[3], Daniel Robledo[4], Solène Connan[2], Valérie Stiger-Pouvreau[2], Leo Berline[3], and Christophe Lett[1]

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Abstract

Unprecedented quantities of brown floating macroalgae Sargassum have been recorded in the tropical North Atlantic Ocean; however, the factors affecting their growth and survival remain poorly understood. To study how environmental conditions influence Sargassum physiology, we use a multi reserves DEB model to quantitatively assess their growth and survival to current temperature, nutrient and light conditions. In the context of DEB theory, estimating a multi-reserves model parameters can be particularly challenging as the accurate calibration in a complex model heavily relies on the quantity and quality of datasets. In the case of holopelagic Sargassum, experimental data is scarce, which hinders our understanding of the effect of temperature, irradiance and nutrient concentrations on the growth and survival of this species.

To address these challenges first we evaluate the sensitivity of the parameter values to the

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*Speaker

available data on holopelagic Sargassum. Then, we explore how different types of experimental data can reduce the incertitude on parameter estimates, thus increasing their identifiability and the prediction power of the algae multi-reserves model. This analysis allows us to determine which types of datasets contain the most information and guides the design of experiences to improve our understanding of Sargassum spp physiology. As a part of the BIOMAS project, (BIOenergetic Modeling Approach for Sargassum dynamics), experimental data from the different Sargassum morphotypes will be integrated to compare model predictions with experimental observations.

Keywords: Multi reserves model, Macroalgae, Data gaps, Parameter identifiability

Stylized facts or fiction?

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Abstract

Stylized facts - generalized descriptions of observed patterns in nature - are indispensable tools in model development, validation, and analysis. They stipulate empirical benchmarks that a robust model must satisfy. Though valuable, stylized facts are inherently simplified, acting as 'useful fictions' with varying degrees of accuracy and literary support. Dynamic Energy Budget (DEB) theory, a cornerstone of ecological modeling, presents a set of core stylized facts to which the prevailing kappa-rule DEB models adhere. However, the strength of support for these foundational facts remains unquantified, and a comprehensive review of potential alternatives is lacking. For example, data on fish growth and toxicokinetics suggest there could be additional or alternative stylized facts that may be inconsistent with current kappa-rule DEB model assumptions, or require a conversation on the domain of applicability. We aim to stimulate the discussion on stylized facts in DEB by presenting our effort to score the empirical support for currently accepted facts, and explore potential alternative formulations and their implications.

Keywords: stylized facts, model development, domain of applicability, consistency

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