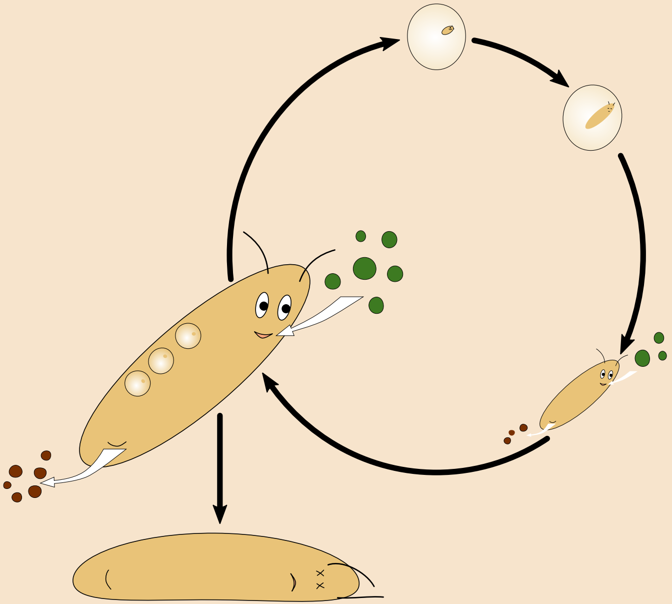
DEB2019

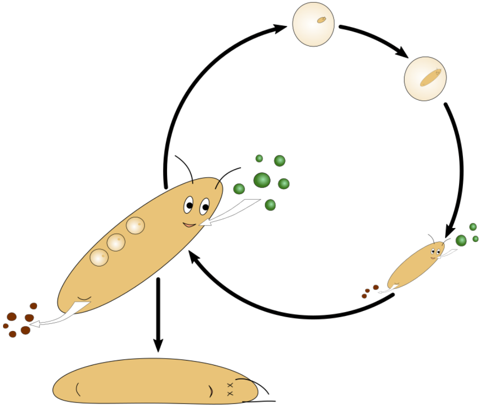
Sixth International Symposium and Thematic School on Dynamic Energy Budget theory for metabolic organization

1-12 April 2019 / Brest (France)



Book of abstracts

About DEB2019



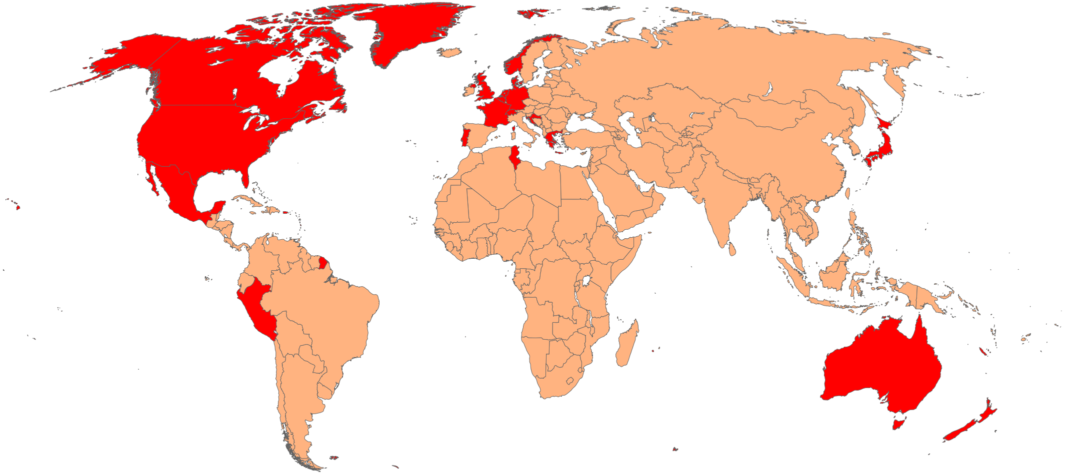
About DEB2019

Dynamic Energy Budget (DEB) theory aims at unifying commonalities of metabolic organization between organisms (animals, plants, bacteria…). This theory is based on a restricted number of assumptions, written out as mathematical formulas that allows quantifying growth, development, reproduction of an organism all along its life cycle as a function of available food and temperature. It also enables modelling the effects of stressors such as contaminants, pathogens, oxygen, pH...

In the actual context of biodiversity erosion, comparison of species functional traits is not the only applications of DEB theory. Prediction of the effects of global change, better understanding the geographical patterns of species, the effects of environmental stressors, optimization of bio-production, management of exploited resources, invasive species control are also examples of applications for which better understanding the metabolism of species and how it is controlled by the environment is key and for which DEB theory allowed knock down scientific some barriers with more than 820 publications.

DEB 2019 is the sixth edition of a series of tele-courses, schools and symposia which take place every two years (see the past conferences at https://deb2019.sciencesconf.org/resource/page/id/11).

The 2019 edition is both the 40th birthday of DEB theory and the 10th birthday of DEB symposiums.



In red, countries of affiliation of DEB2019 participants

Format

DEB 2019 is a three-part international event:

PART 1: 5-week International tele-course - general theoretical part (Jan 24 - Feb 28 2019)

PART 2a: 6-day Thematic school - practical training part (Apr 1 - Apr 6 2019)

PART 2b: 2-day Workshop - expert practical part (Apr 8 - Apr 9 2019)

PART 3: 3-day International DEB Symposium (Apr 10 - Apr 12 2019)

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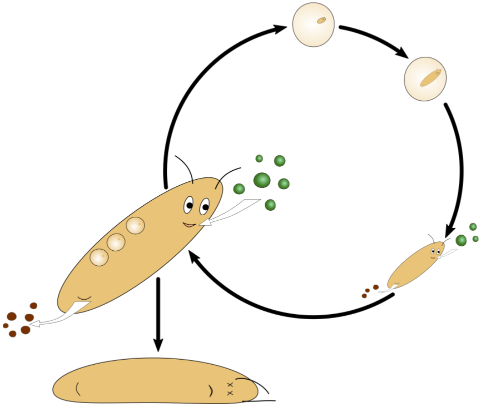

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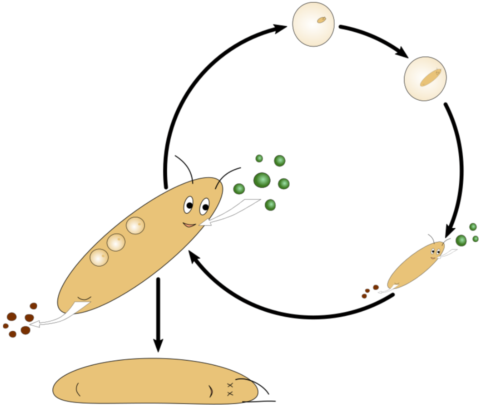
Organization



Organization

Persons involved

Organization committee

Yoann Thomas, *Institut de Recherche pour le Développement.*

Jonathan Flye-Sainte-Marie, *Université de Bretagne Occidentale.*

Laure Pecquerie, *Institut de Recherche pour le Développement.*

Fred Jean, *Université de Bretagne Occidentale.*

Romina Barbosa, *Université de Bretagne Occidentale.*

Julien Gras, *Université de Bretagne Occidentale.*

Karine Rehel-Vallée, *Université de Bretagne Sud.*

Scientific committee

Dina Lika, *University of Crete* (Heraklion, Greece).

Tin Klanjscek, *University of Zagreb* (Zagreb, Croatia)

Cédric Bacher, *Ifremer* (Brest, France)

Gonçalo Marques, *University of Lisbon* (Lisbon, Portugal)

Starrlight Augustine, *Akvaplan-niva* (Tromsø, Norway)

Nicola Mitchell, *The University of Western Australia* (Crawley, Australia)

Tjalling Jager, *DEBtox Research* (De Bilt, The Netherlands)

Administrative and logistics assistants

Nadine Rénier, *Université de Bretagne Occidentale.*

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Founding and partners

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graduate school
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DE LA MER

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ubs

Logistics informations

Dates to remember

Thematic school: April 1st to April 6th, 2019.

Workshop: April 8th to April 9th, 2019.

Symposium: April 10th to April 12th, 2019.

Location of DEB2019 site

DEB2019 school, workshop and symposium will be hosted at **PNBI** (see map p. 17), close to the Institut Universitaire Européen de la Mer (IUEM) of the University of Brest, in Plouzané.

Pôle Numérique Brest Iroise (PNBI)

305 Avenue Alexis de Rochon

29280 Plouzané

France

GPS: 48°21’35’’ N ; 04°33’53’’ W (48.359778, -4.564417)

Map of the DEB2019 site

Important places

IUEM: 48°21’31.6”N 4°33’45.8”W (48.358771, -4.562720)

PNBI: 48°21’35’’ N ; 04°33’53’’ W (48.359778, -4.564417)

Restaurant (RAK): 48°21’36.5”N 4°34’16.0”W (48.360145, -4.571119)

Reaching the DEB2019 site from Brest town center

Note that during Workshop and Symposium a special shuttle link Brest town centre and the DEB2019 site. See time table in page 19. If you don’t use the shuttle you can follow these instructions (travel time is around 45 min).

- In Brest, take the tram, in the direction of **Porte de Plouzané**.
- Alight at the Terminus, then catch **bus number 13**. Alight at the “Piccard” stop
- Follow on walking upward (on Avenue Alexis de Rochon)
- You will find PNBI on your right.
- If you want to reach IUEM, take the first street on your left (rue Dumont d’Urville). You will find the IUEM entrance on your right, across the paved area

Organization

Map of the Brest town centre

Important places

"Liberté" DEB2019 Shuttle stop:
48°23'22.3"N 4°29'06.2"W
(48.389522, -4.485052)

"Français Libres" DEB2019 Shuttle stop:
48°23'03.4"N 4°29'35.4"W
(48.384275, -4.493168)

Le Brestoâ (Symposium dinner):
48°22'53.7"N 4°29'14.2"W
(48.381571, -4.487287)

Train Station :
48°23'15.7"N 4°28'48.5"W
(48.387695, -4.480138)

DEB2019 Shuttle time table

During the DEB2019 Workshop and Symposium a shuttle will allow you to reach the DEB2019 site from Brest town centre in the morning and to return to Brest town centre at the end of the day. Time table is below. Location of the DEB2019 shuttle stops is indicated in page. 18.

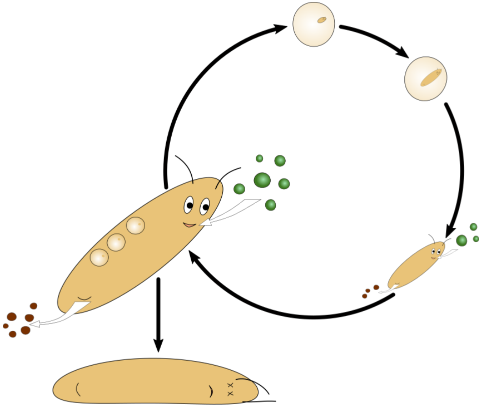
	Mond. 08	*Tues. 09*	*Wedn. 10*	*Thur. 11*	*Frid. 12*
Liberté	7h40	8h05	8h05	8h05	8h05
Français Libres	7h50	8h15	8h15	8h15	8h15
DEB2019 site (De Rochon)	8h20	8h45	8h45	8h45	8h45
DEB2019 site (De Rochon)	21h15	18h00	19h00	17h30	16h00
Français Libres	21h45	18h30	19h30	*	16h30
Liberté	21h55	18h40	19h40		16h40

** Shuttle stop in Brest harbor*

Internet/Wifi connection

- At **PNBI** :
  - If possible you can use the ***eduroam*** network with your institution’s login and password.
  - Other alternative is to connect on :
    - SSID : ***invite***
    - Login : ***debpnbi***
    - Password : ***cmmF=hn2***
- At **IUEM** :
  - If possible you can use the ***eduroam*** network with your institution’s login and password.

Workshop program



Biophysical ecology & Individual to population - April 8

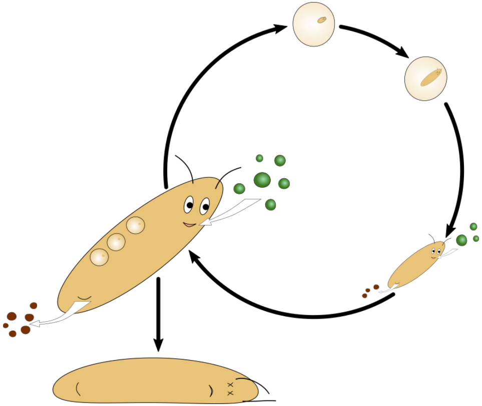
	07:40	Bus Stop Liberté	
	07:50	Bus Stop Français Libres	
08:30	09:00	Welcome coffee	
		Group 1	*Group 2*
09:00	10:30	**Biophysical ecology** Michael Kearney (University of Melbourne, Australia)	**Individuals to Population** B. Kooi (The Netherlands) and R. Nisbet (UCSB, USA)
10:30	11:00	Coffee Break	
11:00	12:30	**Biophysical ecology** Michael Kearney (University of Melbourne, Australia)	**Individuals to Population** B. Kooi (The Netherlands) and R. Nisbet (UCSB, USA)
12:30	14:00	Lunch	
14:00	15:30	**Individuals to Population** B. Kooi (The Netherlands) and R. Nisbet (UCSB, USA)	**Biophysical ecology** Michael Kearney (University of Melbourne, Australia)
15:30	16:00	Coffee Break	
16:00	17:30	**Individuals to Population** B. Kooi (The Netherlands) and R. Nisbet (UCSB, USA)	**Biophysical ecology** Michael Kearney (University of Melbourne, Australia)
18:30	21:00	Workshop Diner Cocktail	
	21:15	Bus to Brest	

Environmental stressors, ecotoxicology and DEB theory - April 9

	08:05	Bus Stop Liberté	
	08:15	Bus Stop Français Libres	
		Environmental stressors, ecotoxicology and DEB theory - Plenary session	
09:00	09:15	**Introductory remarks - Objectives of the workshop** Laure Pecquerie (LEMAR, IRD, France)	
09:15	10:15	**Introduction to DEB theory in ecotoxicology** (assumptions, processes, state variables and parameters) Gonçalo Marques (IST Portugal)	
10:15	11:00	**Impacts of environmental stressors on organisms: Combining an experimental and a modelling approach** Jonathan Flye-Sainte-Marie (UBO, France)	
11:00	11:30	Coffee Break	
		Plenary session	
11:30	12:00	**Contributions and limitations of the DEB modeling approach to the study of environmental stressors at the sub-individual level: views from an experimentalist** Arnaud Huvet (Ifremer, France)	
12:00	12:30	**Contributions and limitations of the DEB modeling approach to the study of environmental stressors at the sub-individual level: views from a modeller and feedback from the NIMBioS working group** Roger Nisbet (UCSB, USA)	
12:30	14:00	Lunch	
		Group 1	*Group 2*
14:00	15:30	**Exploring the impacts on individuals of several physiological modes of action of toxicants using R** Gonçalo Marques (IST Portugal)	**Exploring the impacts on populations of several physiological modes of action of toxicants using Netlogo** Roger Nisbet (UCSB, USA)
15:30	16:00	Coffee Break	
16:00	17:30	**Exploring the impacts on populations of several physiological modes of action of toxicants using Netlogo** Roger Nisbet (UCSB, USA)	**Exploring the impacts on individuals of several physiological modes of action of toxicants using R** Gonçalo Marques (IST Portugal)
	18:00	Bus to Brest	

Workshop program

Symposium program



Overview of the schedule

Day 1 - April 10

09:00	09:30	**Welcome coffee**
09:40	10:00	Opening - F. Jean (IUEM Director) and ISblue direction
10:00	10:50	**Session 1: Theoretical and methodological developments and new applications** Openning conference - **S.A.L.M. Kooijman** *Vrije University (Amsterdam)* **"What did we learn from the Add-my-Pet data base?"**
10:50	11:10	**Domingos Tiago** *Terraprima - Serviàos Ambientais (Portugal)* Minimizing direct greenhouse gas emissions in livestock production: the need for a metabolic theory
11:10	11:30	**De Cubber Lola** *Laboratoire d'Océanologie et de Géosciences (France)* Annelid polychaetes experience metabolic acceleration as other Lophotrochozoans: the example of Arenicola marina
11:30	11:50	**Sangare Nathanaël** *Institut français de recherche pour l'exploitation de la mer (French Polynesia)* Coupling field, laboratory and DEB approach to investigate the pearl-oyster life-cycle in the context of black pearl farming
12:00	13:20	**Lunch**

13:30	14:20	**Session 2: Evolution and biodiversity** Keynote - **Craig White** *Monash University (Australia)* **"The evolution of metabolic rate"**
14:20	14:40	**Sadoul Bastien** *GABI, INRA, AgroParisTech, Université Paris-Saclay (France)* Accounting for genetic variability in fitness-related traits using a Dynamic Energy Budget model, an example on European Seabass
14:40	15:00	**Stubbs Jessica** *School of Biological Sciences, The University of Western Australia (Australia)* From embryo energetics to a full life-cycle DEB model for a Western Australian green turtle population
15:00	15:30	**Break**
15:30	15:50	**Jusup Marko** *World Hub Research Initiative, Institute of Innovative Research, Tokyo Institute of Technology (Japan)* Early-life ontogenetic developments drive tuna ecology and evolution
		Session 1, continued : Theoretical and methodological developments and new applications
15:50	16:10	**Lefebvre Sébastien** *Laboratoire d'Océanologie et Géosciences (France)* DEB theory and stable isotope dynamics: exploring alternative ways
16:10	16:30	**Souloumiac Audrey** *Institut de Radioprotection et de Sureté Nucléaire (France)* Mecanistic and ecophysiologic study of carbon 14 transfer in fish
16:30	16:50	**Dambrine Chloé** *Unité de recherche Sciences et Technologies Halieutiques (France)* Contribution of a bioenergetics model to investigate on growth and survival of European seabass in the North Atlantic

17:00	18:45	**Poster session / Cocktail**
	19:00	Bus to Brest

Day 2 - April 11

	08:05	Bus Stop Liberté
	08:15	Bus Stop Français Libres
09:00	09:50	**Session 3: Effects of anthropogenic and environmental stressors** Keynote - **Roman Ashauer** *Syngenta & University of York (UK)* **"Physiological modes of action are the key to (almost) everything"**
09:50	10:10	**Lika Dina** *University of Crete (Greece)* Linking Adverse Outcome Pathways to Dynamic Energy Budgets: the case of hormone-driven energy allocation for egg loading
10:10	10:30	**Alonzo Frederic** *IRSN, Radionuclide Ecotoxicology Laboratory (France)* Molecular and metabolic mechanisms of transgenerational effects in Daphnia exposed to radionuclides
10:30	11:00	**Break**
11:00	11:20	**Jager Tjalling** *DEBtox Research (Netherlands)* A roadmap for establishing DEBtox in environmental risk assessment practice
11:20	11:40	**Charles Sandrine** *Laboratoire de Biométrie et Biologie Evolutive (France)* Ready-to-use modelling and statistical tools for advanced environmental risk assessment
11:40	12:00	**Lavaud Romain** *Dalhousie University (Canada)* Modeling the impact of hypoxia on the energy budget of Atlantic cod in two populations of the Gulf of Saint-Lawrence, Canada
12:00	12:20	**Aguirre-Velarde Arturo** *Instituto del Mar del Peru (Peru)* Predicting the energy budget of the scallop Argopecten purpuratus in an oxygen-limiting environment
12:30	13:50	**Lunch**

14:00	14:20	**Klanjscek Tin** *Institut Rucer Bockovic (Croatia)* Metabolic scaling of response to toxic stress
14:20	14:40	**Ren Jeffrey** *NIWA (New Zealand)* Effect of ocean acidification on mussel growth: application of a DEB model to green-lipped mussel Perna canaliculus
14:40	15:00	**Marques Gonçalo** *Marine Environment and Technology Center (Portugal)* A generic open source Dynamic Energy Budget model for aquatic and terrestrial organisms to predict toxic effects on the life-cycle on individuals
15:00	15:20	**Mounier Florence** *Aquatic Ecosystems and Global Change Research Unit (France)* Sensitivity of POPs bioaccumulation to Global Change factors. Application of an original DEB-TK approach to the Gironde estuary common sole Solea solea.
15:20	15:50	**Break**
15:50	16:10	**Nisbet Roger** *University of California, Santa Barbara (United States)* DEB, Nanotoxicology and Adverse Outcome Pathways
16:10	16:30	**Pousse Emilien** *National Oceanic and Atmospheric Administration (United States)* Studying costal acidification effect on the Eastern oyster, Crassostrea virginica, through two individual based models
16:30	16:50	**Lagos Paulo** *University of Otago (New Zealand)* Investigating the response of the krill Nyctiphanes australis (Euphausiacea) to stress caused by environmental change: a dynamic energy budget approach

	17:30	Bus to Brest Harbor
	18:30	**Boat trip and Symposium dinner**

Day 3 - April 12

09:00	09:50	**Session 4: Populations and ecosystems in a changing climate** Keynote - **Brian Helmuth** *Northeastern University (USA)* **"When do the details matter? DEB as an integrator of environmental variability multiple stressors and time history effects"**
09:50	10:10	**Guillaumot Charlene** *Université Libre de Bruxelles (Belgium)* Inferring the responses of Southern Ocean benthic species to environmental changes using Dynamic Energy Budget models
10:10	10:30	**Bacher Cedric** *DYNECO - IFREMER (France)* Modelling the response of the disctribution of benthic marine species to climate change
10:30	11:00	**Break**
11:00	11:20	**Juan Bueno-Pardo** *Unité de recherche Sciences et Technologies Halieutiques (France)* A DEB-IBM approach to understand past variation and projecting anchovy abundance in the Bay of Biscay
11:20	11:40	**Koch Josef** *Laboratory of Environmental Toxicology and Aquatic Ecology, Ghent University (Belgium)* Implementing realistic biological variability into an individual-based DEB model for copepods
11:40	12:00	**Lavaud Romain** *Institut des Sciences de la MER de Rimouski (Canada)* Integrating macroalgae & wild bivalve populations to improve ecosystem models for a sustainable development of bivalve culture in eutrophic estuarine complexes
12:00	12:20	**Marn Nina** *Institut Rucer Bockovic (Croatia)* Metabolic and life-history trait responses of sea turtles to environmental cues
12:30	13:50	**Lunch**

14:00	14:20	**Lika Dina** *University of Crete (Greece)* Impacts of climate-related drivers on finfish aquaculture
14:20	14:40	**Queiros Quentin** *MARine Biodiversity Exploitation and Conservation (France)* Investigating overmortality of adult sardines in the Gulf of Lions using DEB approach
14:40	15:00	**Récapet Charlotte** *Ecologie Comportementale et Biologie des Populations de Poissons (France)* Investigating potential causes of mortality at sea in Atlantic salmon through a simulation study
15:00	15:30	**DEB2019 Conclusions and Closing**
	16:00	Bus to Brest

Symposium program

Session 1 : Theoretical, methodological developments and new applications

Conveners: Gonçalo Marques and Dina Lika.

Since 1979, DEB theory has been continuously developed and tested in a multitude of applications. This session contains contributions addressing theoretical and methodological developments as well as new applications of DEB theory. It encompasses extensions of the theory in any direction, including species-specific modules, general theoretical developments, expanding the theory to higher levels of organization or focusing on developing modules for specific features, developing new methodologies for estimating parameters and assessing uncertainties.

The gastrotrich *Chaetonotus zelinkai*.

Opening presentation: What did we learn from the Add-my-Pet data base?

S.A.L.M. (Bas) Kooijman [*]

Emeritus professor, Theoretical Biology Department,
VU University Amsterdam – Amsterdam, The Netherlands

Developing, testing and applying a consistent, coherent as well as quantitative theory on uptake and use of substrates by individual organisms, from start of development till death. The theory, called DEB theory, respects energy, mass, isotope, and time conservation, as well as stoichiometric constrains on transformations. It deals with aging and environmental stressors, such as temperature, substrate limitations, toxicants, anaerobic conditions. DEB theory is formal, so based on a set of explicit assumptions, mechanistic, so the assumptions concern first principles only, and applies to all living organisms, so micro-organisms, animals and plants. It includes sub-organismal, population and ecosystem consequences, symbioses and other syntrophic interactions and patterns in the co-variation of parameter values among species all in an evolutionary perspective. Considerable attention is given to links between models implied by DEB theory and existing empirical models. The testing and application of DEB theory involves innovations in e.g. parameter estimation, and the setup of a database for animal energetics, which presently has more than thousand entries.

Keywords: Add_my_Pet 2017 vs 2019, Motivation, Aims & developments, Estimation in context, Augmented loss functions, Eco-labelling, Applications

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[*] Speaker

Symposium program

Minimizing direct greenhouse gas emissions in livestock production: the need for a metabolic theory

Gonçalo Marques [1], Carlos Teixeira [1], Tânia Sousa [2], Tiago Morais [2], Ricardo Teixeira [2], Tiago Domingos * [2]

[1] *Terraprima - Serviços Ambientais – 2135-199 Samora Correia, Portugal*
[2] *Instituto Superior Técnico - Universidade de Lisboa (IST) – Av. Rovisco Pais, 1, 1049-001 Lisboa, Portugal*

Livestock production is one of the main contributors to global greenhouse gas (GHG) emissions. The tools provided by the Intergovernmental Panel on Climate Change to estimate GHG emissions (Tier 1 and Tier 2) are useless as a tool for advising farmers or national policy on how to minimize GHG emissions. For that, we need a metabolic model that obeys mass and energy balances and that models the tradeoffs between different allocations of energy in the organism, throughout the life-cycle, as a function of environmental variables such as temperature and the amount and type of food. We use the Dynamic Energy Budget (DEB) Theory to build models for four bovine breeds – Alentejana, Angus, Charolais and Limousin. The fitness of DEB models to data is good for all breeds. Differences in DEB breed specific parameters explain differences in GHG emissions, ultimate lengths and weights and von Bertallanffy growth rates. Accumulated methane (nitrogen) production ranges between 0.2 (0.1) and 2 (0.7) kg per kg of beef. In terms of accumulated GHG emissions, Angus breed is a better choice if the cow is slaughtered younger than 200 days (or 450 kg) while for older (heavier) cows, the Charolais breed is a better option.

Keywords: Climate Change, Livestock, Beef, Metabolism, Enteric Fermentation, Manure.

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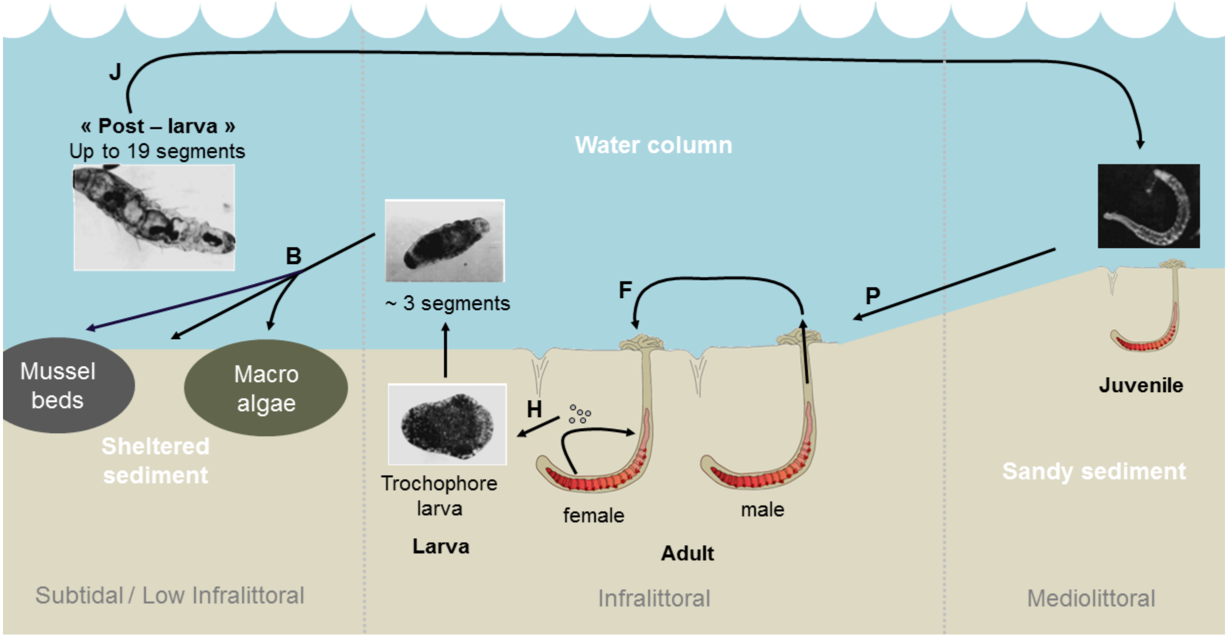

Life cycle of *Arenicola marina* and associated habitats. F stands for fecundation, H for hatching, B for birth (e.g. first feeding, as described in the DEB theory), J for end of the metamorphosis and P for puberty. Adapted from Farke and Berghuis (1979a, 1979b), Reise (1985) and Reise et al. (2001). Pictures of the different life stages of *A. marina* are taken from Farke and Berghuis (1979a).

Annelid polychaetes experience metabolic acceleration as other Lophotrochozoans: the example of *Arenicola marina*

Lola De Cubber * [1], Sébastien Lefebvre [1], Théo Lancelot [1], Lionel Denis [1], Gwendoline Duong [1], Sylvie Gaudron [1,2]

[1] *UMR 8187 - Laboratoire d'Océanologie et de Géosciences (LOG) – Université de Lille - Sciences et Technologies, CNRS : UMR8187, Université du Littoral Côte d'Opale : UMR8187 – 28 Avenue Foch B.P.80 62930 Wimereux (FRANCE), France*
[2] *Sorbonne Universités (UFR 918 & UFR 927) – Sorbonne Universités, UPMC, CNRS – 75005 Paris, France*

Arenicola marina is a polychaete (Lophotrochozoan) showing a complex and poorly known bentho-pelagic life cycle with two larval dispersal phases. In the Add-my-Pet database of Dynamic Energy Budget models, among the 1524 entries, only 11 are annelids, 5 of them being polychaetes for which standard models were applied. The closest phylum with a large amount of data is the molluscs (over 80 entries), also presenting a larval stage. For this phylum, abj-DEB models are applied, which are an extension of std-models considering an acceleration of metabolism between birth and metamorphosis and are applied to most species with a larval phase. Although a preliminary parameter set for a std-DEB model already exists for *A. marina*, a new parameter estimation was performed with the covariation method and a larger data set to assess the suitability of an abj-model for this species, and to infer predictions on larval stages and environmental conditions. The zero-variate data consists in length and age data at different stages of the life cycle, and in the lifespan and the maximum observed length. The uni-variate data set consists in two growth experiments from the literature at two food levels, at one and at several temperatures, and in laboratory data of respiration at several temperatures and fecundity for different lengths. The predictions of the model fit we*l*l to the data (SMSE = 0.24). The acceleration coefficient equals 10, which is similar to the molluscs' values. The field growth curves and the food levels were suitably reconstructed with the new parameter set. The reconstruction of the chronology of the early life stages according to local environmental conditions indicated a first dispersal phase of 7 days followed by a 4.5 months' temporary settlement before a second dispersal in March. We emphasize the need for using abj-models for polychaetes in future studies.

Keywords: Dynamic Energy budget, *Arenicola marina*, Metabolic acceleration, Growth, Respiration, Life cycle.

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Symposium program

Coupling field, laboratory and DEB approach to investigate the pearl-oyster life-cycle in the context of black pearl farming

Nathanaël Sangare * [1], Alain Lo-Yat [1], Gilles Le Moullac [1], Romain Le Gendre [2], Yoann Thomas [3], Benoît Beliaeff [1], Serge Andreföuet [4]

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[2] Institut français de recherche pour l'exploitation de la mer – Ifremer, LEAD, BP. 2059, 98846 Nouméa, New Caledonia
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Spat collection of the black-lip pearl oyster *Pinctada margaritifera* is today the first necessary step leading to black pearl production in French Polynesia atolls. Understanding the factors controlling spat collection spatial and temporal variability is thus essential to optimize both cultural practices and atoll lagoon management. To tackle several of the unknowns, a full life-cycle bioenergetics model following the Dynamic Energy Budget (DEB) theory was developed for *P. margaritifera*. A particular emphasis was given first to the reproduction potential and the larval phase. The DEB model parameters estimation was set from experiment in controlled environment for the larval stage and completed for juvenile and adult stage with patterns from literature. Validation was then performed using *in situ* data from the lagoon of Ahe atoll (Tuamotu, French Polynesia). Various environmental parameters, including chlorophyll-a and temperature, were monitored jointly with pearl oyster reproductive cycle variability (spawning events, synchronicity and fecundity). The application of the full life cycle model clarified how phytoplankton abundances and temperature cycle determine recruitment potential, by affecting the reproduction potential and by controlling larval performances. Laboratory experiment showed that food density highly impacted physical traits of larvae such as age or size at settlement. Measurements of larvae feeding rate and respiration revealed critical metabolic periods, especially before settlement. This multidisciplinary approach, coupling experimental work with modelling, sets a strong basis to explore through DEB concepts, such as the metabolic acceleration, the importance of early life stage on the adult performances. Its coupling with a validated 3D larval dispersal model provide new cues to understand the dynamics of this bottom-dwelling populations.

Keywords: Pearl oyster, Atoll Lagoon, Life cycle, DEB modeling, biophysical modeling.

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Session 2 : Evolution and biodiversity

Conveners: Starrlight Augustine and Laure Pecquerie.

Even the simplest living organism is an extremely complex dynamic system which hampers applying a straightforward physical approach to understand its metabolic, physiological, ecological, or evolutionary behaviour. Still, biological systems can be compared with an evolutionary perspective: different organisms (of different species) have features in common as well as differences that gradually developed during evolution. This session contains contributions that apply DEB theory to exploit this feature and push biology beyond the limitations imposed by descriptions and exploit the power of explanation.

Morevover, the role of biodiversity in ecosystem structure and functioning is central for conservation and environmental quality management, as well as biospherics and earth system studies. Biodiversity is not only about the number of species present, but also the number and nature of the different characteristics and functions which make up a community or an ecosystem, sometimes referred to as traits. Scientists and managers are turning towards such approaches to measure the health and vitality of ecosystems. This session further welcomes DEB contributions developed and applied in the context of apprehending biodiversity loss.

Symposium program

Keynote 1: The evolution of metabolic rate

Craig White [*]

Professor at Monash University, Australia.
Evolutionary Physiology Research Group.

I am an evolutionary physiologist interested in describing and understanding the causes and consequences of physiological variation in animals. My group studies a range of traits, with an emphasis on body size, metabolic rate, water loss, and breathing patterns, and employs a range of approaches including manipulative experiments, comparative studies, experimental evolution, and quantitative genetic analyses. My group work predominantly on insects, but have collected physiological data for over 60 species, including marine invertebrates, aquatic and terrestrial arthropods, and vertebrates (fish, amphibians, reptiles, birds, and mammals).

Keywords: Metabolic rate, Scaling, Growth, Energy allocation, Fitness.

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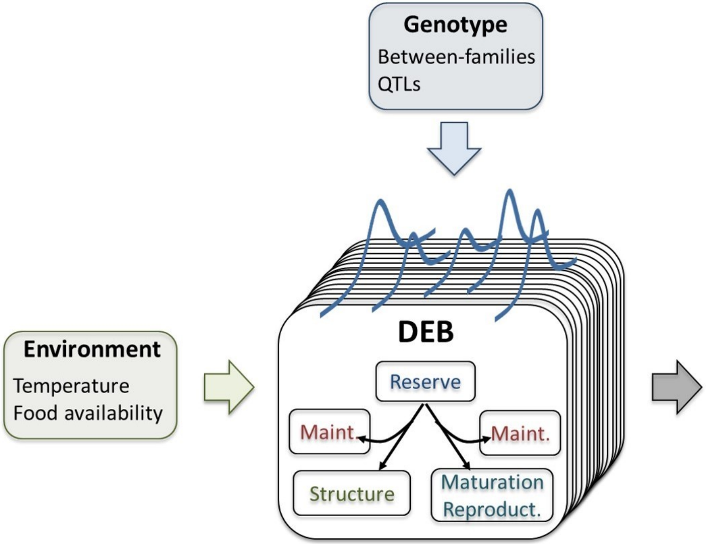
[*] Speaker

Symposium program



Genotype

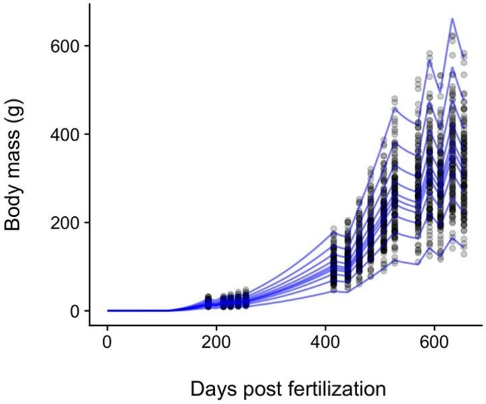
Between-families
QTLs

Environment

Temperature
Food availability

DEB

Reserve
Maint.
Maint.
Structure
Maturation
Reproduct.



Accounting for genetic variability in fitness-related traits using a Dynamic Energy Budget model, an example on European Seabass

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To correctly model the living strategy of individuals and populations in an ecology and evolution context, effects of the environment on fitness-related traits need to be dynamically predicted taking into account the individuals' genotype. This would enable better modeling of the individual variability in growth, survival, and reproductive capacities in a changing environment over time and generations. However, current models either lack the capacity to properly estimate fitness in a dynamic environment or to consider genetic parameters within a population. The Dynamic Energy Budget (DEB) theory was demonstrated to be a powerful tool to describe the life cycle of a wide range of animals in an environment where food and temperature can fluctuate. However, the model is commonly parametrized for the "average" animal of a species, and between-population variability is limited to a consequence of separated environments. We made the hypothesis that inter-individual variation in fitness-related traits can be captured by DEB parameters at the individual level, and that this variability is genetically-driven. Using genotyped European Seabass that were phenotyped for growth over 2 years in a variable but monitored environment, we describe inter-individual variability in DEB parameters. By comparing individuals from 30 half-sib families, we estimated a high heritability (up to 0.7) of several of these parameters, showing the importance of the genotype of the animal. Some of this variability was also translated in terms of behavior, with significant differences in DEB parameters between bold and shy individuals. Altogether, these results highlight the possibility to include a genetic factor explaining inter-individual fitness-related traits in DEB models.

Keywords: Genotype, Inter-individual variability, Heritability.

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[*] Speaker

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Chelonia mydas at Ningaloo.

From embryo energetics to a full life-cycle DEB model for a Western Australian green turtle population

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Ningaloo reef in Western Australia supports a significant population of green turtles (*Chelonia mydas*). Despite the abundance of this species, much of the research and monitoring of the Ningaloo *C. mydas* population has focussed on the nesting environment and relatively little is known about their in-water biology. Dynamic Energy Budget (DEB) theory provides a mechanistic framework with which to investigate the full life-cycle energetics of this vulnerable species. Like all sea turtle species, *C. mydas* are long-lived, slow-growing and occupy several different habitats throughout their life-cycle. These traits make these animals difficult to study in the marine environment and consequently, there is little information available on growth rates in the wild. In contrast, the environmental conditions during the terrestrial incubation of sea turtle embryos can be easily controlled in a laboratory, allowing for accurate measurements of developmental physiology during this life stage. Such data can be used to estimate DEB parameters for a full life-cycle model. Here, as part of the BHP-CSIRO Ningaloo Outlook Marine Research Partnership, we conducted incubation and respirometry experiments on *C. mydas* embryos to determine growth rates at different temperatures. This data was combined with limited data available for the juvenile and adult stages to parameterise a full life-cycle DEB model for *C. mydas.* Model predictions showed good agreement with observed data for all life stages. Energy allocation throughout the life-cycle was investigated, as were maternal effects on hatchling size and reserve energy. The parameters were then used to simulate different food and temperature conditions to investigate growth and reproduction under different scenarios. These simulations provide insights into how the Ningaloo population of green turtles may respond to future environmental conditions associated with climate change.

Keywords: Chelonia mydas, Ningaloo Outlook, Embryo energetics, Maternal effects, Life-cycle model.

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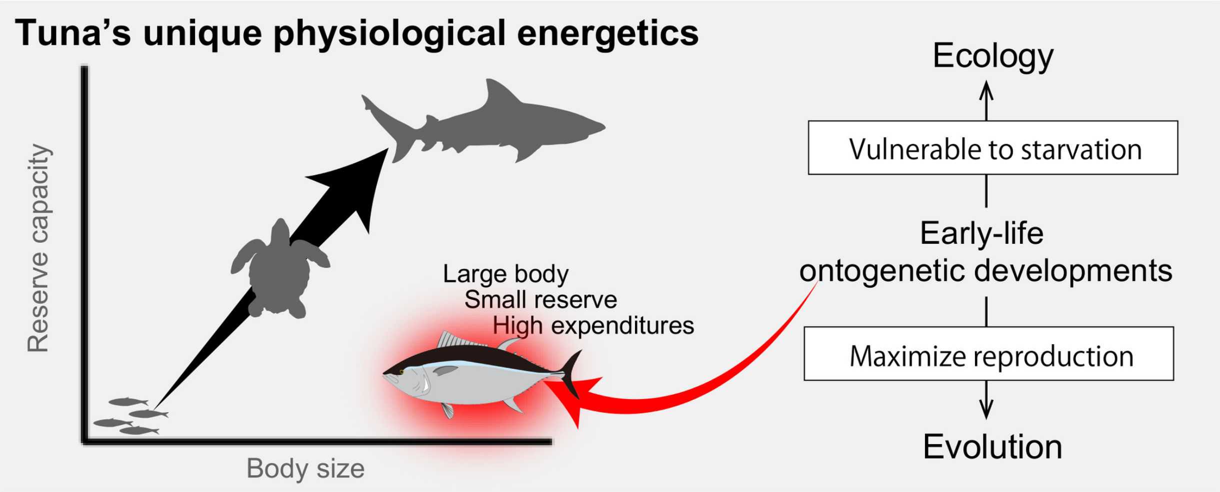
Tuna's unique physiological energetics
Reserve capacity
Body size
Large body
Small reserve
High expenditures
Ecology
Vulnerable to starvation
Early-life
ontogenetic developments
Maximize reproduction
Evolution

Early-life ontogenetic developments drive tuna ecology and evolution

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Tunas are a highly valuable biological resource. Exceeding $40 billion in annual consumer market value, tuna fisheries make a meaningful contribution to the global economy. In recent decades, however, we have tapped into this value with great zeal, threatening to leave little for future generations. Evidence shows that adult biomass of all tropical and temperate tuna populations declined on average 59.5% and 80.2% from 1954 to 2006, respectively. It is therefore of little surprise that several commercial tuna species have been red-listed by the International Union for Conservation of Nature (IUCN).

To better understand tuna ecology and evolution, we adopted a data-driven modelling approach that accounts for the full life cycle-from an egg to an adult individual and its eggs. The results show that critical ontogenetic developments occupy only about 2% of a typical tuna lifetime. Namely, accelerated ontogeny during the larval stage enables tunas to reach large adult size, but does not improve their capacity to build energy reserve. Post larval stage morphological and physiological adaptations further support tuna migratory and predatory lifestyle at a cost of high energy expenditures. All this makes tunas truly unique among large fish as small reserve and high expenditures conspire to become major physiological determinants of tuna ecology and even evolution. For example, high expenditures and small reserve stimulate tuna's voracious appetite, while high expenditures and large body enhance predatory prowess. Exceptional energy demand is thus met with even greater energy intake.

Furthermore, the actual reproductive output of tunas approximates the theoretical maximum. This is unusual from an evolutionary perspective, because evolution should maximise fitness, and fitness involves a tradeoff between reproduction and survival. In tunas, however, large adult size enabled by accelerated ontogeny likely takes survival out of the picture, and maximising fitness thus becomes equivalent to maximising reproductive output.

Keywords: Accelerated ontogeny, Bluefin tuna, Skipjack tuna, Ecology and evolution, Energy speculators.

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δ13C
DEBBIE
Anthelme Gaudron

DEB theory and stable isotope dynamics: exploring alternative ways

Sébastien Lefebvre * [1], Marine Ballutaud [1], Carlos Martinez Del Rio [2], Laure Pecquerie [3]

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Using stable isotope analyses to decipher trophic relationships depends on two strong assumptions: i) a constant and known trophic enrichment factor (TEF) and ii) isotopic steady state, which depends on the tissues isotopic turnover (measured by *lambda*, the instantaneous incorporation constant). These two aspects of isotope dynamics have been questioned for 20 years and are now challenged using both theoretical in silico modelling and experimental approaches. The consequence of violating these assumptions is a distorted representation of the inferences derived from isotopic analyses, e.g. in reconstructing species diet, trophic niche and food web. Our ”strong” assumptions are wrong: TEF and *lambda* are interconnected and both are functions of bioenergetics and scale with body mass. We hypothesize that integrating their process based variations and their connection will improve inferences from isotope measurements. Most popular models classically used to assess isotope incorporation dynamics are phenomenological and are inappropriate to tackle these problems. More mechanistic models recently developed such as the Dynamic Isotopic Budget (DIB) model provides a promising sound alternative. DIB is based on Dynamic Energy Budget theory which predicts many types of intra- and interspecific scaling relationships. The drawback of DIB is that it is in its present form too complex for ecological applications. We developed a simpler dynamic model based on Von Bertalanffy (VB) model that explicitly link TEF and *lambda*. We calibrated this VB model using DEB parameters, made testable predictions, and examined whether these predictions are consistent with the more mechanistic DIB models. Our aim is to quantify TEF and *lambda* in a wide range of animal species using both types of models. Then, we will evaluate the consequences of incorporating dynamics on diet and trophic niche estimations.

Keywords: Von Bertalanffy, Trophic enrichment factor, Isotopic turnover rate.

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*Speaker

Mecanistic and ecophysiologic study of carbon 14 transfer in fish

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Carbon-14 (^{14}C) is one of the two radionuclides which are released in greatest amounts into rivers by the nuclear power plants in routine operation. In France, ^{14}C contributes to a major fraction of the estimated annual dose absorbed by local populations living in the vicinity of nuclearized rivers, mainly by ingestion of radiocontaminated fish. However, mathematical models used to assess the transfer of ^{14}C to the aquatic ecosystems are unable to explain ^{14}C values observed in sampled fish. One of the reason for this is that these models are very simplistic, neglecting the potential influence of changes in ^{14}C speciation, biochemical transformations occurring along trophic chains and the potential influence of fish physiology as a function of environmental factors, such as temperature or food.

In this context, the present PhD project aims to adapt the conceptual approach known as the ”Dynamic Isotope Budget” (DIB), an extension of the Dynamic Energetic Budget (DEB) used to describe stable isotope fluxes in organisms, to the case of ^{14}C transfers among water, sediment, phytoplankton, zooplankton, and fish. In this aim, Cyprinus carpio is selected as a robust laboratory species, commonly found during radioecological monitoring in French rivers and available in the Add-My-Pet collection. First, a literature search is conducted and size and reproduction data are used to improve the parameterization of the DEB model for *C. carpio*. Second, sensitivity analyses (MORRIS, SOBOL’) are carried out to identify most influent parameters. Finally, ongoing experiments are conducted to quantify transfer efficiencies of ^{14}C in different processes of the DIB model using different forms of ^{14}C (glycerol, arginine, glucose, as precursors in lipid, protein and glucids metabolism).

Keywords: radioactive isotopes, Carbon 14 fluxes, freshwater ecosystem, fish, common carp.

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*Speaker

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Symposium program

Contribution of a bioenergetics model to investigate on growth and survival of European seabass in the North Atlantic

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European seabass (*Dicentrarchus labrax*) is a species of concern for both its ecological and economical values. ICES assessments have recently highlighted the worrying state of the Northern stock, probably due to over fishing and a series of poor recruitments. The extent to which poor recruitment is due to environmental change is difficult to assess, as processes driving seabass life cycle are poorly known. Here we explore how food availability and temperature may affect survival and growth of wild seabass. We developed a bioenergetics model based on the Dynamic Energy Budget (DEB) theory. We applied it over the Bay of Biscay – English Channel areas and over the full seabass life cycle. We calibrated the model using different datasets of size and weight at age: two from aquaculture experiments (data on larvae and juveniles raised at 15 and 20°C) and one from the wild (data on juveniles and adults collected during surveys or fish market sampling). By estimating the scaled functional response that rules the food availability and using average temperature conditions experienced by seabass in our calibration for the wild dataset, the model was able to reproduce a major difference encountered in the species life traits: farmed fish mature earlier than wild fish (at age 4 versus 7 on average). We explored survival and growth of larvae and juveniles by formulating scenarios on food levels and temperatures in order to evaluate the temperature limits and starvation ability, which partly conditions the recruitment success. Then, using the model with two series of average temperatures (corresponding to English Channel and Bay of Biscay), the model showed small differences in growth that may challenge the basis of current assessment models. We plan to incorporate this model into a full life cycle and spatially explicit individual-based model for studying the population connectivity.

Keywords: Dicentrarchus labrax, Dynamic Energy Budget theory, Growth, Starvation, Survival.

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[*] Speaker

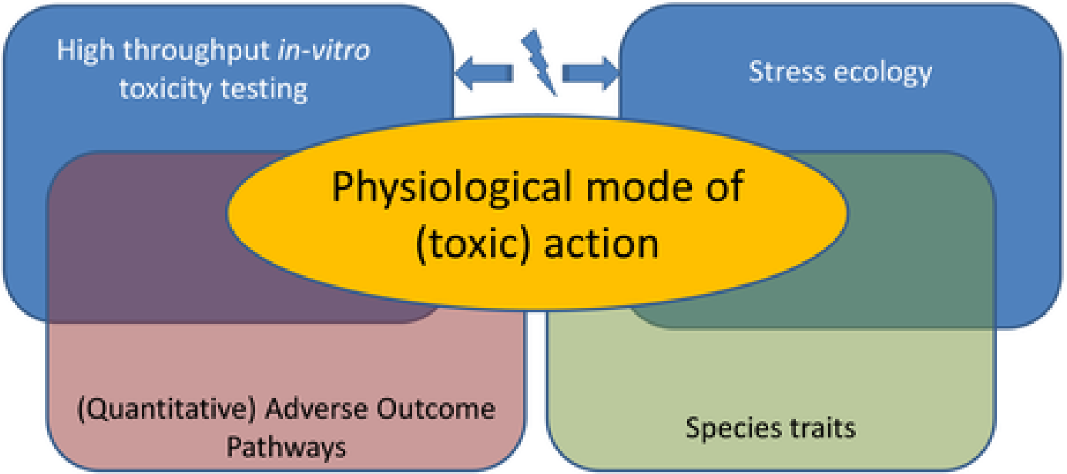
Session 3 : Effects of anthropogenic and environmental stressors

Conveners: Tjalling Jager and Jonathan Flye-Sainte-Marie

Sub-optimal conditions, and hence ‘stress’, is an inescapable part of organism’s lives. Nature will challenge organisms with stressors such as resource limitation, disease or parasitic infections. However, human activities have introduced additional stress, for example in the form of emissions of new chemical compounds (e.g., pesticides and industrial chemicals) and the redistribution of naturally-occurring ones (e.g., oil compounds and heavy metals). Mechanistically understanding the actions of stressors (and their interactions) on the life history of organisms is a scientific challenge, but also has considerable practical application in efficiently managing human environmental impacts. Mechanistic modelling is essential for this task, DEB theory provides an excellent basis for the development of useful models, and indeed has a long track record in the interpretation and prediction of stressor effects.

This session contains contributions that deal with the action of (or combinations of) stressors on individuals in a DEB context. These contributions can be applications of DEB modelling to a specific case, but also presentation of novel model concepts (e.g., in more realistically linking exposure to effects), critical analyses of model performance, regulatory developments, or software development to support application.

Symposium program



Keynote 2: Physiological modes of action are the key to (almost) everything

Roman Ashauer [*]

Senior Scientist Eco-modelling, Syngenta Crop Protection
& Honorary Fellow, University of York (UK)

In my team we investigate the fate and effects of synthetic chemicals in the environment with an emphasis on ecotoxicological effect models and aquatic systems. By systematically studying toxic effects of pollutants we derive general principles and use those to develop tools for the environmental risk assessment of chemicals. Our research consists of modelling, field work and lab experiments. Current research questions are:

- Why do organisms differ in their sensitivity to chemicals?
- What are the general principles that govern toxicity of different chemicals?
- How do critical transitions propagate from cells to organisms and ecosystems?
- How to do quantitativein-vitro to in-vivo toxicity extrapolation?

We are particularly interested in the development of ecotoxicological effect models, for example toxicokinetic-toxicodynamic models. In order to develop, parameterise and test these models we carry out experiments, mostly with aquatic invertebrates. In recent and on-going projects we have investigated pesticides, industrial chemicals, pharmaceuticals and engineered nanomaterials. Our research has also led to the development of new tools for the risk assessment of chemicals. For example methods for the assessment of time-variable exposure that we developed are currently being applied in the risk assessment of pesticides and more recent work that links in-vitro to in-vivo toxicity data via models has great potential.

Keywords: Predictive ecotoxicology, Toxicokinetics, Toxicodynamics, Research strategy.

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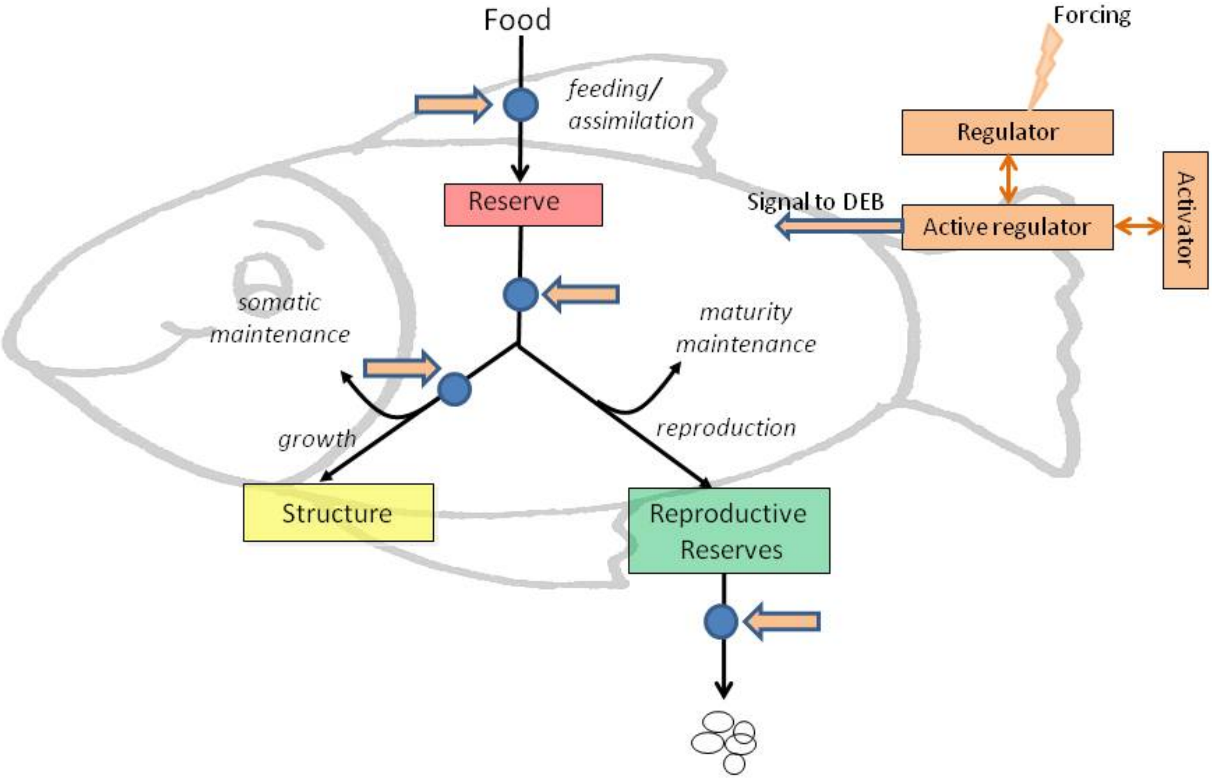
[*] Speaker

Symposium program



Linking Adverse Outcome Pathways to Dynamic Energy Budgets: the case of hormone-driven energy allocation for egg loading

Konstadia Lika * [1], Erik Muller [2,3], Cheryl Murphy [4], Roger Nisbet [5], Diane Nacci [6], Christopher Remien [7], Irvin Schultz [8], Karen Watanabe [9]

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Ecological risk assessment aims to characterise the adverse impacts of a single or multiple stressors on living organisms, populations and ecosystems. Two approaches have been recognized as powerful tools in assisting ecological risk assessors: Adverse Outcome Pathways (AOPs) and Dynamic Energy Budget (DEB) models. AOPs describe conceptual links between measurable molecular, cellular, or organ-level events that lead to an adverse effect relevant in risk assessment, but only few studies provide quantitative links to individual performance metrics and none goes beyond the individual level. DEB theory, however, is a consistent quantitative framework that captures the metabolic dynamics of an organism through its entire life cycle and provides the link effects on individuals to those at the population and ecosystem levels. Quantitative AOPs linked to DEB models are better equipped to improve ecological risk assessment. Quantitative AOPs have been developed to simulate the endocrine regulation of fish vitellogenin and egg production but these models do not consider the entire energetic budget of an organism. In DEB framework, an organism allocates energy to a reproduction buffer that can be potentially converted to eggs. The strategies of handling the buffer are species-specific and are not explicitly specified. In this study we demonstrate how to link the mechanistic models of the hypothalmus-pituitary-gonadal (HPG) axis that simulate vitellogenesis to a DEB model. We simplify the HPG axis to include a forcing function, a regulator (estradiol-17β), an activator (estrogen receptor) and an active-regulator (estradiol-17β – estrogen receptor complex). The output of this module, the rate of vitellogenin secretion, serves as the link with the DEB model. The incorporation of the reproductive hormone module into the DEB model is achieved through the concept of synthesizing units. We parameterize the model using published data on rainbow trout and simulate scenarios of endocrine disruption under multiple stressor situations.

Keywords: Adverse Outcome Pathways, Dynamic Energy Budget theory, Suborganismal processes, Rainbow trout.

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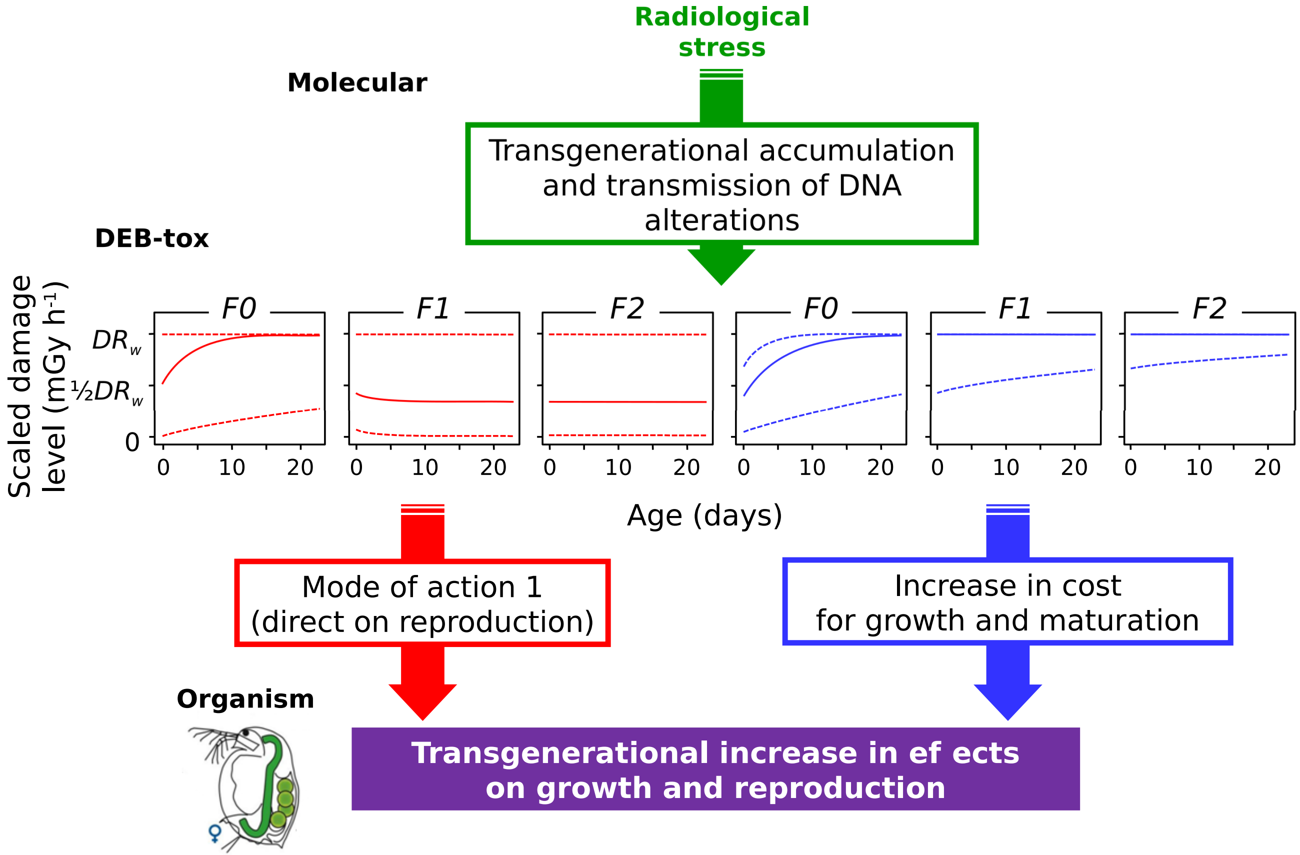

Radiological stress

Molecular

Transgenerational accumulation and transmission of DNA alterations

DEB-tox

Mode of action 1 (direct on reproduction)

Increase in cost for growth and maturation

Organism

Transgenerational increase in effects on growth and reproduction

Molecular and metabolic mechanisms of transgenerational effects in *Daphnia* exposed to radionuclides

Fréderic Alonzo * [1], Marie Trijau [1], Elise Billoir [2]

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Understanding how radioactive contaminants affect wildlife species at every level of biological organization is a major challenge in radioecology. Mechanistic links among observed effects are necessary to predict consequences for survival, growth and reproduction which are critical for population dynamics. With its short life cycle, the cladoceran *Daphnia magna* is particularly suitable to address toxicity over several generations, on a much more relevant time scale to natural biota. Multigenerational toxicity tests were conducted with depleted uranium (U), americium-241 (Am-241) and cesium-137 (Cs-137), inducing respectively a chemical toxicity, an internal alpha radiotoxicity and an external gamma radiotoxicity. Experimental results showed in all cases that toxic effects on survival, body size, fecundity increased in severity across generations, demonstrating that measured effects in one generation might not be representative of toxicity in offspring generations, and ultimately of population response. Reduction in body size and fecundity induced by depleted U, Cs-137 and Am-241 were analyzed using DEBtox models with respectively internal concentration, external gamma dose rate and internal alpha dose rate as dose metrics. For each radionuclide, a combination of several modes of action was necessary to explain observed effects. A damage compartment with hereditary damage level was introduced in order to explore possible modes of action associated with the increase in toxicity across generations. Modelling was performed using a Bayesian framework, in order to quantify uncertainty in parameter estimations and model predictions. Studies of DNA alterations, using a qPCR technique, confirmed that molecular damage was accumulated in daphnids exposed to depleted U and Cs-137 and transmitted to their progeny, as a possible underlying mechanism causing the increase in effect severity over generations. Further studies of DNA methylation recently investigated the role of epigenetic processes in the transmission of effects from parents exposed to Cs-137 to their unexposed progeny.

Keywords: *Daphnia*, Radionuclides, Toxicity, Multigeneration.

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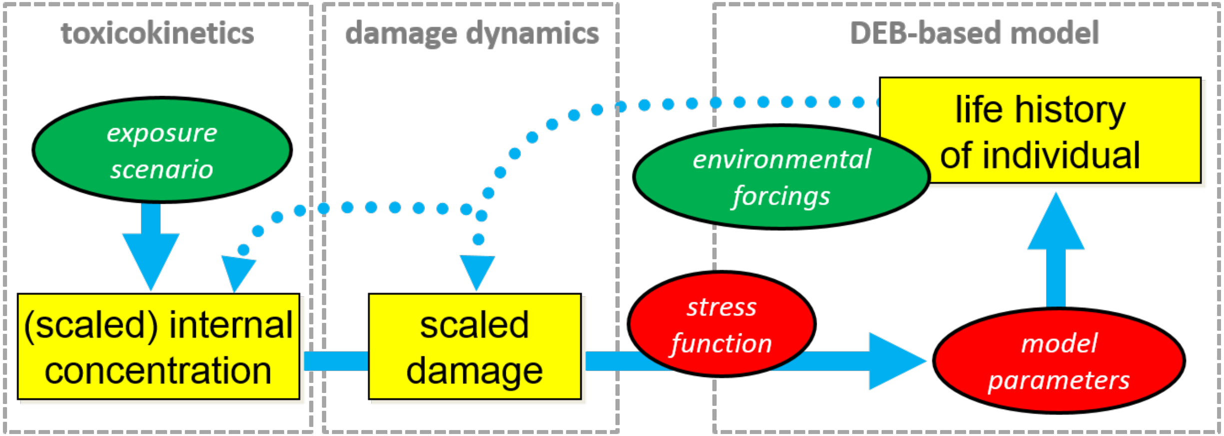
[*] Speaker

Symposium program



A roadmap for establishing DEBtox in environmental risk assessment practice

Tjalling Jager *[1]

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Most frameworks for chemical risk assessment work on the principle of comparing the results from an exposure assessment (what are organisms exposed to) and an effect assessment (the relationship between exposure and toxic effects). Exposure assessment is dominated by mechanistic fate models, but effects assessment currently still relies heavily on crude descriptive methods. The last decade has witnessed a rapidly increasing interest in mechanistic effect models, culminating in 2018 in a dedicated EFSA opinion on toxicokinetic-toxicodynamic (TKTD) models for pesticide risk assessment. For animals, this opinion focussed on GUTS for survival modelling and DEBtox for sub-lethal effects (DEBtox here as in: DEB-based models used to analyse/predict toxic effects on sub-lethal life-history traits). GUTS was judged ”ready to be used in risk assessment” by EFSA; DEBtox was judged to have ”great potential” but ”currently limited to research applications.” Clearly, GUTS has a number of advantages over DEBtox when it comes to risk assessment, most specifically its simplicity, its ability to work with standard toxicity data, an easy-to-interpret and irreversible endpoint (death), and a large number of case studies with pesticides and aquatic organisms. In the next few years, GUTS will act as a trailblazer for DEBtox in pesticide risk assessment, familiarising all stakeholders with basic TKTD modelling. It is highly likely that this process will lead to an increasing demand for similar approaches to deal with sub-lethal effects. However, to facilitate the uptake of any DEBtox model into risk assessment practice, we need to address the issues that are currently hampering it. In this contribution, I will present my analysis of the issue and suggest ways forward.

Keywords: DEBtox, toxicity, ecotoxicology, risk assessment.

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*Speaker

Symposium program

Ready-to-use modelling and statistical tools for advanced environmental risk assessment

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Among the consequences of the development of our societies, chemical pollutants and their impacts on living organisms have become a priority issue for regulatory agencies with guidelines reinforcing the requirements for the approval of active substances. Before any decision, information must be collected on their physico-chemical properties, toxicity and ecotoxicity, and the associated risks must be assessed. In this perspective, many toxicity tests are carried out within laboratories, according to standardized protocols whose data are then analyzed by appropriate and reliable mathematical models and statistical inference methods. Classical outputs are critical effect concentrations for the biological traits of interest, that may be obtained by fitting an exposure-response/effect model. Such a model consists of a deterministic part describing the mean tendency of the data, and a stochastic part depending on the type of the data (namely, binary, count or continuous data). Choosing the most appropriate model may thus appear awkward, but can be supported by ready-to-use tools. Such tools should be specifically designed for ecotoxicologists and risk assessors, in order to help them in performing statistical analyses of standardized toxicity test data, in a user-friendly way, with a freely available graphical web interface and without requiring to invest in the underlying statistics and computer technologies. Faced with this statement, our team developed several ready-to-use tools offering a collection of services for statistical inference and mathematical simulations applied to ecotoxicology. This presentation gives an overview of these tools: (1) the R-package 'morse' gathering together exposure-response/effect models that can be easily fitted to standard toxicity test data within a Bayesian framework; (2) the web-platform MOSAIC, in particular its GUTS module (*General Unified Threshold model of Survival*) allowing to fit toxicokinetic-toxicodynamic (TKTD) models like GUTS directly online; (3) the GUTS Shiny application to simulate GUTS models online under exposure concentration profiles varying over time.

Keywords: User, Friendly software, Dose response models, TKTD models, GUT.

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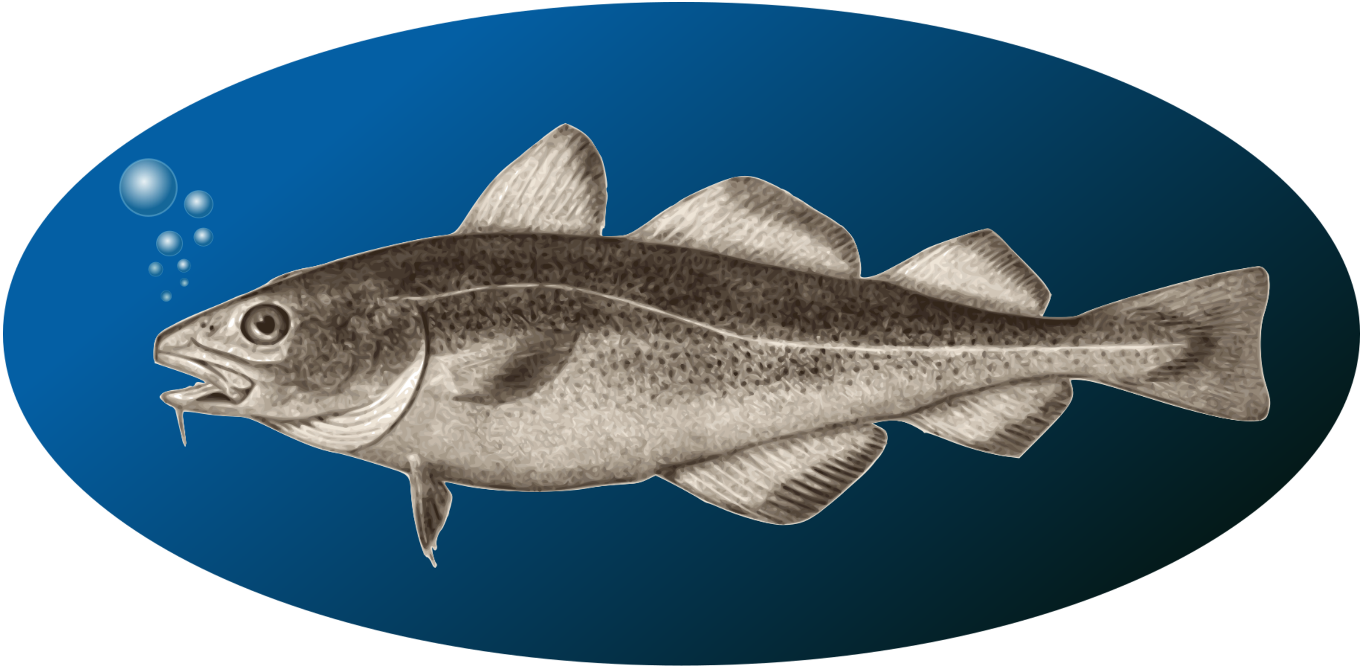
[*] Speaker

Symposium program



Modeling the impact of hypoxia on the energy budget of Atlantic cod in two populations of the Gulf of Saint-Lawrence, Canada

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Like many marine species around the globe, several stocks of Atlantic cod (*Gadus morhua*) live in increasingly hypoxic waters. In the Gulf of Saint Lawrence (GSL) in Canada, the deep channels traversing the semi-enclosed sea exhibit year-round hypoxia, identified as one of the limiting factor for the recovery of GSL cod in its northern part. While many individuals in the northern GSL are known to venture in deeper, warmer, and more hypoxic waters of the Gulf channels, those in the southern GSL live in a shallower, colder, and more oxygenated environment. In this study, we use the modeling framework of the Dynamic Energy Budget (DEB) theory to disentangle the effects of hypoxia, temperature and food on the life-history traits of these two populations of cod in the GSL. Following recent advances by Thomas et al. (2018) on the mechanisms for the effects of hypoxia within the context of DEB theory, we implemented a correction of ingestion depending on dissolved oxygen (DO) saturation. We successfully developed and validated a set of parameters for a GSL Atlantic cod DEB model. Using simulations of historical growth trajectories from 1990 until 2004 estimated from data collected through fisheries research surveys, we found that temperature explained about half (48%) of the difference in length and 59% of the difference in mass between the two populations. The remaining proportion was attributed to exposure to hypoxia and food input. We also used our model to explore scenarios of duration, frequency, and intensity of hypoxia on cod's life-history traits, which showed that decreasing DO linearly reduces growth and reproduction while young cod seem to avoid impairing conditions resulting in limiting effects on developmental stages.

Keywords: Hypoxia, Temperature, Atlantic cod, Growth, Gulf of Saint Lawrence.

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*Speaker

Milky water event in Paracas bay, Peru.

Predicting the energy budget of the scallop *Argopecten purpuratus* in an oxygen–limiting environment

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Low concentrations of oxygen determine marine species distribution and abundance along the Peruvian coast with consequences for human activity such as fishing and aquaculture. In order to assess bioenergetic consequences of oxygen limitation on the Peruvian scallop *Argopecten purpuratus*, we first developed a Dynamic Energy Budget (DEB) model of growth and reproduction calibrated on field experimental datasets. Then, we included oxygen availability as an additional forcing variable using a simple rule based on the ability of the scallop to regulate oxygen consumption. The resulting model was tested using growth/reproduction monitoring and simultaneous high frequency environmental records in Paracas Bay (Peru) at two different depths: suspended in the water column and on the sea bottom. Simulations indicated that scallops' growth and reproduction was not food-limited. The negative observed effects of hypoxia on growth and reproduction could be explained by a decrease in both assimilation and reserve mobilization. However, hypoxic conditions in summer were not sufficient to explain the observed losses in somatic tissue weights and the disruption of reproduction. The latter two patterns were better simulated when assuming increased somatic maintenance costs due to the presence of H_2S during milky turquoise water discolouration events observed during summer.

Keywords: DEB theory, Bioenergetics, Hypoxia, Hydrogen sulfide, Growth, Reproduction, Peru.

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Metabolic scaling of response to toxic stress

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Stressed organisms maintain homeostasis by activating mitigative metabolic processes such as cellular repair and scavenging of Reactive Oxygen Species (ROS). These require materials and energy, which can only be achieved by diverting energy from other metabolic processes. Therefore (i) all (ROS-mediated) stress has an effect, and (ii) as materials and energy devoted to mitigation become significant, at least some metabolic processes become noticeably reduced. Given that available energy is finite, as stress increases mitigation costs reach a point where no additional energy can be spared for mitigation; plasticity of the energy budget, therefore, limits the extent of the mitigative responses. If damage creation is faster than damage repair, damage accumulates. The accumulated damage reduces efficiency of metabolic processes, thus creating a positive feedback of damage on damage creation, and – for an exposure above some critical level or ”tipping point” - a runaway spiral leading to ever-increasing effects of stress.

We investigate the extent to which the energy budget can adjust to meet the requirements of stress mitigation varies with basal metabolism. We create a simple toxicokinetc-toxicodynamic model that accounts for basic processes involved in toxicity: bioconcentration, damage creation by metabolism and the bioconcentrated toxicant, and damage repair. The resulting model predicts scaling of the critical exposure with body weight.

To test the prediction, we used 50% mortality (LC50) due to copper exposure as the measure of the critical exposure, and weight of grown organisms as the measure of metabolism. Preliminary results suggest that, in agreement with theoretical predictions, the slope is negative for algae and ciliates, both of which can reasonably be described as V1-morphs. Larger organisms (fish, crab, mussels, copepods, etc) do not show a clear trend. We discuss reasons for the patterns, and suggest new approaches to interpretation of species sensitivity distributions.

Keywords: Stress, Toxicants, Metabolism, Damage, ROS, Scaling.

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[*] Speaker

Symposium program

Effect of ocean acidification on mussel growth: application of a DEB model to green-lipped mussel *Perna canaliculus*

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The effect of ocean acidification (OA) on shellfish species are of a special concern as they are very important in both ecological and economical terms. The green-lipped mussel (*Perna canaliculus*) is the most important bivalve in aquaculture in New Zealand. The mussels may be particularly sensitive to the increase of OA. The mussel industry has recently experienced major spat failures and slower growth rates with socio-economic repercussions, which would be exacerbated by OA. To investigate effect of OA on growth of green-lipped mussel, we have conducted growth experiments in the laboratory. These mussels were exposed to two levels of CO_2 concentrations (400 and 1,100 µatm). The results show significant reductions in shell length and flesh weight growth, decrease in feeding rate and increase in the respiration rate at increased CO_2 level. These changes were interpreted using a DEB model and the decline in growth rate was a result of decrease in assimilation, increase in specific costs for structure and maintenance. The effect is also reflected by the decrease in energy conductance and change of energy allocation. After the parameterisation of a DEB model for the mussel with the experimental data, the model was used to simulate the growth and reproduction of the mussel at various OA levels. This study aimed to provide scientific information for mitigation of the OA impact in mussel aquaculture.

Keywords: Green–lipped mussel, DEB parameters, Ocean acidification.

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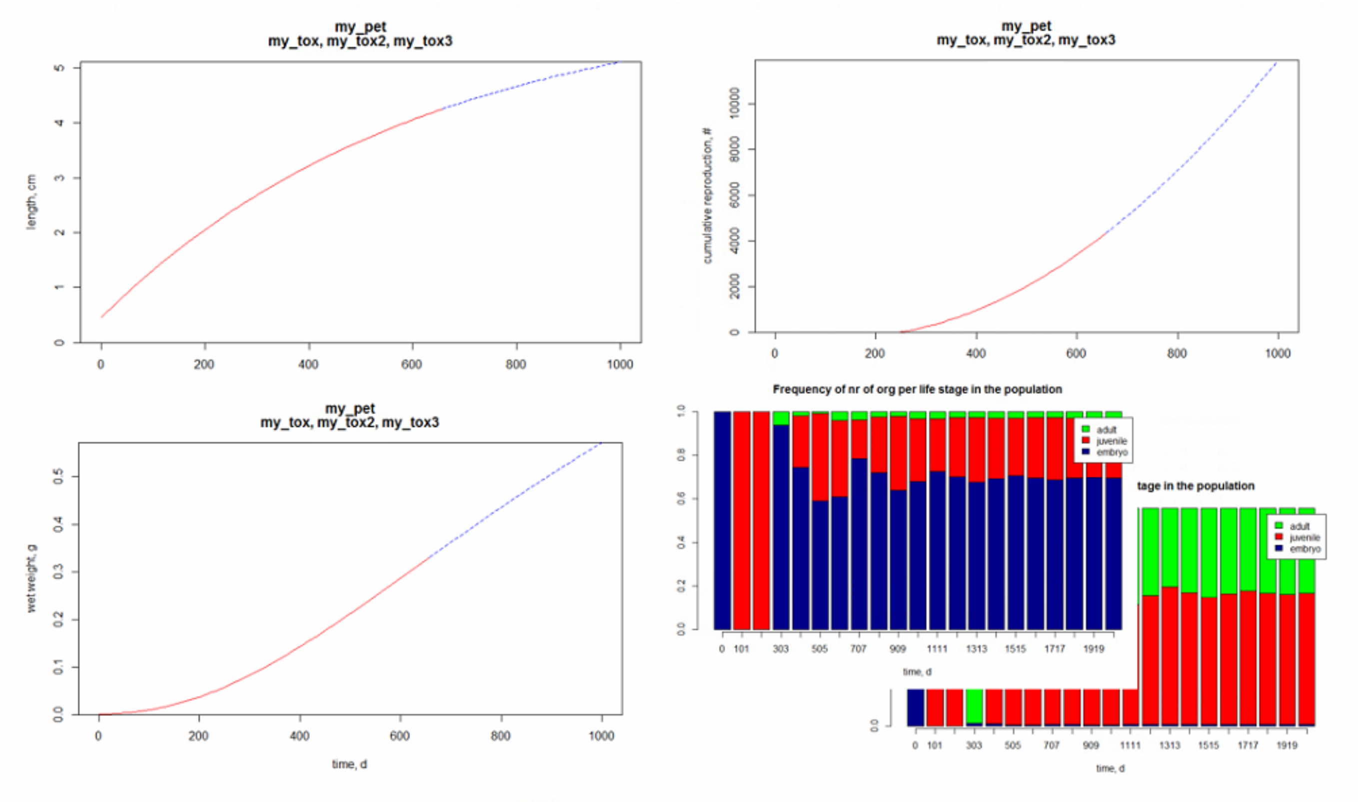
Symposium program



A generic open source Dynamic Energy Budget model for aquatic and terrestrial organisms to predict toxic effects on the life-cycle on individuals

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Dynamic Energy Budget (DEB) models have been demonstrated to be applicable for interpreting ecotoxicological effects in terms of effects on physiological processes in a variety of taxa. However, the development of DEB models for different species involves solving differential equations, implementing them into software, and parameterizing the models is not always straightforward. In this context, OpenDEBtox, a generic toxico-kinetic/toxico-dynamic (TK-TD) modelling framework based on DEB theory, has been developed in the R freeware for lethal and sub-lethal effects of chemicals and is available open source on EFSA's Knowledge junction. OpenDEBtox allows great flexibility to simulate and predict effects of single chemicals and mixtures on growth, reproduction and survival for individuals of different species. OpenDEBtox needs two types of input: 1) species specific DEB parameters describing the lifecycle of the organism 2) parameters describing the effect of the toxicant (DEBMoA and toxicity parameters). The first can be taken from the Add-my-Pet database and the latter can be taken from the purpose built DEBecotox database, which contains a summary of all available DEB-based studies in the open literature. The different DEBMoA have distinct effects on the life cycle traits of an individual organism, affecting growth and reproduction in different ways. The separation of TK and TD processes provides a tool to quantify interspecies differences, thus providing a basis for predictive modelling across taxa and chemical space. As such, OpenDEBtox can be extended to modelling the impact of non-chemical stressors including limitation of food sources, temperature or combinations of multiple stressors. This is important to investigate combined effects for which very little data are available and a general framework for data interpretation is currently lacking. OpenDEBtox not only produces predictions at the individual level, but also predicts simple population endpoints such as growth rate and population profiles in terms of number and mass.

Keywords: DEB, Ecotoxicology, DEBMoA, Mixtures.

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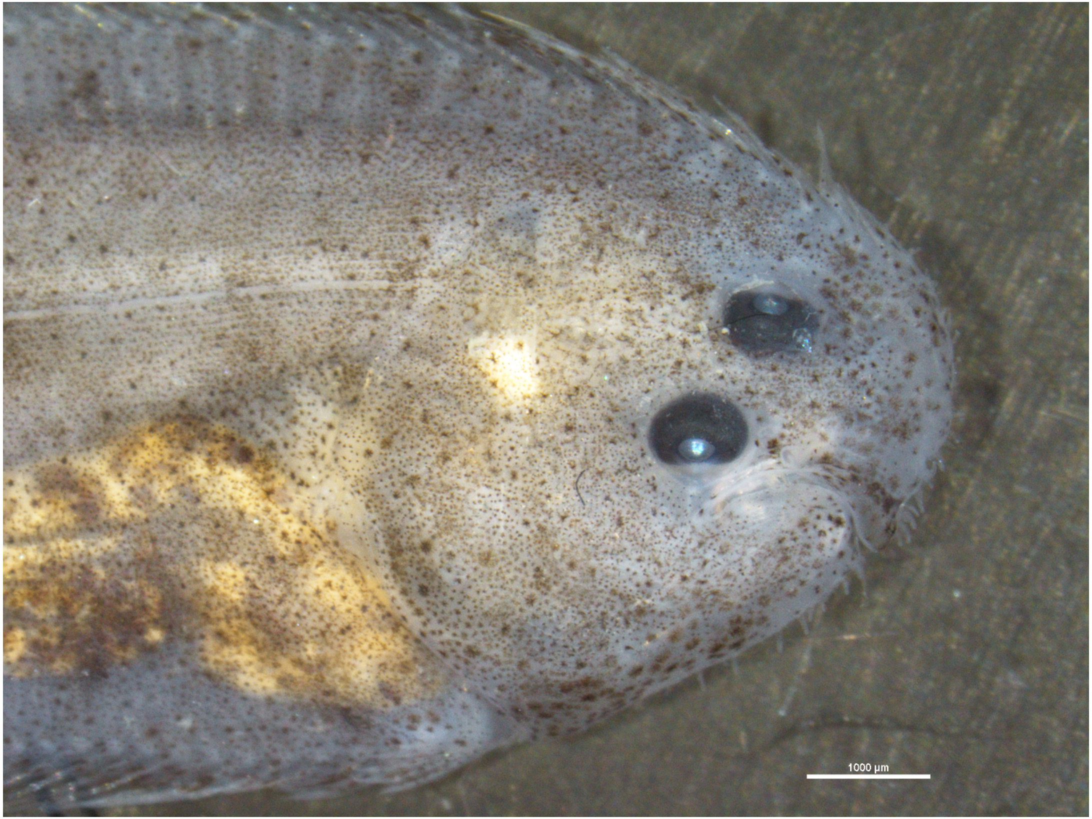
[*] Speaker



Juvenile common sole (*Solea solea*).

Sensitivity of POPs bioaccumulation to Global Change factors. Application of an original DEB-TK approach to the Gironde estuary common sole *Solea solea*

Florence Mounier * [1], Véronique Loizeau [2], Laure Pecquerie [3], Hilaire Drouineau [1], Pierre Labadie [4], Hélène Budzinski [4], Mathilde Lauzent [4], Gabriel Munoz [4], Jérémy Lobry [1]

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Estuarine nursery grounds are essential transitory key habitats for various fish species. However, these areas are particularly impacted by all the components of Global Change. In particular, contamination by Persistent Organic Pollutants (POPs) significantly impacts the functionality of nursery areas affecting growth and condition of juvenile fish. To study adverse effects of chemical pressure on ecosystems, a comprehensive knowledge of bioaccumulation mechanisms of pollutants in biota may be a prerequisite to predict internal concentrations under natural fluctuating conditions in growing individuals. In that way, we developed a toxicokinetic (TK) model whose uptake and elimination fluxes depend on biological traits dynamics (notably food ingestion and growth). To be able to predict these biological traits in dynamic environmental conditions (concerning particularly food quality, food availability and temperature) we used a mechanistic bioenergetic model based on the DEB theory. First, we implemented this TK model to describe CB153 and L-PFOS (2 representative compounds of 2 different POPs families) bioaccumulation in the juvenile sole, considered as a key species for assessing nursery function in western European coasts. Then, a global sensitivity analysis highlighted that beyond the impact of TK parameters values (Assimilation Efficiency and Elimination rate) on estimates of internal concentrations at maturity, diet composition and prey contamination have a major role in POPs bioaccumulation in the Gironde estuary (the largest estuary in Western Europe), far ahead of temperature, birth date, food availability and quality. Finally, we compared model predictions of fish contamination in CB153 and L-PFOS to measurements in juvenile sole from the Gironde estuary to assess realism of environmental and TK parameters used in simulations and we concluded on the most plausible values of TK parameters in a natural environment.

Keywords: Toxicokinetic models, Global change, Sensitivity analysis, *Solea solea*, PCBs, PFASs.

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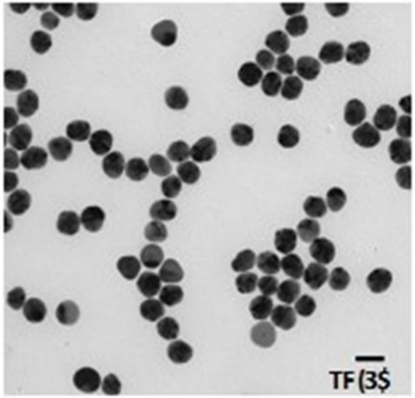
[*] Speaker

10 um diameter

40 nm diameter



DEB, Nanotoxicology and Adverse Outcome Pathways

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For over a decade the use of engineered nanomaterials (NMs) has increased steadily, raising concerns about ecological impacts. We review experience gained from 10 years of research (2008-2018) using DEB models within the program of the University of California Center for Environmental Implications of Nanotechnology (UC CEIN). Study organisms included bacteria, freshwater and marine phytoplankton, invertebrates, fish and plants. NMs were predominantly metal or metal oxides.
DEB modeling featured as one of CEIN's approaches because of the potential for linking processes at different levels of organization. This is particularly challenging with NMs because: (i) data on toxicity mechanisms commonly originate in high throughput or high content studies of subcellular processes, and (ii) the interaction of NMs with physico-chemical environment is very dynamic. We illustrate these from work on phytoplankton. A DEB model relates changes in photosynthetic efficiency (from high content experiments) to population growth rate in two marine species exposed to metal oxide NMs. Batch culture experiments with a freshwater species identify an important toxicity mitigating mechanism involving interaction of a metabolic product (dissolved organic carbon - DOC) with silver NMs in the environment – modeled by coupling a DEB module to a module describing chemical kinetics in the environment. The generality of this mechanism was shown in subsequent studies of remediation of cadmium toxicity by sulfidized nano-iron, where the presence of DOC greatly increased the potential for remediation.
The research had wider implications. A DEB-inspired model of damage dynamics influenced the development by a NIMBioS working group of new formalism that integrates two approaches to ecotoxicity: ”top-down” DEB models focusing on the organism and ”bottom-up” Adverse Outcome Pathways (AOPs) describing key events at molecular level that cause damage. This methodology is being used to relate DEB processes to metabolomic signatures from phytoplankton exposed to copper NMs and dissolved copper.

Keywords: Ecotoxicology, Nanotechnology, Adverse Outcome Pathway, Damage.

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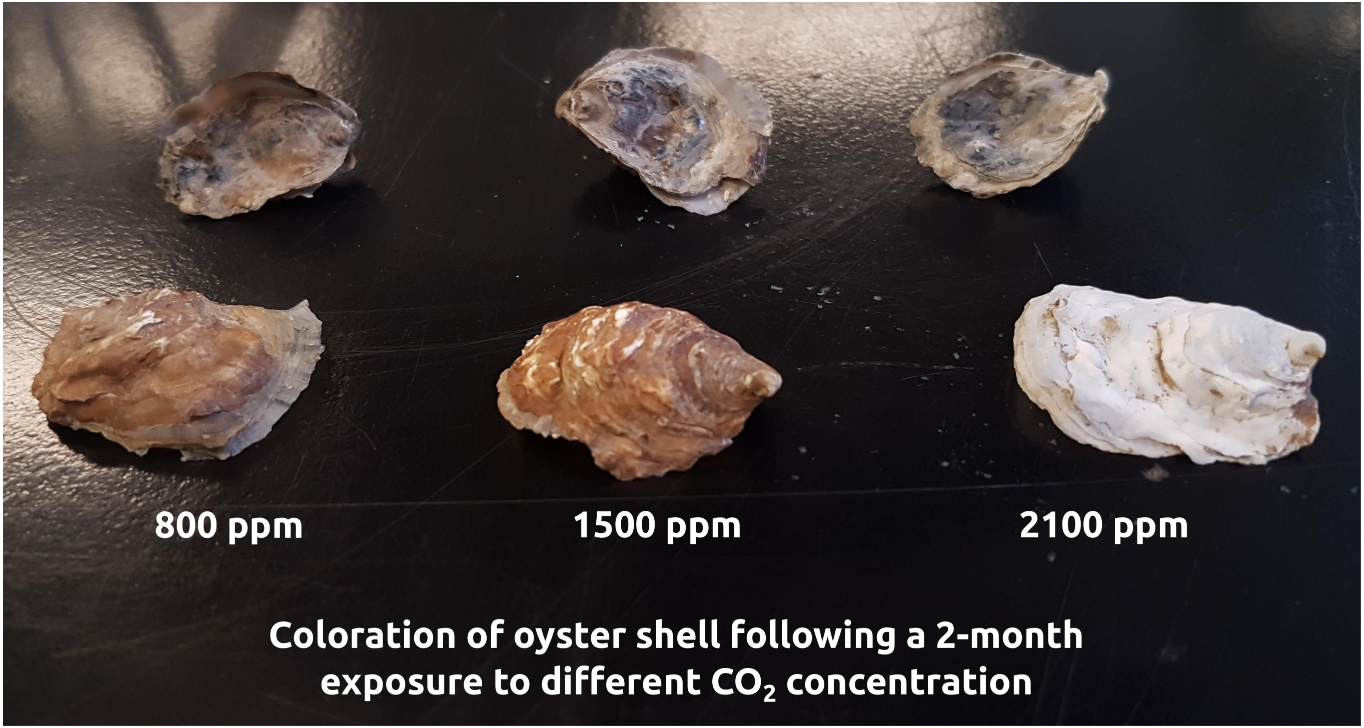
*Speaker



Coloration of oyster shell following a 2-month exposure to different CO_2 concentration

Studying costal acidification effect on the Eastern oyster, *Crassostrea virginica*, through two individual based models

Emilien Pousse *[1], Daphne Munroe [2], John Klinck [3], Eileen Hofmann [3], Dylan Redman [1], Mark Dixon [1], Melissa Krisak [1], Erin Cuyler [1], Matthew Poach [1], Gary Wikfors [1], Shannon Meseck [1]

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Global carbon dioxide emissions have significantly increased since the 1900. The ocean absorbs one third of the CO2 emitted, resulting in the ocean becoming more acidic. Coastal ecosystems, where high nutrient levels and rapid growth of plankton further reduce pH are especially vulnerable to waters acidification. Facing abnormal CO2 levels, marine organisms may expend more energy to regulate their body chemistry and to build and maintain shells. The Eastern oyster (*Crassostrea virginica*), an economically important bivalve in the United States, is particularly sensitive to ocean acidification (OA) with lower growth and effects on physiological rates. The effect of OA on the eastern oysters bioenergetics, was explored through laboratory experiment and two models; Dynamic Energy Budget (DEB) and individual based model described by Hoffman et al., 2006. DEB model has been widely applied on bivalves and has allowed to deal with the effect of physical parameters on physiological rates and maintenance costs. Hoffman's model relies on a net production corresponding to the energetic balance between assimilation and respiration, and a growth possible only when the length/weight relationship of a given individual is superior to the mean for this species. Both models will be compared on the basis of their ability to reproduce oyster growth by taking into account effect of CO2 concentration on physiological rates and maintenance costs. To calibrate both models a 10-week experiment where 900 oysters were exposed to different CO2 levels (2100, 1500, 800 ppm) was carried out. Half of the oysters was unfed, while the other half was exposed to natural seawater. Each two weeks 180 individuals were sampled for growth and weight. On weeks 2, 4, 8 and 10, respiration rates were measured in 7 individuals per condition. Feeding rates were also obtained in 8 individuals through a method based on biodeposits analysis.

Keywords: Eastern oyster, Ocean acidification, Carbon dioxide, Individual based models.

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Symposium program

Investigating the response of the krill *Nyctiphanes australis* (Euphausiacea) to stress caused by environmental change: a dynamic energy budget approach

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Ocean warming and increases in ultraviolet radiation (UVR) over the past century have resulted in important changes in marine plankton communities, including reductions in pelagic primary productivity. To examine the potential effects on secondary production, we utilized adults of Nyctiphanes australis as a model species to understand how the physiology and energy utilization of zooplankton might respond to changes in temperature and elevated UVR under a Dynamic energy budget (DEB) framework.

To assess and predict the effects of climate change on marine ecosystems, a comprehensive knowledge of the physiological costs of stress on key species such as krill is needed. To this end, we quantified changes in oxidative stress, pigments content, feeding rates and respirometry rates, lipids and amino acids content of animals exposed simultaneously to several doses of UVR and temperatures, following the natural fluctuation dynamics found during months of summer and winter. The obtained data was used to parameterize a standard DEB model in complement with zero- and uni-variate data available in the literature. Here we predict how krill may respond to environmental changes such as altered growth, reproductive output and energy utilization with the finality to identify environmental thresholds of such change.

Preliminary analysis of the DEB model suggested that growth and the effect of different diets were adequately predicted. However, reconstructions of energy balance and respiration rates were still slightly underestimated, especially at intermediate ranges of temperature and UVR doses. Nonetheless, in general terms, the results suggested overall robustness of the DEB model and supported the applicability of the model to predict physiological stress under variable environmental conditions.

Keywords: Krill, Secondary Production, Energy balance.

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[*] Speaker

Session 4 : Populations and ecosystems in a changing climate

Conveners: Cédric Bacher and Yoann Thomas.

Climate change is likely to affect the spatial distribution of a number of species. In the framework of niche theory, species distribution models have been developing using correlative and static approaches based on the primary effect of abiotic factors. On the other hand, models of trophic networks have shown that biotic interactions are key drivers of the response of species or trophic groups to environmental changes. However, in spite of the increasing number of applications of DEB theory, only a few examples illustrate the possibility to assess population changes at the ecosystem scale. Upscaling from individuals to populations and ecosystems poses a number of challenges that we will address and discuss in this session, e.g., how individual variability (including adaptation through natural selection) and environmental variability affect population response; how to represent the interactions between multiple species; how connectivity, habitat and biotic interactions shape species distribution in a changing environment.

Keynote 3: When do the details matter? DEB as an integrator of environmental variability multiple stressors and time history effects

Brian Helmuth *

Professor at Marine Science Center, Northeastern University, Boston, USA
Marine Ecological Forecasting, Ecophysiology, and Physical Biology

My research explores the effects of climate and climate change on the physiology and ecology of coastal marine organisms. Specifically, I use thermal engineering techniques, including a combination of field work, remote sensing and mathematical modeling, to explore the ways in which the environment determines the body temperatures of coastal marine animals such as mussels and seastars. Combined with energetics models and measurements of physiological performance, this approach provides a quantitative method of mapping patterns of growth, reproduction, and survival in economically and ecologically important coastal species. My most current research explores the role that environmental heterogeneity in space and time plays in driving "rescue effects" following extreme events, and explores the idea that climate refugia at very small scales may ultimately contribute to much larger-scale, biogeographic patterns. A major goal of these approaches is to inform decision makers with scientifically accurate and useful forecasts, and my lab group also examines cutting-edge methods of communicating science and climate adaptation strategies, for example using virtual reality methods.

Keywords: Climate change, Digital elevation models, Ecophysiology, Heat budget, Intertidal zone, Scale.

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*Speaker

Symposium program

Inferring the responses of Southern Ocean benthic species to environmental changes using Dynamic Energy Budget models

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The Southern Ocean is facing rapid environmental shifts related to global climate change. This central issue is currently the focus of an intense research effort to understand and characterize the response of marine benthic species and populations.
Our knowledge of the impact of environmental changes on Antarctic species physiology has mostly been studied using short-term experimental designs constrained by strong financial and technical limitations. The use of dynamic models such as the Dynamic Energy Budget (DEB), which study the relationship between species functional traits and environmental characteristics helps to spatially interpolate the results of these experiments. DEB models describe a part of the species fundamental niche using simple observations from species life cycle that can be extracted from the literature. The sensitivity of the species to changes occurring in their surrounding environment can also be simulated.
In this study, we calibrated a DEB model for several common and abundant benthic species of the Southern Ocean presenting contrasting feeding diets and ecological niches width (i.e. the sea urchin *Sterechinus neumayeri*, the sea star *Odontaster validus*, the bivalves *Laternula elliptica* and *Adamussium colbecki*, the gastropod *Nacella concinna* and the fish *Trematomus bernacchii*).
We simulated species sensitivity to environmental changes, assessing the impact of changes in temperature and food availability on species metabolic performance (e.g. changes in growth rate, reproductive performance, maximal size and age). The limits and potential of this model developed for Antarctic benthic species are discussed with a special attention devoted to their application to other case studies and the improvement of our understanding of the potential response of Antarctic benthic communities to future environmental changes.

Keywords: Southern Ocean, Marine benthic species, Environmental changes, Metabolic performances.

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Symposium program

Modelling the response of the distribution of benthic marine species to climate change

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In a context of climate change, understanding the response of species to changes in the environment and the implications for their geographic distribution is of paramount importance. Through the formulation of relationships between the organism and its environment, species distribution models (SDM) provide a tool to assess how species distribution would respond to environmental stressors. Our study presents the development and a first application of a mechanistic and generic SDM, using a multi-agent modelling platform: NetLogo. The model simulates the spatial and temporal population dynamics of a marine bentho-pelagic species with an individual-based mechanistic approach of the life cycle. It couples a Dynamic Energy Budget model of the individual life history traits in relation to temperature and food concentration (e.g. phytoplankton), larval dispersal due to currents (oceanographic connectivity) and competition for space at the recruitment phase. The model is applied to the blue mussel *Mytilus edulis* along the coast of Brittany and scenarios of environmental changes target the effect of seawater warming based on the results of a climate model (Representative Concentration Pathway RCP8.5, model CNRM-CM5). We show that oceanographic connectivity drives the population dynamics and local changes are likely to affect distant population structure. Simulations show that seawater warming modifies the demographic structure of *M. edulis* and the phenology of the reproduction but temporal changes are smaller than the differences due to local environmental conditions.

Keywords: Habitat, Connectivity, Biogeography, Phenology, IPCC scenario, Spatial ecology, Individual–based model.

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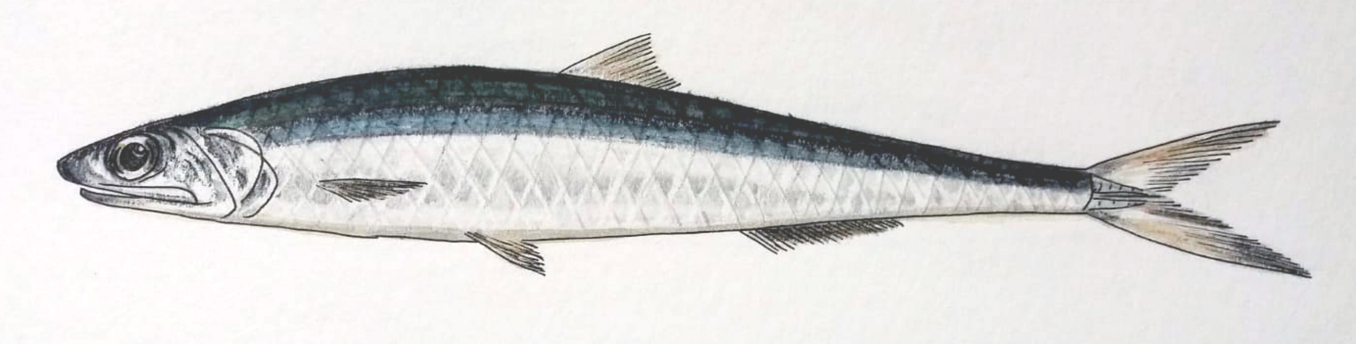
*Speaker



A DEB-IBM approach to understand past variation and projecting anchovy abundance in the Bay of Biscay

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European anchovy populations are strongly related to variations in recruitment and environmental ”bottom-up” forcings. In order to better understand the mechanisms underlying these fluctuations at the individual and population scales, an Individual Based Model was coupled to a Dynamic Energy Budget model, with outputs of the physical-biogeochemical POLCOMS-ERSEM model as driving forcing in the Bay of Biscay. The calibration of the model was done by adjusting some natural mortality parameters and including a density-dependent control of the population through an iterative process, while for validation, the historical age structure and population biomass between 2000 and 2015 in the Bay of Biscay were considered. Fishing mortality in the model was introduced as an external factor with values of instantaneous mortality rates obtained from the stock assessment reports, while different hypothetical fishing scenarios were also considered for comparison. After validation, the model was used to project the evolution of the population along the 21st century. To do that, the POLCOMS-ERSEM model was run forced with IPCC climate scenarios RCP4.5 and RCP8.5 (+2 and +4 °C average temperature increase respectively). Our results show that the collapse of the population occurred in 2005 was caused by a combination of high fishing pressure and environmental features, while lowering the fishing pressure after 2005 was key for the recovery of the population. On the other hand, simulations on future scenarios of climate change show a positive relationship between temperature and population performance, mediated by processes at the individual level favouring larger size of age 1 individuals and higher fecundities. Our model provides important insights on the separated effects of environment and fishing pressures on the population of European anchovy in the Bay of Biscay, capturing also the consequences of these forces at the individual scale.

Keywords: Anchovy, Hindcast, Projection scenarios, Bay of Biscay, Individual based model, Fishing mortality.

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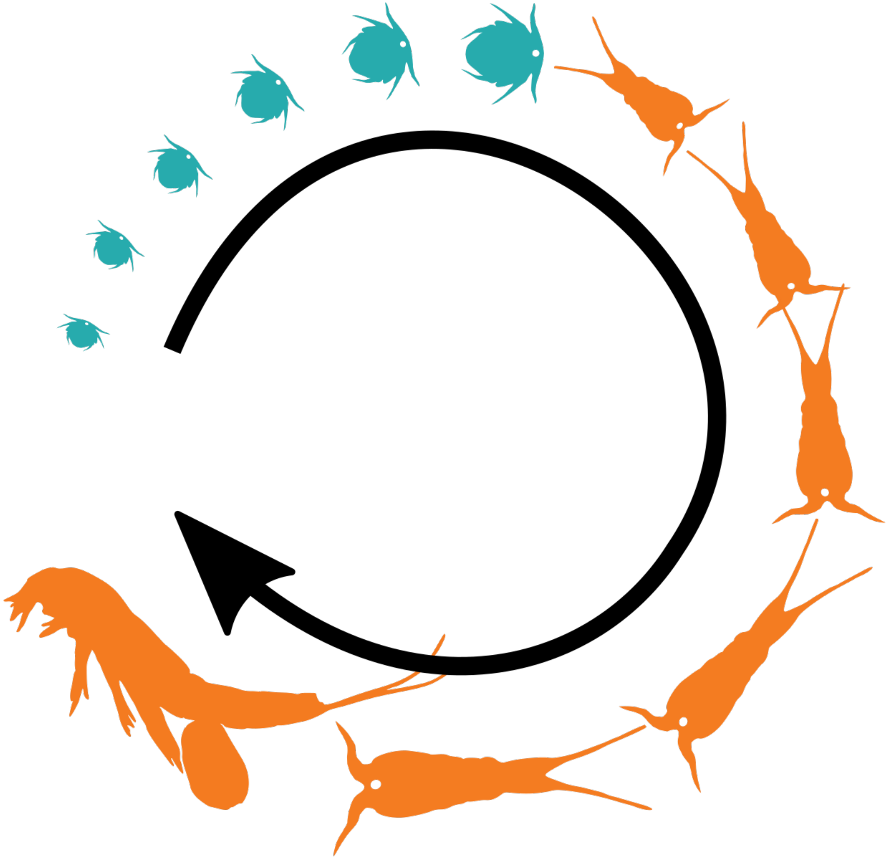
[*] Speaker

Symposium program



Implementing realistic biological variability into an individual-based DEB model for copepods

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One of the biggest advantages of individual-based population models (IBMs) is the possibility to simulate biological variation among individual animals. Inter-individual variation is known to promote the ecological success of populations by making them more resilient to environmental changes and stress events. While inter-individual variation can be measured in virtually all populations, reproducing such variation in population models accurately is not always straightforward. That is mainly because variation can be measured in apical endpoints like development time, size at a certain age or life stage, or reproduction success, but not on the underlying physiological parameters of the organism. In IBMs that make use of the Dynamic Energy Budget (DEB) theory, the development of an organism depends on 12 primary parameters, all of which potentially vary among individuals to some extent. While previous studies included stochastic scatter for individual parameters (one at a time), the degree of variation in this parameter has always been chosen rather arbitrarily. In this study we used experimental data on the development time and brood sizes of the copepod *Nitocra spinipes* reared at control conditions to make realistic estimates of the variability in DEB parameters for this species. As a first step, a global sensitivity analysis was performed to identify the parameters that are linked most closely to the observed endpoints. Subsequently, stochastic scatter was introduced to these parameters by drawing them from a probability distribution (multiple distribution types were tested and compared ranging from uniform to log-normal distributions). The degree of variation per parameter was adjusted by means of an optimisation algorithm that makes use Monte Carlo simulations. The Kolmogorov-Smirnov test statistic was used to assess the difference between measured versus simulated data. A simulated annealing approach was then used to optimise the variation parameters.

Keywords: Copepod, Variability, Variation, Sensitivity analysis, Parameter estimation, Individual–based.

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Integrating macroalgae & wild bivalve populations to improve ecosystem models for a sustainable development of bivalve culture in eutrophic estuarine complexes

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Carrying capacity of coastal systems for bivalve culture has typically been investigated through numerical modeling using Nutrient-Phytoplankton-Zooplankton-Detritus-Shellfish representation. Phytoplankton availability is a key to bivalve production and tightly depends on nutrient cycle within the system. In Malpeque Bay (Prince Edward Island, Canada), previous studies highlighted the need for integrating other components such as macroalgae and wild bivalve populations (Filgueira et al 2014), which modify nutrient availability, in order to reconcile phytoplankton simulations with observations. The impact of blooming macroalgae, particularly significant in eutrophic environments, was integrated to an existing ecosystem carrying capacity model applied in Malpeque Bay. We use the first dynamic energy budget (DEB) model for a macroalgae species, *Ulva lactuca*. Based on the Synthesizing Units concept, it provides a mechanistic implementation of the assimilation of nutrients and energy through photosynthesis. Model development was supported by experimental work to estimate key parameters. Additionally, DEB models for wild bivalve populations of blue mussel, eastern oyster, softshell clam and northern quahog were integrated to the modeling framework. The addition of these new modules increases model veracity and provides new insights into aquaculture-coastal ecosystem interactions, especially in quantifying the influence of species with commercial, recreational and aboriginal value.

Keywords: Green macroalage, Nutrients, Photosynthesis, Synthesizing units, Growth.

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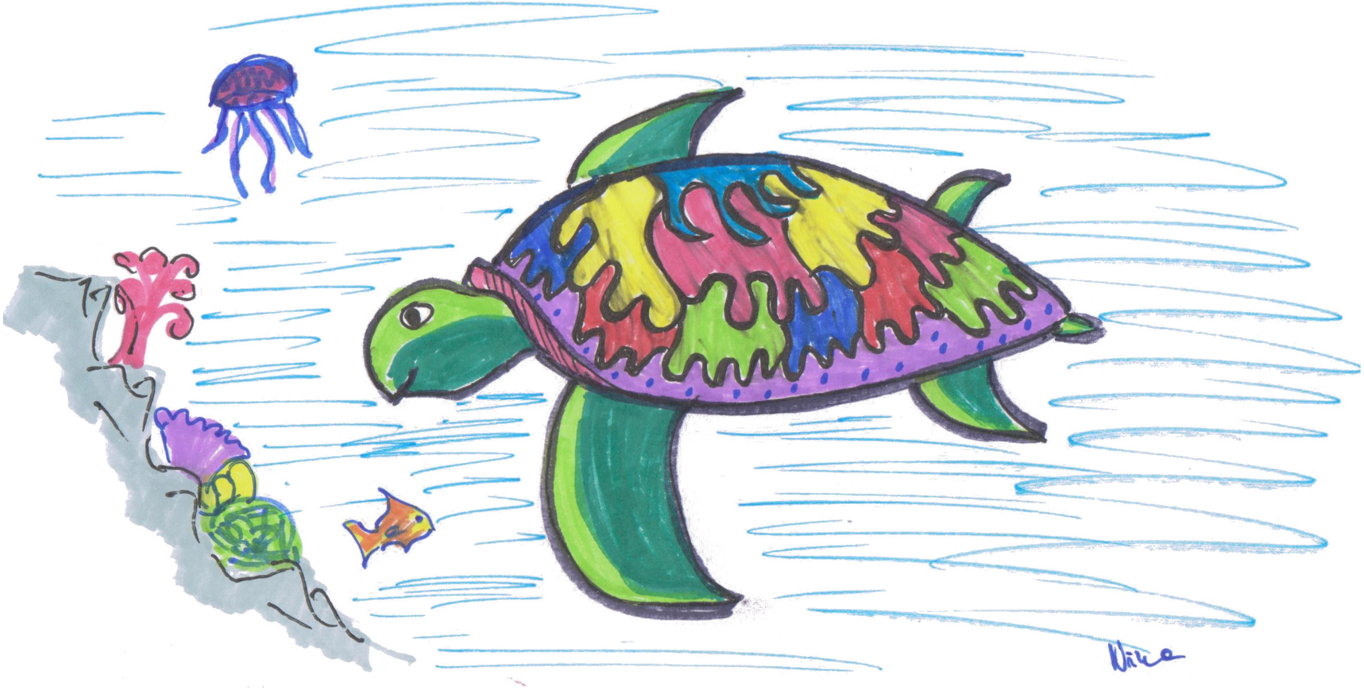

Metabolic and life-history trait responses of sea turtles to environmental cues

Nina Marn *[1,2], Marko Jusup [3,4], Sidonie Cateu [5], Tarzan Legović [1], S.A.L.M. Kooijman [6], Tin Klanjšček [1]

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All seven species of sea turtles are large, long-living, slow maturing, and cold blooded creatures. They have evolved roughly 200 million years ago, and have since changed little compared to their environment. Despite a low probability of being named ”the dynamic group of the year”, sea turtles live an extremely adventurous live. Most species of sea turtles have a benthic and an oceanic life phase, live in the ocean but reproduce on land, and connect two (coastal and open ocean) habitats by migrations sometimes spanning an entire ocean. During their life span, they grow from size of a golf ball to an admirable > 100 kg heavy turtle with a shell larger than a meter, and their life is so perilous that only one in a 100 will live long enough to reproduce. All species of sea turtles are on the IUCN Red list. Despite some recent successes in global conservation efforts, many regional management units of sea turtles are still in decline. Understanding how the environment affects the metabolic responses of turtles can aid our understanding of species, and is important for strategically planning conservation measures. We focused on one of the best studied sea turtle species - loggerhead turtle (*Caretta caretta*) - to study how food availability and temperature affect the energy budget and life history traits of an individual sea turtle. We used the standard DEB model because it reproduces the life cycle of the North Atlantic loggerheads well. We compared the characteristics of North Atlantic and Mediterranean turtles, to deduce which characteristics result from environmental pressures, and which from metabolic adaptations - detected as changes in DEB parameter values. Finally, we zoomed into growth patterns of the turtles, to explore the ways in which the patterns can be reproduced by simulating changes in metabolic and/or environmental characteristics.

Keywords: Sea turtles, Population differences, Standard DEB model, Comparative energetics.

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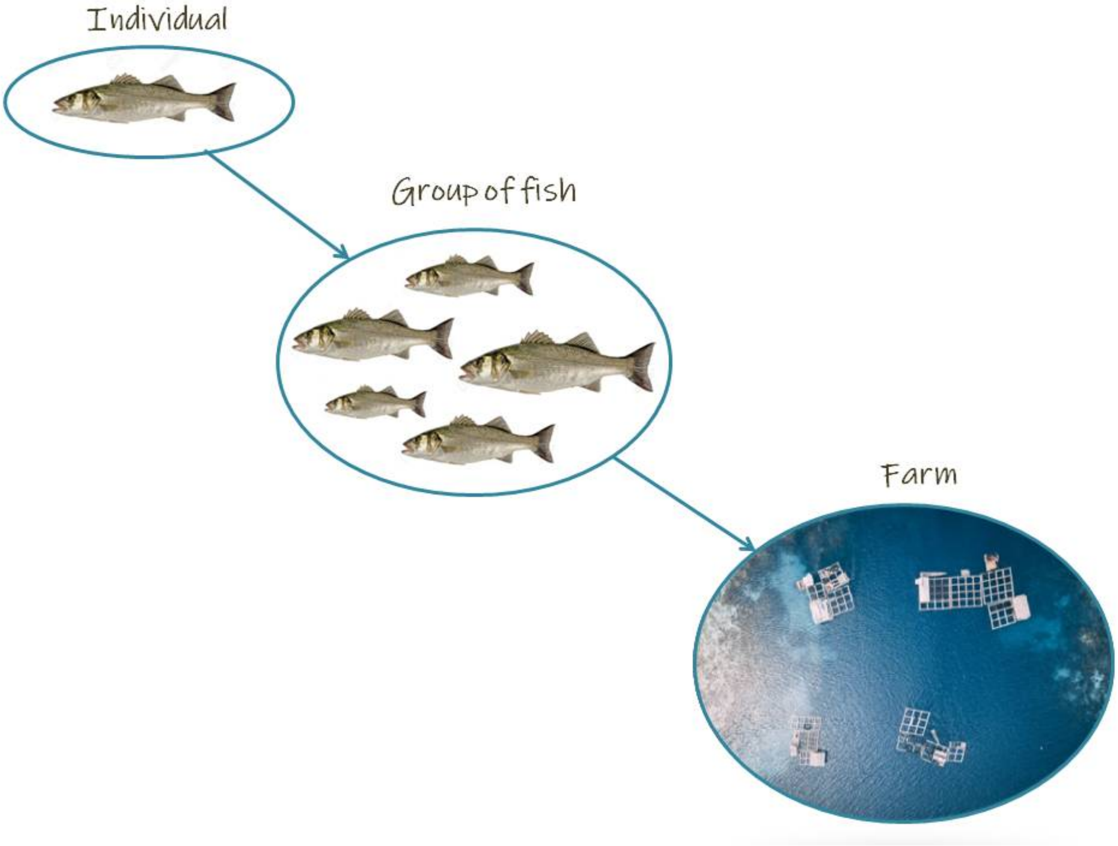
Individual
Group of fish
Farm

Impacts of climate-related drivers on finfish aquaculture

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Impacts of climate change (CC) on marine aquaculture are of an increasing concern. CC is likely to have a significant impact on the biology of aquaculture species and affect the productivity of aquaculture, as future warming is expected for the decades to come. The effects of climate-related drivers such as sea-surface temperature changes and extreme events, like storms and heatwaves, are rarely self-intuitive and, thus, give rise to both future threats and opportunities. Robust forecasting requires accurate predictions of physiological responses to environmental drivers. Dynamic Energy Budget (DEB) theory is a powerful framework capable of linking individual performance to environmental drivers. We parameterized a DEB model for European sea bass (*Dicentrarchus labrax*) using life-history data from published literature and personal observations and tested its validity using growth and feeding data from farms located on sites representatively covering the geographic distribution of the aquaculture activity in Greece. Inter-individual variability of farmed fish was introduced through: 1) an individual initial weight and 2) a factor that acts as an individual-specific multiplier for some of the model parameters and produces scatter in maximum size, and age and size at puberty. We use the model to forecast spatial and temporal implications of CC on fish performance and attributes relevant to aquaculture production for two chosen Intergovernmental Panel on Climate Change (IPCC) scenarios, the most likely and the worst-case scenario. The results are then implemented in a computer-based Decision Support System that simulates and visualizes the impacts of the CC scenarios on biological and economic indicators. The developed tool will ccontribute to the assessment and improvement of aquaculture practices.

Keywords: Climate change, aquaculture, Dynamic Energy Budget theory, European sea bass.

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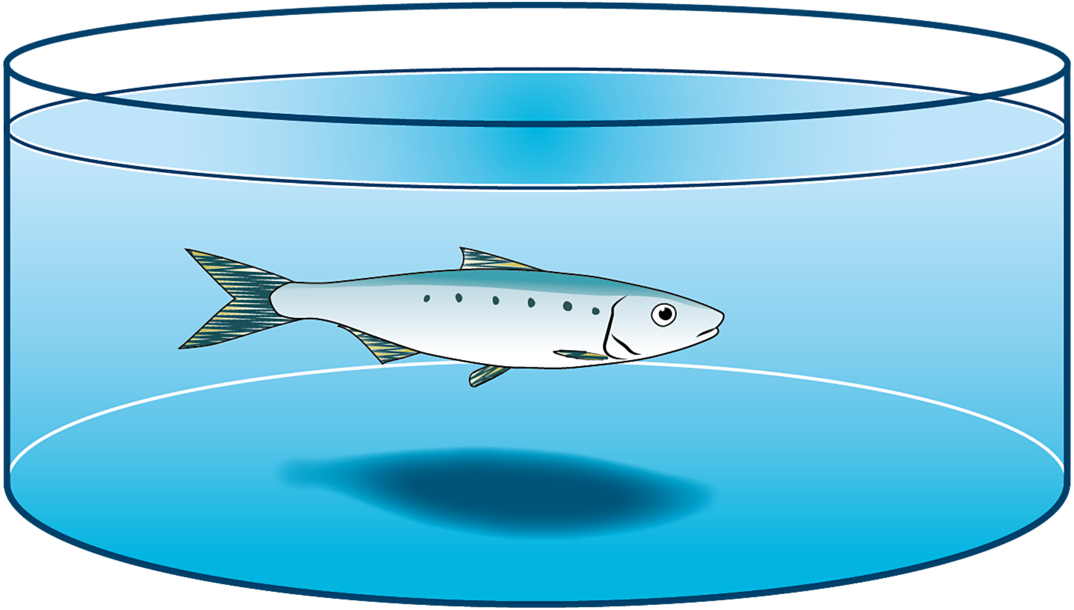
Symposium program



Investigating overmortality of adult sardines in the Gulf of Lions using DEB approach

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The sardine (*Sardina pilchardus*) used to be a major component of the commercial fisheries in NW Mediterranean Sea, but landings have fallen drastically over the last decade due to a marked decline in fish size and condition. Surprisingly, these changes were not explained by changes in recruitment, which remained high, nor related to overfishing, or top-down control by tunas and marine mammals. Rather, a shift in population demography was observed with the disappearance of the oldest individuals (> 2 years), probably resulting from higher adult mortality. It was put forward that these changes derive from bottom-up control (i.e. changes in plankton composition). Such a hypothesis has been further supported by experimental work that highlighted the effects of both food size and quantity on sardine size, condition and reserve lipids. Yet, the adult overmortality hypothesis associated to the reproduction remained to be validated. To do so, we used the Dynamic Energy Budget (DEB) approach to investigate the effects of food size and quantity on reproductive investment of sardines (e.g. precocity of the reproduction, overmortality following reproduction). Sardines are known to be capital breeders, i.e. store energy to finance later breeding. Here, we modulated feeding conditions (e.g. size, quantity, quality) to identify thresholds, which could lead to either survival or death of adults after the reproduction and compared them with observations in the wild. The calibration of the DEB model was based on morphometric data and data on respiration rates and ammonia excretion provided by the experimental studies. The integration of this DEB model into a population model should finally help in understanding the dynamic of sardine populations facing modification of planktonic prey populations and integrating other stressors such as fishing pressure or increasing temperature.

Keywords: Dynamic Energy Budget, *Sardina pilchardus*, Food size, Reproduction.

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Investigating potential causes of mortality at sea in Atlantic salmon through a simulation study

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Migratory species are particularly sensitive to environmental changes, because their life-cycle depends on a variety of habitats. Change in only one habitat or in the temporal coupling between conditions in different habitats can thus have far-fetching consequences for them. Evaluating those perturbations can be challenging when some of those habitats are difficult to monitor. For example, the freshwater habitats of migratory fishes are intensely monitored to understand the impact of climate change but we have far less information on potential changes in the quality of their marine habitats. For this reason, the causes of recent changes in the demographics of marine Atlantic salmon (*Salmo salar*) have been difficult to pin down. More specifically, the decrease in survival observed since the mid-twentieth century might be due to increasing temperature, to lower quantity and quality of the food resource, but also to changes in the interactions with predators, parasites or pollutants. Some of these causes are size-dependent (e.g. predation) whereas others are rather related to the ability to pay maintenance costs (e.g. immunity, antioxidant defences). Because the changes in size and age at maturation of anadromous salmons were not parallel to the changes in survival, interactions between different environmental factors might have changed over time. I will thus present a simulation study based on dynamic energy budget models combined with individual-based models to explore how changes in environmental factors can differentially impact survival, size and age at maturation. In particular, the ability of such models to discriminate between different sources of mortality, given qualitative or quantitative temporal variation in cross-sectional data (here size and age at maturation), will be discussed.

Keywords: Anadromous fishes, Sea age at maturation, Marine, Stage survival, Multiple stressors, Interspecific interactions.

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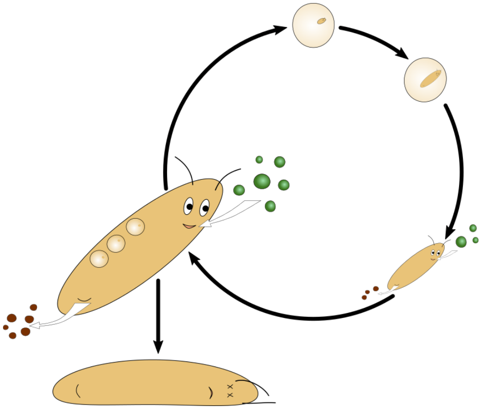
Posters communications



Modelling the response of *Abatus cordatus*, an endemic sea urchin of the Kerguelen Islands, to a changing environment

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The Kerguelen islands are part of the vast French sub-Antarctic territories, displaying a rich marine biodiversity and providing a natural laboratory for the study of coastal marine fauna and flora, which are currently challenged by environmental changes. The responses of benthic communities to these changes remain however poorly understood.

In the framework of a Long Term Ecological Research and monitoring program (PROTEKER, Institut polaire français Paul-Emile Victor program n○1044) the present study aims at modelling the response of *Abatus cordatus*(Echinodermata: Echinoidea) to environmental changes. *A. cordatus* is a detritivorous sea urchin, endemic to the Kerguelen Islands. It has long been studied and a considerable amount of experimental data is available.

A DEB model was developed to predict the potential changes of the species individual physiological performances (growth and reproduction rates) and population structure (density of the different development stages, cohort dynamics) around several stations of the Kerguelen Islands, according to different climatic scenarios proposed by IPCC reports. This approach is used for the first time in the context of the sub-Antarctic region, and provides the potential of being extended to further case studies (other regions, other biological models/scales), in order to support management and conservation plans.

Keywords: Sea urchin, Sub-Antarctic, Population dynamics, Environmental changes.

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Evaluation of different energy budget models for precocious maturation in Atlantic salmon

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Organisms are currently facing rapid environmental change. Their ability to react depends on mechanisms inherited from their evolutionary history. In particular, energy acquisition and processing are the nexus between an organism's environment and life-cycle. Theoretical bioenergetics describes these processes through physical and chemical principles common to all living organisms. This emerging field of research currently covers several approaches, which mainly differ by the mechanism of energy constraint: energy acquisition, energy distribution to cells, or the dissipation of thermal energy. The first approach has proved extremely effective at integrating environmental effects (e.g. temperature, quality and quantity of food) into the life cycle and demography of organisms at the species level. In particular, the theory of dynamic energy budgets, as well as other approaches based on distinct theoretical assumptions (e.g. DEBlipid), now have practical applications in ecotoxicology, management of exploited populations or aquaculture. Our aim is to evaluate the impact of these theoretical assumptions on the models' ability to describe the complex life cycle of a commercially and culturally important species, Atlantic salmon. Simple bioenergetics models have already been developed for the growth of Atlantic salmon. However, Salmonids exhibit a wide variation in breeding strategy, ranging from early male maturation before migration to several years at sea before maturation. Current data suggest that these strategies are linked to body size or lipid stores. The acquisition or treatment of energy therefore seems essential. We will present a comparison the performance of different models to describe empirical data on growth, mortality, and maturation from the beginning of autonomous feeding to sea migration.

Keywords: DEB model, Salmonids, Breeding strategy, Environmental effects, Genetic effects.

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Modelling benthic species population biogeography from individual traits

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Under the pressure of climate change, species may experiment variations in their spatial distribution and abundance. Understanding the responses of species to environmental variations and the consequences on their individual performances and biogeography is thus essential. To this end, individual-based mechanistic species distribution models (SDM) explicitly incorporate known processes at individual level to spatially evaluate the response to environmental variations through their physiological tolerances. These SDMs also make it possible to study the emergence of observed characteristics at the population level (e.g. demographic structure and dynamics). The goal of our project is to develop a generic mechanistic and individual-based model of population dynamics, in order to study the biogeographic response of benthic species facing various climate scenarios. The aim will be to test and prioritize the factors driving the populations dynamics and spatial distribution, depending on the species, habitat and stressor. The development of a generic approach, using a metabolic theory at individual scale (Dynamic Energy Budget theory), and including spatial interactions (population connectivity), will provide a conceptual framework for a comparative approach to the response of various species, in a variety of ecosystems and habitats. To achieve this goal, we will (1) develop and calibrate a generic mechanistic and individual-based model (IBM) by using a multi-agent platform, (2) validate the model on target species at various temporal and spatial scale, based on field surveys, (3) test the model sensitivity and (4) predict the species distribution in future climate change scenarios.

Keywords: Climate change, Population dynamics, Individual based model.

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MORSE: An R-package dedicated to ecotoxicology

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Chemicals effects on living animals are usually measured on life history traits from standardized toxicity tests. This ensures the control of experimental conditions and the reproducibility of toxicity tests which generally concern survival, reproduction or growth of animals. The statistical analysis of the data leads to the estimation of toxicity thresholds. If toxicity tests are carried out with a reasonable number of concentrations of the chemical substance and if the responses/effects are statistically significant, a regression model is recommended to estimate LCx and/or ECx at the end of the experiment. However, choosing the most appropriate model may be difficult while it may strongly impact the threshold estimates. Moreover, these models prevent the full exploitation of available data, monitored over time, leading to a statistical bias in time-dependent toxicity thresholds. They are also defined for constant exposure concentrations, making not possible the extrapolation to more realistic, time-variable exposure profiles. Such situations can be accounted for with toxicokinetic-toxicodynamic models, as the General Unified Threshold model of Survival for survival data. Nevertheless, proper and relevant estimates of parameters for these models is rarely possible within a unique software, nor hardly feasible for non-statisticians. To bridge this gap, we developed ready-to-use functions within an R-package entitled 'morse', freely available at https://CRAN.R-project.org/package=morse. 'morse' is based on a Bayesian framework to provide parameter estimates as probability distributions, from which uncertainties can be propagated to model outputs. This poster illustrates: how simple it is to fit an exposure-response/effect or a GUTS model with only few lines of R code; how to estimate LCx either from a classical exposure-response/effect or a GUTS model; how to make predictions of the survival rate under untested time-variable concentration profiles; and how to get an estimate of the new concept of x% lethal profile (LPx) as recently promoted by EFSA.

Keywords: Dose, Response model, GUTS models, Ready-to-use functions, R software.

Energy as a driver of high *Arctic muskox* population dynamics

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Energy is a critical driver of animal life-history and fitness, therefore also population dynamics. The muskox (*Ovibos moschatus*) experiences harsh climatic and seasonal environmental conditions in the Arctic that dictate all aspects of its life, including habitat selection, movement, and food availability. There is considerable variability in survival and reproductive rates across different years and populations in free-ranging muskoxen. Little is known of muskox energetics or the cause of variability in population fitness. We developed a dynamic energy budget based individual model (DEB-IBM) for the muskox that covers all aspects of mammalian life-history. We parameterize a baseline muskox model using data from a well-studied captive research herd, and explore model application to a wild population in the high Arctic to assess the biological significance of seasonal environmental variability. Our baseline model successfully reproduced observed life-history traits as well as patterns of growth, body condition, feeding, metabolic rates, and reproduction of well-fed captive muskoxen. Adaptation of the baseline model to the wild population on Victoria Island, Canada, required re-parameterization of only three variables that controlled seasonal food availability and the dynamics of upregulated assimilation in reproductive females. The modified model captured the significant inter-annual carry-over costs of reproduction, such that reproductive females accumulated less storage energy after a summer of nursing compared to females with no calves at heel. Limited food availability in winter months reduced fecundity in wild muskox by 42% compared to well-fed captive animals. Our results highlight the strong interplay between energetics and individual fitness components, and opens the door to future applications of the model for understanding environmental influences on population dynamics.

Keywords: Population, Mammal, Individual based model, Arctic.

Homogenizing life-history traits of the semelparous polychaete *Hediste diversicolor* using DEB

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Hediste diversicolor is a euryhaline marine polychaete species of the Nereididae Family that has been well studied in ecological, ecotoxicological and aquaculture contexts. Discrepancies arose from life-history traits collected in the literature. A standard DEB modelling approach using the co-variation method and the package ”add my pet” was initiated to increase coherence in the life cycle of this species. This species was well studied in experimental approaches and this has allowed benefiting from results in controlled conditions. Some complications remain. *H. diversicolor* die after its first spawning event (semelparous) making predictions on its maximum length or weight unrealistic and, sub-consequently increasing the difficulty of the parameterization with these parameters as pivots into the calibration procedure. Second, measurements of length dimensions are quite complicated in this ”elastic” species (and frequently losing terminal setigers by autotomy) leading researchers to multiply metrics to measure length (e.g. number of setigers, total length, and length of the three first segments....). Calibration exercise was mostly done on univariate data from experimental results, and parameter set was then used to homogenize the zero-variate data regarding food density, temperature and age. Calibration is satisfactory. Noticeably, the volume-specific maintenance rate is very high, the specific cost for structure is higher and maturity at birth and puberty are lower respectively than the generalized animal values. While Annelids are still understudied in the deb context, these parameters seem in accordance with other species from this phylum. The work is still in progress. Two directions are being explored: costs and benefits in using an ”abj” model and in implementing surface-specific maintenance rate as this species is a Lophotrochozoan and euryhaline species. Future applications in aquaculture will be discussed.

Keywords: Annelid, Aquaculture, Semelparous.

DEB model for a developing tadpole

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We try to understand the energy budget dynamics of a developing tadpole. The data we use was originally gathered to study how different pathogens affect the energetics and performance of tadpoles. Infectious diseases of amphibians currently receive broad attention because they are linked to the mass population declines of amphibian species worldwide – especially due to the spread of two closely related severe fungal pathogenes, *Batrachochytrium dendrobatidis* and *Batrachochytrium salamandrivorans*.

At first glance, tadpoles may seem a typical example of a distinct developmental stage in the life of an organism. However when observing a developing tadpole in detail, it becomes evident that the transition towards the adult stage is more a continuous process than a sudden event. Visual signs of the development are the emergence of limbs, the transformation of the mouth and the resorption of the tail. Those signs are commonly used to divide the life cycle of frogs into 46 sub-stages defined by Gosner (1960).

Tadpoles of the species *Pseudacris regilla* were kept in the laboratory for several weeks during which they almost completed their metamorphosis. Measurements taken from them include their Gosner stage, food uptake, oxygen consumption and body length (which can be converted to body weight using a known weight-length relationship).

A DEB model fits the experimental data best when some of the parameters are assumed to vary with the developmental state. The trend is particularly strong for the feeding rate, with tadpoles gradually reducing their food uptake when approaching metamorphosis.

Although the model was formulated to describe development of tadpoles, some parts of it might be transferable for other scenarios. Continuously changing parameters might be more a rule than an exception for many organisms.

Gosner, K.L., 1960. A simplified table for staging anuran embryos and larvae with notes on identification. Herpetologica, 16(3), pp.183-190.

Keywords: Tadpole, Development, Metamorphism, Gosner stage, Pseudacris.

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A dynamic energy budget model for small yellow croaker *Larimichthys polyactis* : parametrisation and application in its main geographic distribution waters

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Global fishery resources have generally declined. Appropriate management is necessary for optimum utilisation of fish stocks. Small yellow croaker *Larimichthys polyactis* is an important fisheries species in the northwest Pacific Ocean, a major decline in abundance has been attributed to overfishing and environmental changes. To provide a basis for understanding population dynamics, we have applied a dynamic energy budget (DEB) model to small yellow croaker in the Yellow and East China Seas. The model was parameterised using the improved version of the covariation method following AmP procedure. The method requires minimum physiological information. It is based on the methodology of fitting multiple models to multiple datasets in a single parameter estimation. The available data for the species consist of information on life history and development aspects including age-at-birth, age-at-puberty, the life span and reproduction as well as growth data of age-length and length-weight relationships. The plausible parameter values were obtained as the model achieves overall goodness of fit. The application of the model has shown that it can successfully reproduce the behaviour of small yellow croaker in the main distribution waters. The growth simulations in both length and weight were within the range of observations. The model output of fecundity matched the observations reasonably well. We discuss the need for further improvement of the model and collection of environmental data.

Keywords: Small yellow croaker, DEB parametrisation, Fisheries, Growth, Reproduction.

GUTS Shiny App: a web platform to simulate survival rate under time-variable exposure concentration profiles

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Environmental Risk Assessment rests on fitting standard dose-response models to toxicity test data and estimating LC/EC50 values. This practice prevents the full exploitation of data, which are monitored over time, leading to a statistical bias in the estimated time-dependent toxicity thresholds. Moreover, standard models are defined for constant exposure concentrations, making impossible the extrapolation of the results to more realistic, time-variable exposure profiles. Toxicokinetic-toxicodynamic (TKTD) models help in describing chemical effects by considering the exposure dynamics. They offer the possibility to calculate LC/ECx for any exposure duration t, even at time points outside the experimental design. They also support a mechanistic understanding of the chemical mode of action, the derivation of time-independent effect parameters and the prediction of risks under time-variable exposure profiles. Nevertheless, they are not widely used in practice, due to their mathematical complexity that requires advanced methods such as numerical integration and non-linear optimization.

Recently, among TKTD models, EFSA promoted the use of General Unified Threshold models of Survival (GUTS) for regulatory risk assessment of pesticides for aquatic organisms. GUTS models are fitted on experimental data to estimate parameters, the survival rate is predicted under environmental exposure scenarios, and predicted numbers of survivors are compared to observed data. Validated is based on three criteria: % of data predicted within uncertainty limits, normalized root mean square error and final survival probability prediction error. This poster presents the GUTS Shiny App (http://lbbe-shiny.univ-lyon1.fr/guts-shinyapp/), a web platform to simulate GUTS models for any time-variable exposure concentration profile. Uncertainty on input parameters may be propagated to the model outputs. Following EFSA recommendations, the GUTS Shiny App allows the estimation of the multiplication factor causing an additional x% of mortality at the end of the profile (the LPx). If the user downloads observed data, the GUTS Shiny App automatically delivers EFSA validation criteria.

Keywords: GUTS simulations, Uncertainty propagation, x% lethal profile, Validation criteria.

MOSAIC: a web interface for statistical analyses in ecotoxicology

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In ecotoxicology, toxicity tests are standardly conducted in order to measure acute or chronic effects of potentially toxic substances on reproduction, growth and/or survival of living animals. Based on statistical models, mainly exposure-response/effect models, these data are analyzed to derive toxicity thresholds associated with their uncertainty, thus helping risk assessors in taking argued decisions. But choosing the most appropriate model and tracking uncertainties is not always an easy task if not implemented in ready-to-use software.

MOSAIC (http://pbil.univ-lyon1.fr/software/mosaic/) is developed to meet this request for a freely available user-friendly web interface dedicated to the mathematical and statistical modelling of standard toxicity test data. Its simple use makes MOSAIC a turnkey decision-making tool for ecotoxicologists, regulators and risk assessors. Without immersing in extensive mathematical and statistical technicalities, users are provided with advanced and innovative methods to get quantitatively robust estimates of toxicity thresholds in support of their daily work in environmental risk assessment.

Most of MOSAIC functionalities are based on Bayesian inference. From the joint posterior distribution of parameters, Bayesian inference allows a clear handling of uncertainties, that is propagated to the derivation of the toxicity thresholds. In this poster, we first illustrate how to derive LCx and ECx estimates in few steps from standard toxicity data. Then we illustrate how to perform an SSD analysis including censored data, that is defined as intervals. At last, we present the most recent tool available in MOSAIC, which is dedicated to the use of toxicokinetic-toxicodynamic (TKTD) models, especially General Unified Threshold models of Survival (GUTS models), to fit survival data as a function of both time and concentration. This new functionality could become the new paradigm to derive precise LCx estimates with a better precision than the ones obtained from classical exposure-response/effect models.

Keywords: Dose-response model, GUTS models, Ready-to-use functions, R software.

Mixture toxicity with an individual-based model on the dynamic energy budget theory: effects of Cu and Zn on *Daphnia magna* populations

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The current regulatory framework of risk assessment regulatory framework considers the effects of single substances that are assessed through standardized laboratory tests, e.g. the 21-day *Daphnia magna*reproduction test. However, in the environment, individual organisms are being exposed to mixtures of chemicals. Protection goals in EU legislation (e.g. Water Framework Directive) state that protection of populations is needed to maintain ecosystem functioning. In our research, we developed an Individual-Based Model of the Dynamic Energy Budget theory (DEB-IBM) to predict effects of metal mixtures on *Daphnia magna* populations. The DEBtox model was calibrated using apical effects (i.e. growth, reproduction and survival) of Cu and Zn assessed in standardised tests. To validate our model and determine the most appropriate mixture toxicity mode, a population experiment (75 days) with *D. magna*exposed to Cu and Zn (both single and mixtures) was performed. We tested three implementations of mixture toxicity in DEB-IBM: independent action (where effects are considered independent), concentration addition (where the compounds have the same toxic mode and act as dilutions of each other) and effect addition (where effect levels are summed). Each implementation was evaluated for predictability against the population experiment based on the normalised mean square error (NMSE). All three implementations perform well compared with the data, indicating that none of the mixture models is preferred at the population level. We extrapolated the experiment with DEB-IBM to untested concentrations and determined effect levels for Cu and Zn based on equilibrium population density. The effect levels of the three implementations were compared. The current implementation of mixture toxicity in DEB-IBM could accurately predict mixture toxicity effects observed in a population experiment. The concentration addition model was the more conservative mixture toxicity mode. More fine-tuning and comparison with experiments is needed to further validate our approach and increase confidence in predictions.

Keywords: Population dynamics, Population level effects, Ecological modelling, Metal risk assessment, *Daphnia magna*.

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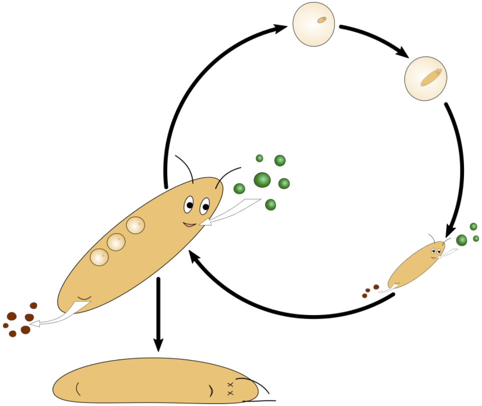

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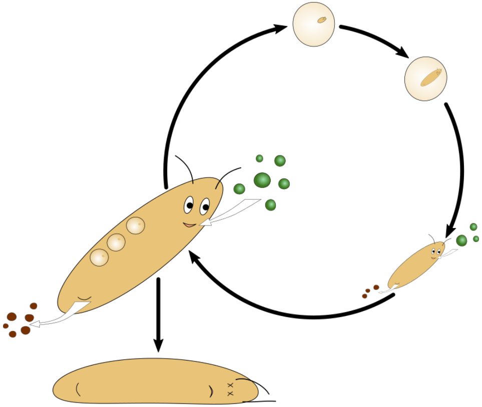

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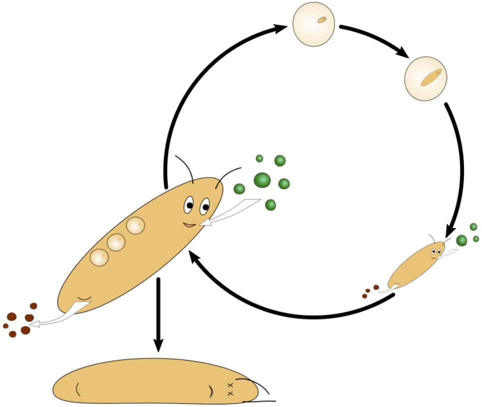

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