”Agent-based population models of small pelagic fishes explain changes in life-history traits through Dynamic Energy Budget Theory”

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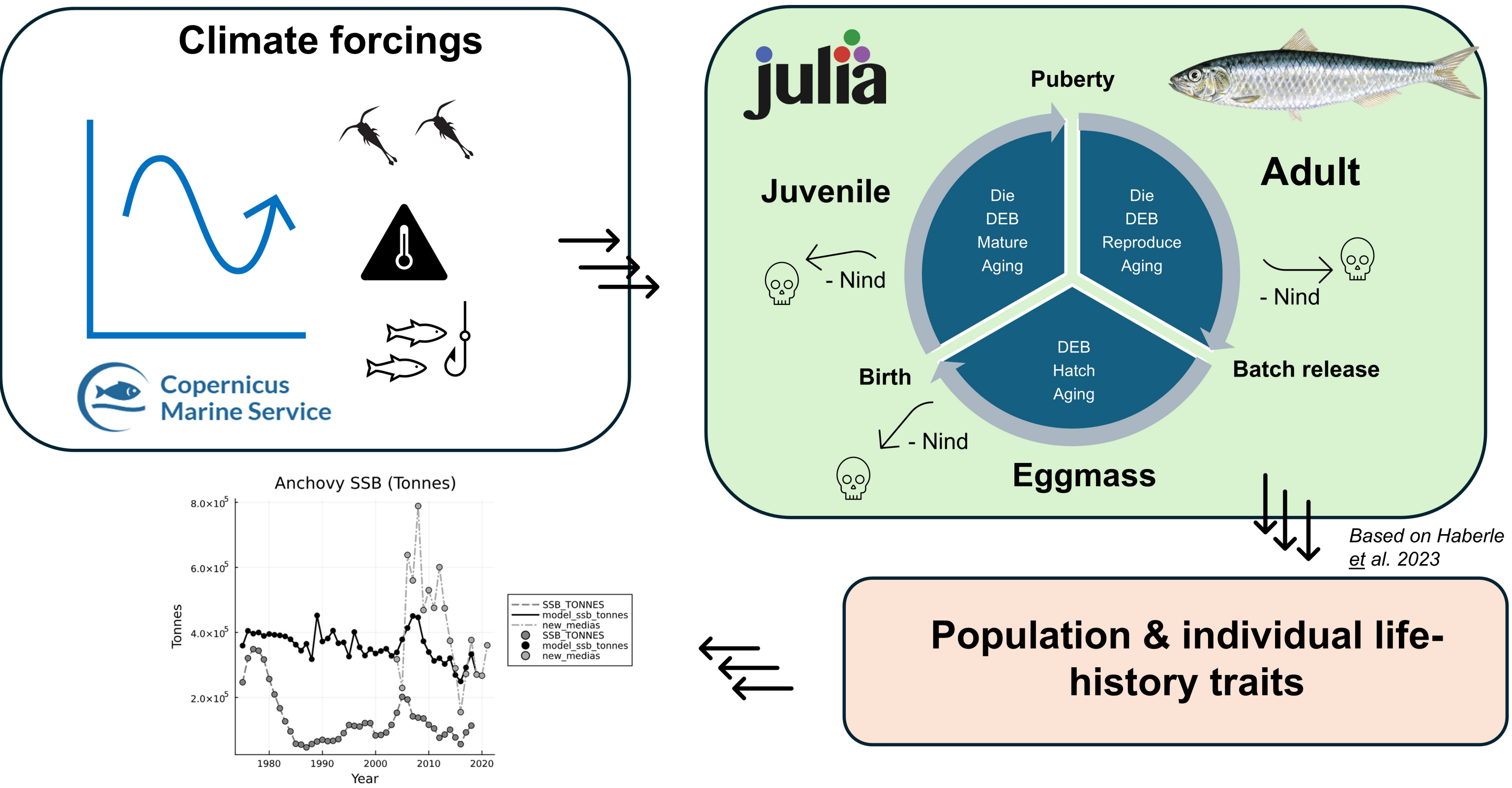
Abstract

Sardines and anchovies are vital components of marine food webs and fisheries, yet the causes behind their shrinking sizes at all life stages remain unclear. Improving our ability to predict sardine and anchovy population dynamics is crucial for sustainable management and understanding their responses to climate change, including changes in life-history traits. To address these challenges, we developed an agent-based population model using the high performance programming language Julia. This model simulates the bioenergetics of sardines and anchovies across all life stages based on the Dynamic Energy Budget Theory, accounting for temperature, food availability, and age-specific natural and fishery-induced mortality. The model account for stochastic variability and transmission of key parameters influencing growth and reproduction through generations. In this way, the model provides a platform to test various hypotheses for the observed size reduction: are the fish maturing earlier and remaining smaller due to rising temperatures, increased fishing pressure, or shifts in the plankton community? Using climate and evolutionary simulations, we demonstrate that environmental and anthropogenic forcings alone cannot account for the observed reduction in body size and the concomitant shift toward earlier reproduction in sardines and anchovies. Our analyses indicate that selection for fast-growing, small-bodied individuals is the most plausible mechanism driving these trends.

Keywords: Demography, Life history traits, Small pelagic fishes, Agent based model, Natural Selection.

*Speaker



Climate forcings
Copernicus
Marine Service
julia
Puberty
Juvenile
Adult
Die
DEB
Mature
Aging
Die
DEB
Reproduce
Aging
- Nind
- Nind
DEB
Hatch
Aging
Birth
Batch release
- Nind
Eggmass
Based on Haberle et al. 2023
Population & individual life-history traits
Anchovy SSB (Tonnes)
Tonnes
Year
SSB_TONNES
model_ssb_tonnes
new_medias

From mechanistic population dynamics models to functional traits projections : the case of sand reworking by lugworms in the context of climate change

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Abstract

A major challenge in marine ecology is understanding population and ecosystem dynamics under environmental change. The integration of bioenergetic dynamic budget (DEB) models with individual-based models (IBMs) has significantly advanced our understanding of population responses. However, scaling these approaches to community and ecosystem dynamics remains challenging in coastal and benthic systems, where ecosystem engineers disproportionately influence ecosystem function and structure through their effect traits on ecosystems.

In this study, an IBM was developed to analyze the sand reworking activity of two benthic engineers (*Arenicola marina* and *A. defodiens*) under climate change scenarios. The model integrates a DEB-IBM framework with a sand reworking module based on the DEB model's ingestion flux and individual structural volume. Calibrated with data from the literature, the model generates robust predictions of bioturbation activity. Climate projections, including changes in sea surface temperature under RCP8.5 scenarios, and ad-hoc changes in chlorophyll-a levels ($\pm$10% from 2010-2020 satellite observations), were incorporated to assess population dynamics and associated sand reworking across species' distribution ranges by 2100.

The results reveal significant spatial variations in sand reworking patterns, with a general decline observed in regions where populations are currently most abundant. This decline in bioturbation activity could drive substantial changes in community structure and ecosystem functioning. To fully grasp the impacts of climate change on sandy ecosystems inhabited by these species, further studies should explore the links between sand reworking activity and sediment oxygenation.

Keywords: ecosystem engineers, functional traits, sand reworking, climate change

*Speaker

Exploring heritability of DEB parameters as phenotypical traits

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Abstract

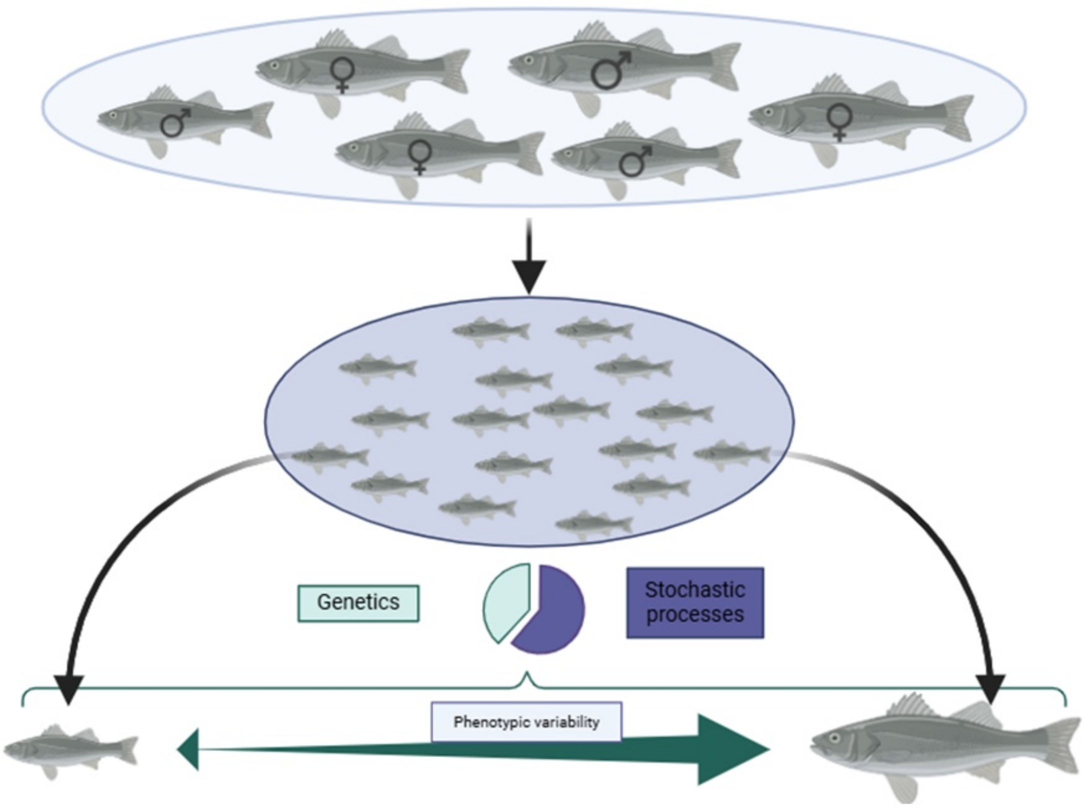
It has been suggested that genetically related fish living together can develop substantial differences in size over time. This variation may arise due to initial random differences in assimilation rates, which are then amplified by unbalanced social interactions (Kooijman, 2009). In this study, we propose that even minor genetic differences may contribute to the significant variation in growth trajectories consistently observed among kinship fish.

To test this hypothesis, we assessed the heritability (proportion of phenotypic variation in a given trait that is attributable to genetic relatedness) of growth-related traits. Considering that Dynamic Energy Budget (DEB) parameters at the individual level can be regarded as phenotypic traits, we examined the heritability of two DEB parameters directly linked to energy assimilation and energy mobilization: specific maximum assimilation rate and energy conductance.

We quantified the heritability of these parameters in two aquaculture-reared fish species: 2,515 European seabass (*Dicentrarchus labrax*) and 600 Gilthead seabream (*Sparus aurata*). Genetic relatedness between individuals was determined using genome-wide single-nucleotide polymorphism data. Individual-specific DEB parameters were estimated based on repeated measurements of length, weight, and muscle fat density (Palmer *et al.,* 2024). Finally, phenotypic variance was partitioned into genetic and unexplained variance using linear mixed modelling. The heritability of the specific maximum assimilation rate was found to be 0.48 in seabream and 0.42 in seabass, while the heritability of energy conductance was 0.42 in seabream and 0.39 in seabass. These findings indicate that nearly half of the observed variation in these DEB parameters can be explained by genetic relatedness.

Keywords: DEB parameters as traits, Between individual variability, Genetic relatedness, Heritability

*Speaker


Genetics
Stochastic processes
Phenotypic variability

Global patterns of climate change impacts on desert lizard communities

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Abstract

Desert faunas are highly vulnerable to ongoing climate change due to their proximity to physiological limits. However, interspecific variation in functional traits complicates species-specific vulnerability assessments at a global scale. Leveraging recently published comprehensive trait databases and phylogenetic trees, we compiled a complete parameter dataset for constructing biophysical models for 235 desert lizard species. Using species-specific model parameterization, we projected the impacts of climate change on desert lizards worldwide. Our analysis revealed significant variations in thermal tolerance and field body temperature across taxonomic groups and desert realms. Furthermore, we identified heterogeneity in climate change impacts among different taxa, particularly concerning hydration risk, hyperthermia, and shifts in feeding demand, both across and within desert realms. Climate change refugia-defined as warm desert regions with high lizard diversity and low predicted physiological stress-are projected to persist to varying degrees across different desert regions. However, few of these refugia fall within existing protected areas. Our findings underscore the critical role of interspecific variation in functional traits in assessing species' vulnerability to climate change and highlight the urgent need to enhance the protection of refugial areas within the world's warm deserts to safeguard lizard biodiversity.

Keywords: Climate changeDesert lizardsBiophysical modelingFunctional traitsClimate refugia

*Speaker

Does DEB theory predict optimal values for the metabolic scaling exponent?

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Abstract

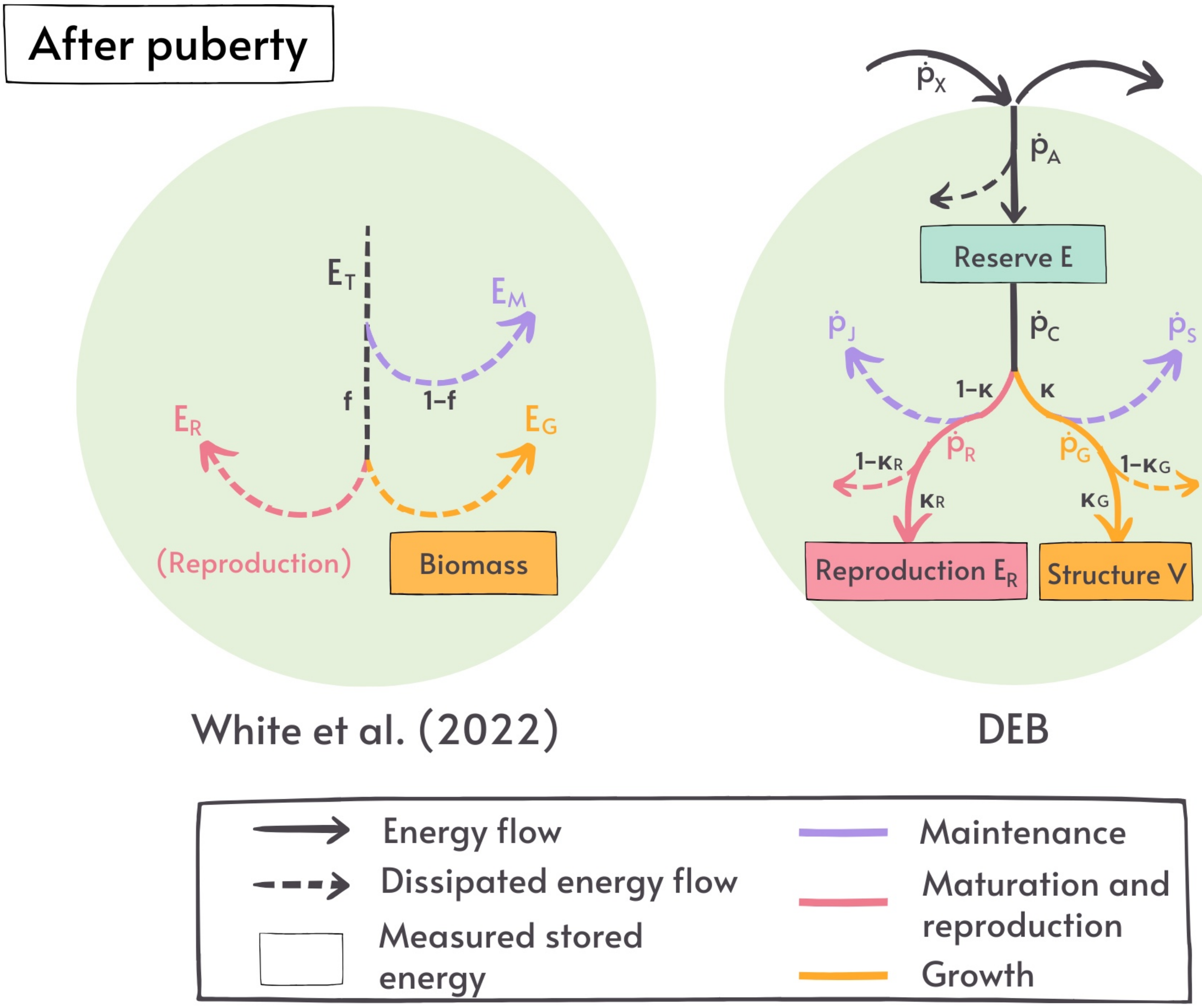
The metabolic scaling exponent describes the relationship between body mass and metabolic rate. It was often postulated to be fixed, at least at any given biological scale, with different values depending on the main mechanistic constraints considered. However, empirical studies have shown that the scaling exponent varies across different taxonomic groups and life stages. A recent evolutionary study used an energy balance model to investigate the relationship between the scaling exponent and dissipated energy. However, this model required strong assumptions.

We aimed to investigate the relationship between the ontogenetic scaling exponent and fitness while accounting for the whole energy balance of organisms and realistic mechanistic constraints. We simulated potential organisms by varying four DEB parameters and estimated two measures of fitness and two measures of the scaling exponent. The DEB parameters were constrained so that the mass at birth, mass at puberty, and ultimate mass were equal between all simulated organisms.

Preliminary results show that the relationships between fitness estimates and allometric scaling exponents were mainly mediated by variation in two parameters: the allocation coefficient and the costs of structure. The highest fitness values were obtained in organisms with a high scaling exponent before puberty (higher than 1) but a low scaling exponent after puberty (between 0.3 and 0.9), hence for low values and low costs of structure. The results suggest that "optimal" values for scaling exponents do emerge from a mechanistic model, but they do not converge with the values often postulated based on more simple mechanisms.

Keywords: intrinsic rate of increase, lifetime reproductive success, optimality theory, evolutionary constraints

*Speaker


After puberty
E_T
E_M
f
1–f
E_R
E_G
(Reproduction)
Biomass
White et al. (2022)
$\dot{p}_X$
$\dot{p}_A$
Reserve E
$\dot{p}_C$
$\dot{p}_J$
$\dot{p}_S$
1–κ
κ
$\dot{p}_R$
$\dot{p}_G$
1–κ_R
1–κ_G
κ_R
κ_G
Reproduction E_R
Structure V
DEB
Energy flow
Dissipated energy flow
Measured stored energy
Maintenance
Maturation and reproduction
Growth

Theory and ecological trait data standards can improve the utility of functional trait databases

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[3]Institute of Ecotechnics Synergia Ranch, New Mexico, USA – United States
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[8]Fisheries Resources Institute, Fisheries Research Education Agency, Japan – Japan
[9]Amsterdam Institute for Life and Environment (A-LIFE), VU University, The Netherlands – Netherlands

Abstract

Trait databases have an important role to play in the future of ecology and evolution. Yet there are challenges in how to structure them, how to prioritise content, and how to limit bias towards traits based on ease of measure or taxonomic peculiarities. Theory can guide which traits (and metadata) to measure, but it is less prescriptive about how to best structure and store data. Ecological trait data standards aim to address this question and to facilitate efficient re-use of trait data. Here we explore how both theory and trait data standards can be used to inform the design of a functional trait database of life history observations required quantify the processes of energy and mass exchange and allocation during individual ontogeny. We specifically use Dynamic Energy Budget (DEB) theory and its associated parameter database, which has $>$ 5500 species across the tree of animal life, and the traits.build framework for trait database construction. We present a database of over nearly 33,000 'zerovariate' life history trait measurements that have passed through the filter of the DEB parameter estimation process.

Keywords: Life history, Bioinformatics, traits.build, Metabolic theory, Functional traits

*Speaker

Modeling Microbial Activity To Improve Sustainability Of Sub-Surface Flow Treatment Wetlands

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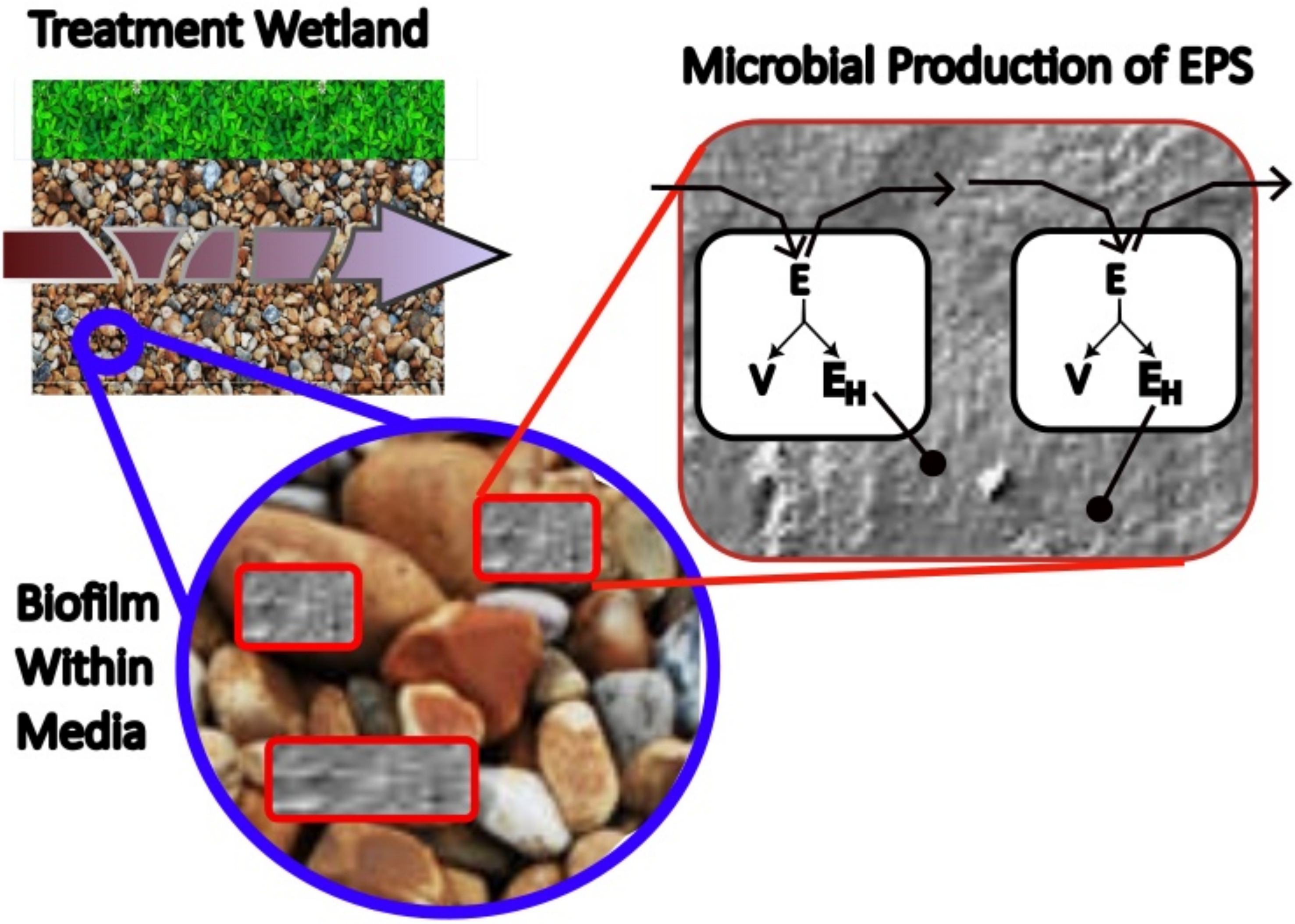
Abstract

Sub-surface flow treatment wetlands (SSF TW) are wastewater treatment systems designed to emphasize specific processes found in natural wetland ecosystems. SSF TWs can contribute to United Nations Sustainable Development Goal 6, "Clean Water and Sanitation." among others.
Microbes play a central role in SSF TW, where transformations of organic matter and nutrients take place as wastewater flows through a matrix of porous media and extracellular polymeric substance (EPS) produced by microbes. Biofilm – the total mass of microbes and EPS - is a critical component as well as a challenge to SSF TW system operation because microbes produce EPS in response to local environmental conditions. Biofilm contributes to clogging of pore spaces within TW media, can cause premature declines in pollutant removal efficiency, and ultimately leads to the end of system service life.

While a number of mechanistic numerical models are available to study internal SSF TW processes, none separates estimates of microbial biomass and production from EPS mass and production. This represents a broad gap in our understanding of how microbial dynamics actually contribute to TW system efficiency, clogging, and service life.
The objective of this study is to improve sustainability of SSF TW by developing a DEB model of microbial activity and EPS production. Departures from the Standard DEB model include: multiple taxa, multiple substrates, multiple reserves, and assignment of EPS production to DEB model maturity and reproduction. The model will quantify EPS production, as well as microbial biomass, growth, and pollutant reduction capacity (e.g. denitrification) observed in SSF TWs.

Keywords: Sustainability, wastewater treatment, bacteria, EPS

*Speaker


Treatment Wetland
Microbial Production of EPS
E
V
E_H
E
V
E_H
Biofilm Within Media

Long-term dynamics of a simplified DEB-based ecosystem model

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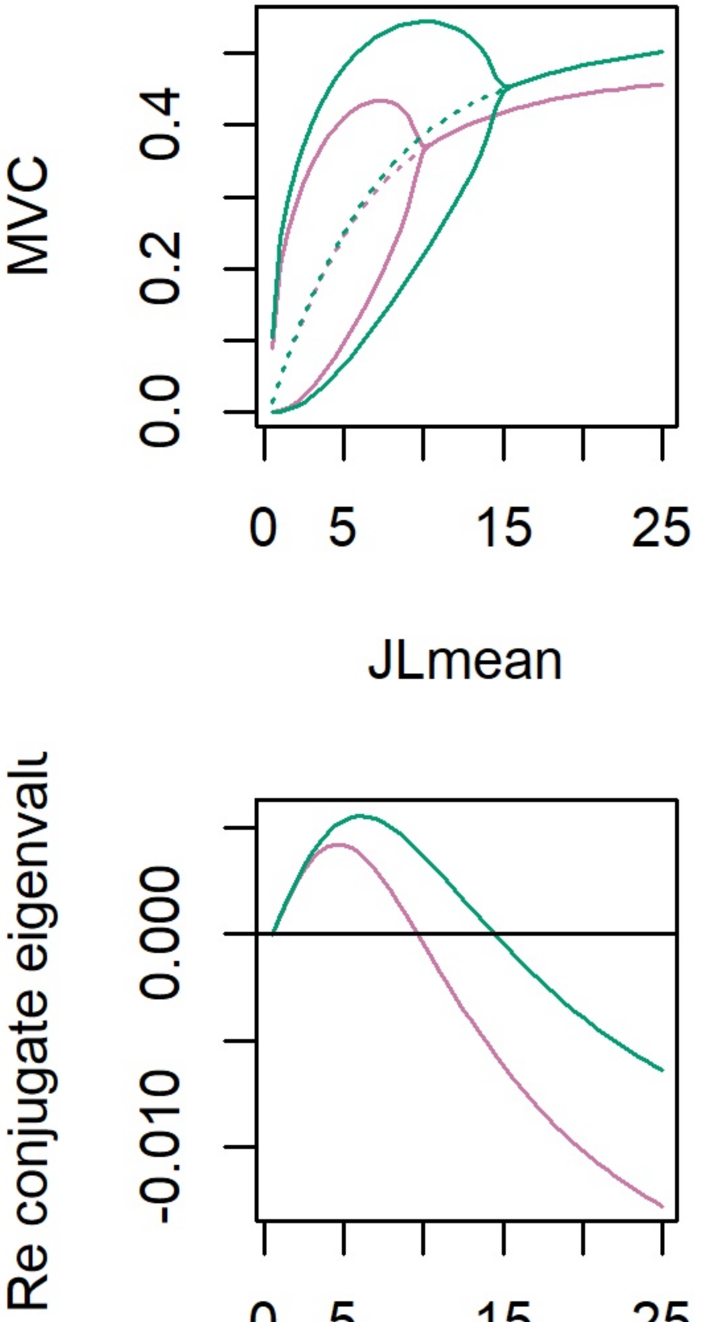
Abstract

Recently we presented a stoichiometric carbon and nitrogen model of an entire ecosystem based on Dynamic Energy Budget (DEB) theory (van der Meer et al. 2022 Ecol. Model.). The living matter of the ecosystem was represented by producers, consumers, and decomposers, each with either one (consumers and decomposers) or two (producers) reserve compartments. Additionally four types of detritus were considered, resulting in a model with 11 state variables. The dynamics of the nutrients carbon dioxide and ammonium followed automatically from the dynamics of the other state variables, because of the law of mass conservation. The model contained 33 parameters and 27 conversion constants.
Although the model is relatively simple compared to many ecosystem models that are generally used by applied ecologists, analyzing the system dynamics of this model in response to, for example, the forcing functions light and nutrient availability, or to parameter variability is still a daunting task. Here we therefore present a simplified version of the model that only considers producers and consumers, both with no more than one reserve compartment. By leaving out detritus and decomposers, we implicitly assume that decomposition is an infinitely fast process. Hence, losses during consumer feeding and death are supposed to be immediately transferred into inorganic nutrients. We further assume that carbon dioxide is not limiting any process rate. The simplified model has four state variables and only 12 parameters and 8 conversion constants.
This simplification allows for a detailed analysis of the long-term model dynamics by means of bifurcation analysis. We show that the dynamical behavior of the model resembles that of the Rosenzweig-MacArthur model, but since the DEB model is based on first principles such as area-volume relationships and rules of mass conservation, we are able to provide a more mechanistic interpretation of the link between environmental forcing and parameter values and dynamical model behavior.

Keywords: Canonical community model, bifurcation analysis, Rosenzweig, MacArthur model, paradox of enrichment

*Speaker



MVC
0.0
0.2
0.4
0
5
15
25
JLmean
MVC
0.0
0.6
1.2
0.4
0.8
Ntotal
Re conjugate eigenvalu
-0.010
0.000
0
5
15
25
JLmean
Re conjugate eigenvalu
-0.04
-0.01
0.4
0.8
Ntotal

Exploring food composition effects on fish metabolism and growth

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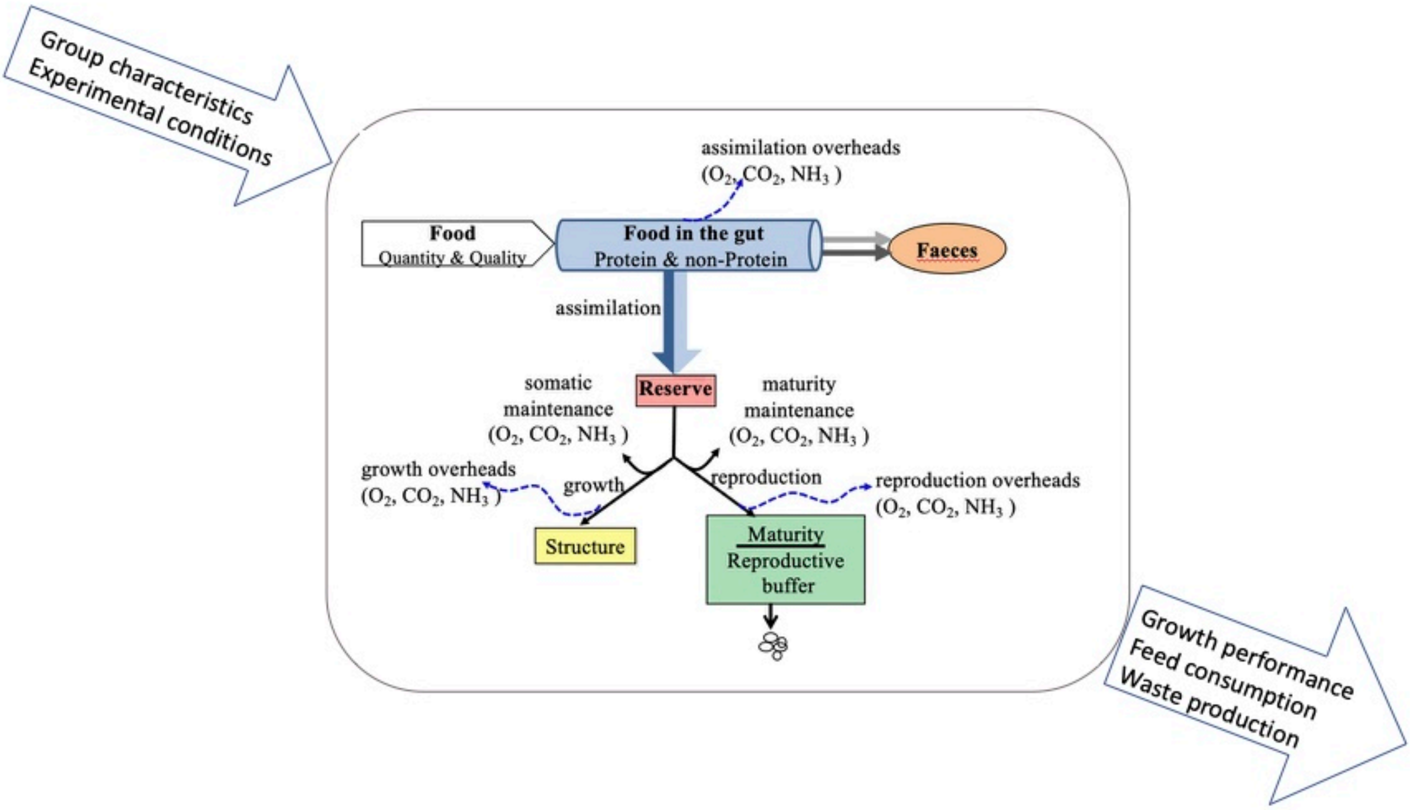
Abstract

The description of flow and transformation of energy and nutrients within a fish is key for fish research as it allows to optimize growth and reduce production costs of farmed animals, ensure animal welfare, and minimize environmental impact. In this work, we developed a nutritional bioenergetics model for fish based on Dynamic Energy Budget (DEB) theory, explicitly incorporating the digestion process. The model applies the concept of synthesizing units to distinguish between protein and non-protein food components regarding their contribution to the formation of reserves. This approach allows predictions of measurable quantities of interest to fish researchers, technicians and aquaculture operators, including feeding rate, oxygen consumption, carbon dioxide, ammonia and solid waste production, under different temperatures and various feeding conditions, both in terms of quantity and macronutrient composition. Without additional assumptions, the model also quantifies the effects of the dietary protein-to energy ratio on food intake and assimilation. For instance, lower food intake is prediced for fish fed high-energy diets (rich in fats) compared to diets with low energy content (poor in fats); a pattern that aligns with experimental observations in fish. The model has been parametrized and validated for rainbow trout (*Oncorhynchus mykiss*), Atlantic salmon (*Salmo salar*), European sea bass (*Dicentrarchus labrax*), and gilthead seabream (*Sparus aurata*), performing well under a variety of diverse datasets across different culture systems and experimental protocols.

Keywords: DEB theory, nutritional bioenergetics, finfish farming, protein, to, energy ratio

*Speaker


Group characteristics
Experimental conditions
assimilation overheads
(O_2, CO_2, NH_3)
Food
Quantity & Quality
Food in the gut
Protein & non-Protein
Faeces
assimilation
Reserve
somatic
maintenance
(O_2, CO_2, NH_3)
maturity
maintenance
(O_2, CO_2, NH_3)
growth overheads
(O_2, CO_2, NH_3)
growth
reproduction
reproduction overheads
(O_2, CO_2, NH_3)
Structure
Maturity
Reproductive
buffer
Growth performance
Feed consumption
Waste production

Towards a Dynamic Theory of Societal Metabolism: Insights from DEB Theory

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Abstract

Societies, like organisms, function as autopoietic systems, sustaining themselves through resource use, knowledge accumulation, and environmental interactions. This metabolic process is central to societal metabolism (SEM), studied through frameworks such as Societal Exergy Analysis (SEA), Economy-wide Material Flow Accounting (Ew-MFA), and Multi-Scale Integrated Analysis of Societal and Ecosystem Metabolism (MuSIASEM). However, these approaches rely on static accounting and lack a dynamic representation of metabolic processes and transitions.

In contrast, Dynamic Energy Budget (DEB) Theory provides a thermodynamically consistent framework for modeling biological metabolism, incorporating endogenous state variables and dynamic metabolic processes. To develop a comprehensive dynamic SEM theory, several improvements are necessary: (1) explicit distinction of metabolic processes such as assimilation, growth, and dissipation, (2) inclusion of endogenous state variables for material stocks, active and passive systems, and embodied information, (3) recognition of embodied information as a key driver of societal metabolism, influencing technological evolution and decision-making, and (4) ensuring that the model is consistent with empirical data.

This work serves as a basis for a dynamic SEM model that integrates these elements, enabling better assessments of sustainability, resource efficiency, and the impacts of environmental change on societies.

Keywords: societal metabolism, information, modeling

*Speaker

Filling in the data gaps for critically endangered leatherback turtles through mechanistic modelling

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Abstract

Leatherback turtles (*Dermochelys coriacea*) are highly migratory and long-lived, making these sea turtles vulnerable to numerous threats throughout their lives. All seven leatherback turtle populations are in various stages of population decline according to the IUCN Red List, despite global conservation efforts. The longevity of a population hinges on the ability of sufficient individuals to acquire enough energy to grow and produce a sufficient number of offspring within their lifetime. Growth and reproduction are constrained by the environment, generally with warmer and energy abundant environment resulting in faster growth, larger sizes, and more produced offspring. Quantifying the relationship between the environment and these life-history traits is complicated by the fact that leatherback turtles spend the majority of their life at open sea, and that rearing leatherbacks in captivity is extremely difficult. Here, we complement an existing Dynamic Energy Budget (DEB) leathearback model with newly acquired data on captive-reared juveniles and literature data on reproduction, and explore to what extent a well parameterized DEB model of a leatherback turtle can: (i) predict functional and life-history traits, including reproductive potential, of leatherback turtles; (ii) elucidate the effects of environmental conditions (food availability and temperature) on those traits; and (iii) predict the traits for two distinct (North-West Atlantic and East Pacific) leatherback turtle populations.

Keywords: dynamic energy budget model, environmental simulations, reproductive potential

*Speaker