



DEB-in-Practice

Advanced data analysis

Starrlight Augustine

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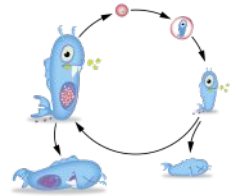
University of Lisboa/ Vrije
Universiteit

Dina Lika

lika@uoc.gr

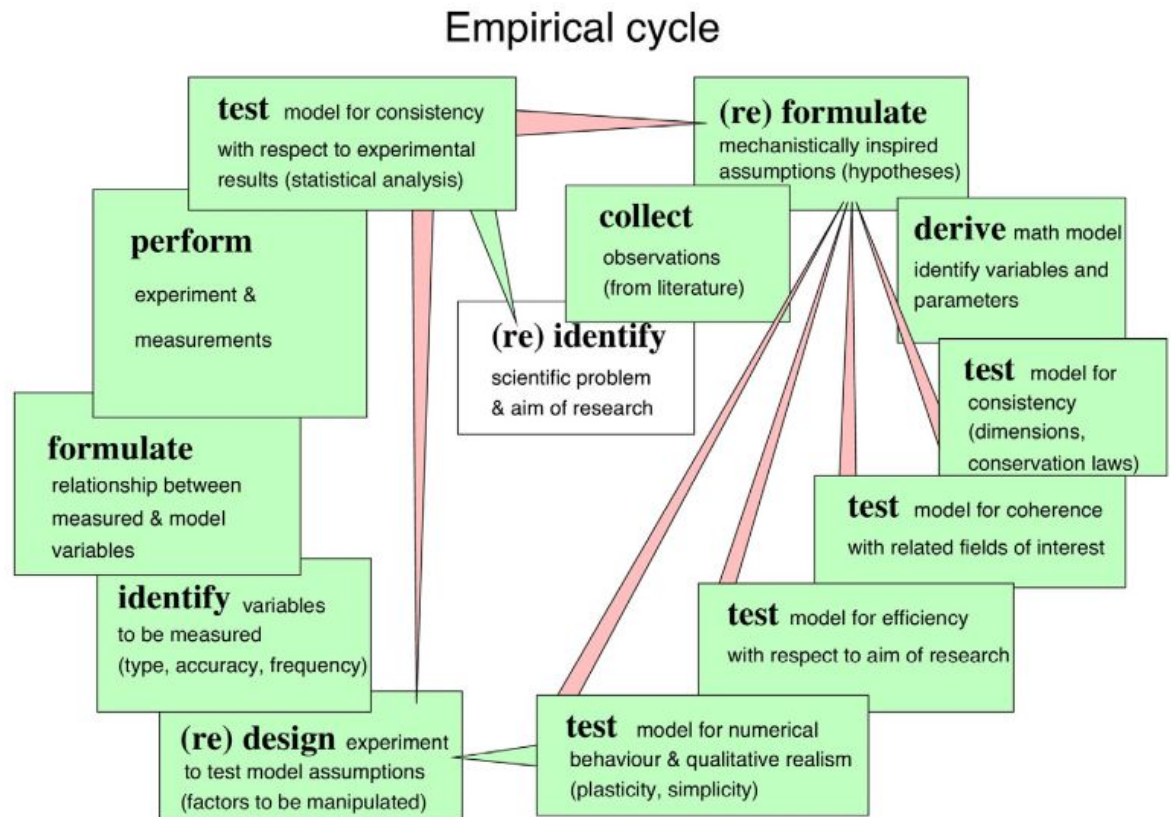
University of Crete

Empirical cycle

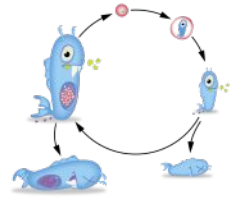


Avoid thinking in terms of “the” model -> families of related models

“All models are wrong, some are useful”

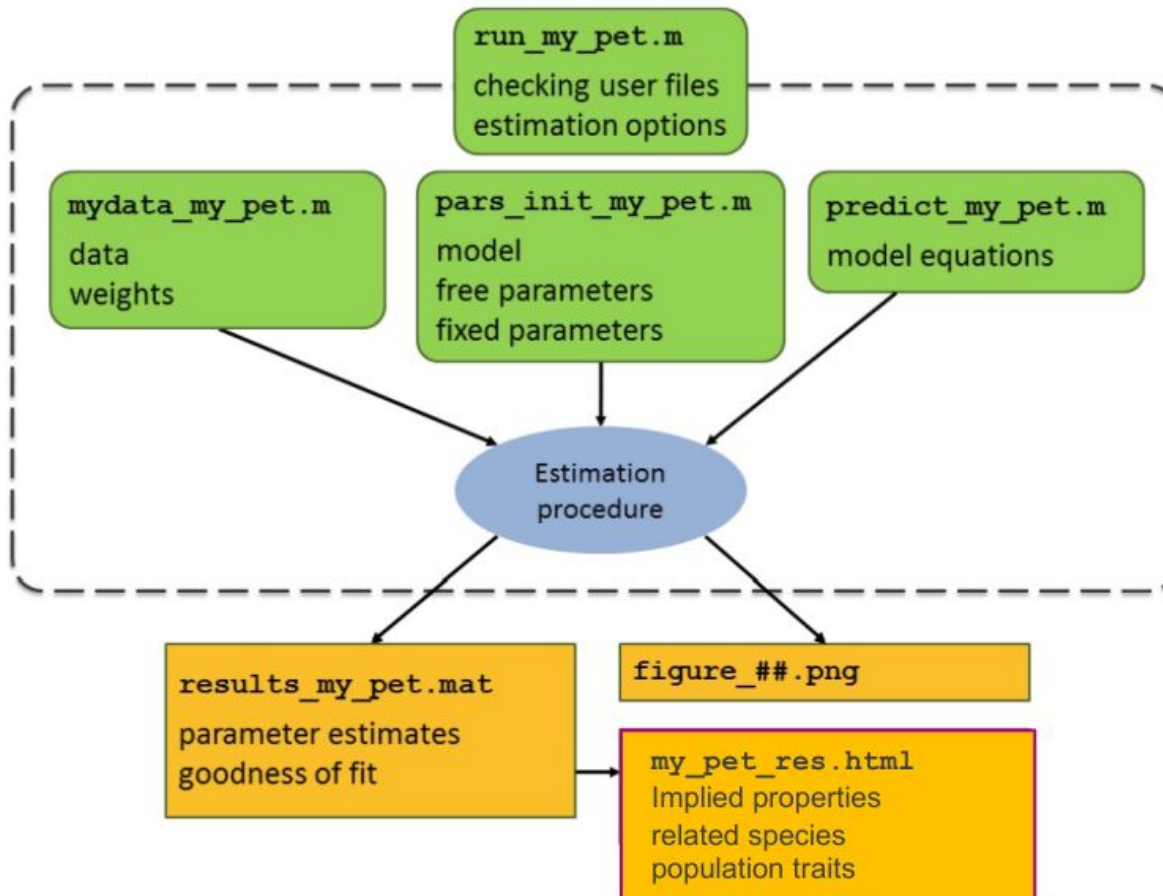
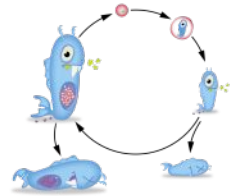


Modular Framework

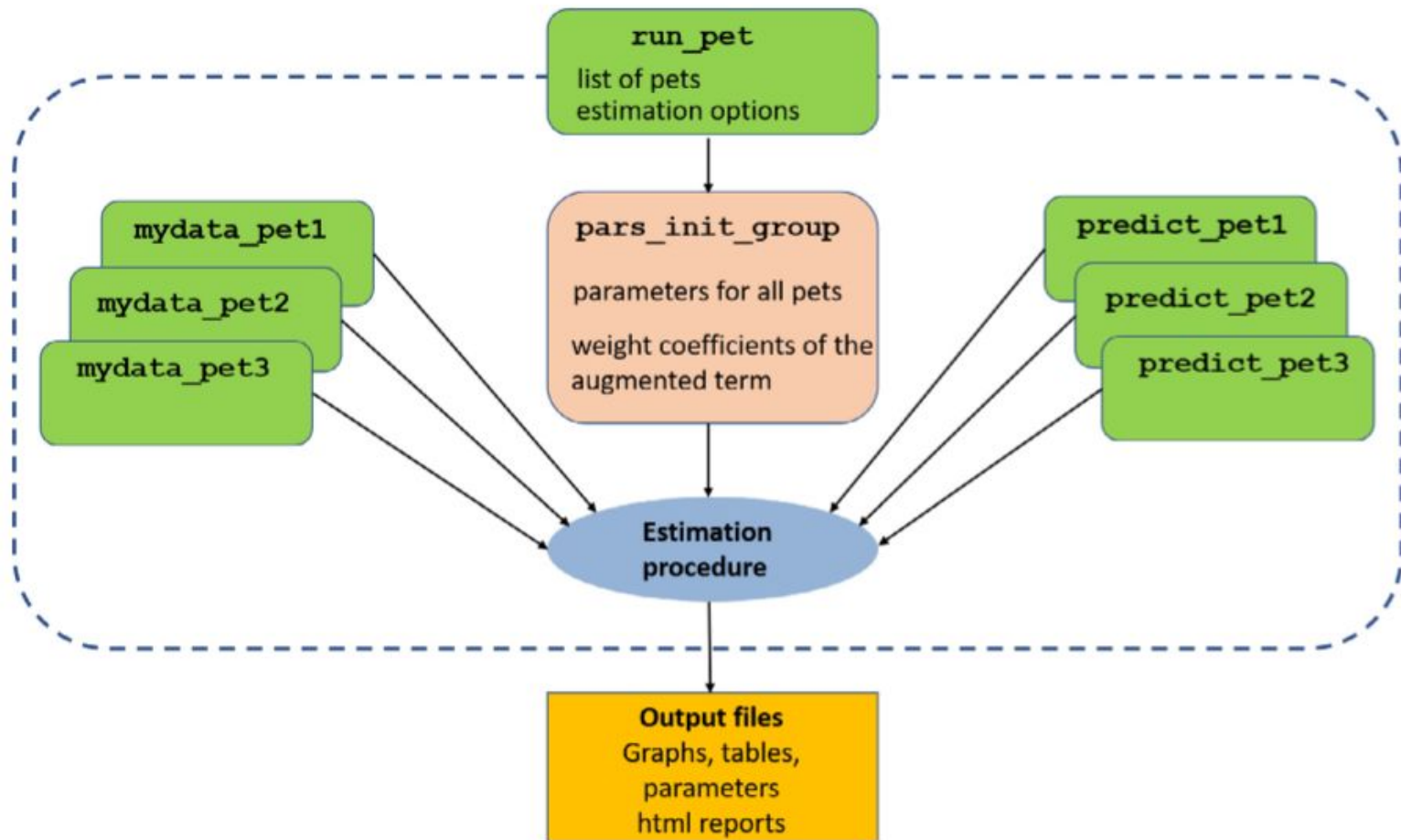
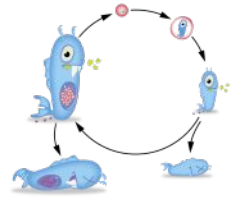


- possible to develop and test modules independently -> walk up and down levels of complexity

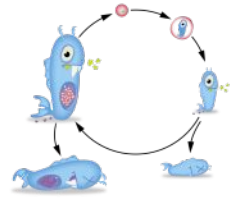
AmP procedure



“Augmented” loss function



Combining different entries



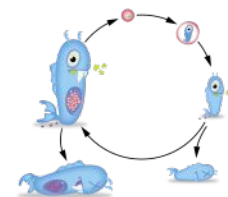
a continuum between parameters being the same or different:
parameters are allowed to vary between (related) species, but not that much

extension of the loss function is a function of weight coefficients and parameters, but not of data or predictions.

DEB theory takes parameter values to be individual-specific, but the differences are small enough for the mean values to represent the species, eco-type or population.

If enough is known about each individual, the different entries might even represent individuals, rather than species

essential feature for DEB theory, since evolutionary selection is at the level of individuals, and treating parameters as individual-specific evolutionary changes in parameter values, as studied in the field of adaptive dynamics, can be included naturally



By fitting each species one-by-one, large differences in parameter values can show up. But is this the result of real differences between species or an artifact caused by data not determining parameters accurately

How much can we reduce the differences in parameter values, without affecting the goodness of fit too much?

Since, in our view, parameter values represent species diversity, we are looking for a reduction in this diversity that is still allowed by data

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RESEARCH ARTICLE

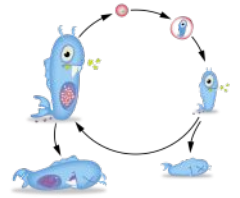
Functional Ecology



Substantial intraspecific variation in energy budgets: Biology or artefact?

Tomos Potter¹  | David N. Reznick² | Tim Coulson¹ 

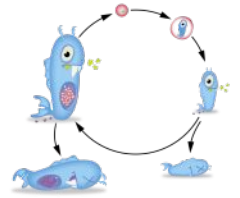
Augmented loss function



$$F_{sb} = \sum_{i=1}^n \sum_{j=1}^{n_i} \frac{w_{ij}}{n_i} \frac{(d_{ij} - p_{ij})^2}{d_i^2 + p_i^2} + \sum_{k=1}^N \frac{w_k \text{var}(\theta_k)}{\text{mean}(\theta_k)^2}$$

with $d_i = \frac{1}{n_i} \sum_{j=1}^{n_i} d_{ij}$ and $p_i = \frac{1}{n_i} \sum_{j=1}^{n_i} p_{ij}$

“Augmented” loss function



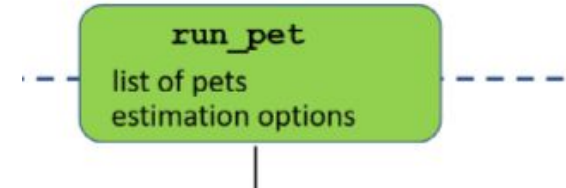
```
|close all;  
global pets
```

```
pets = { ...  
    'Clarias_gariepinus', ...  
    'Clarias_gariepinus_x_Heterobranchus_longifilis', ...  
    'Heterobranchus_longifilis', ...  
    'Heterobranchus_longifilis_x_Clarias_gariepinus', ...  
};
```

```
estim_options('default');  
estim_options('max_step_number', 1e3);  
estim_options('max_fun_evals', 5e3);
```

```
estim_options('pars_init_method', 1);  
estim_options('results_output', 3);  
%estim_options('method', 'no');
```

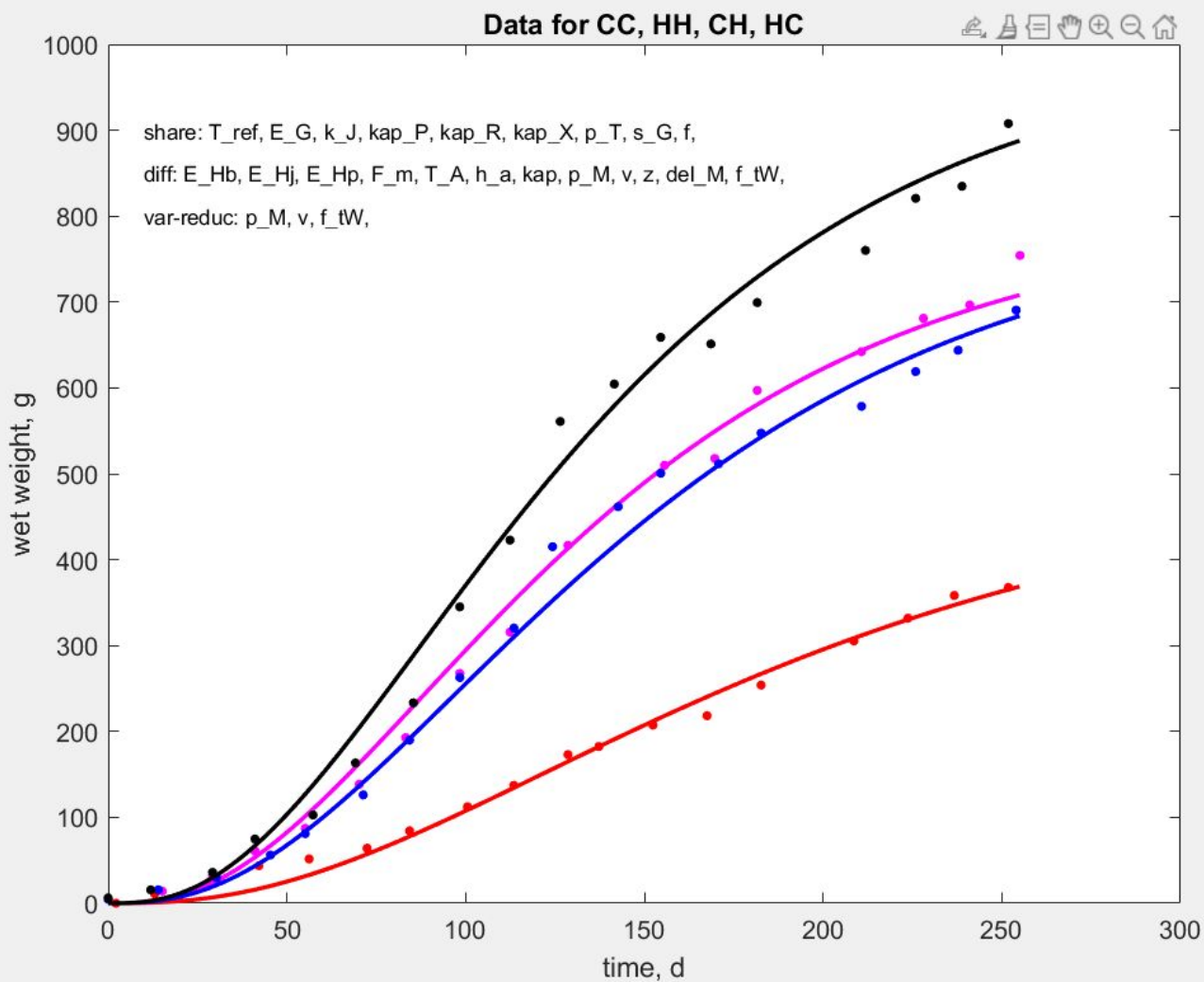
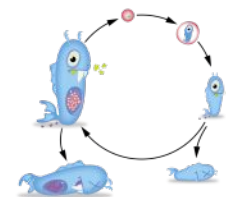
```
estim_pars;
```



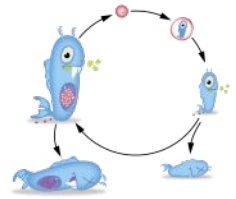
```

pets = { ...
  'Clarias_gariepinus', ...
  'Clarias_gariepinus_x_Heterobranchus_longifilis', ...
  'Heterobranchus_longifilis', ...
  'Heterobranchus_longifilis_x_Clarias_gariepinus', ...
};

```



Parameters with reduced variance in the Augmented loss function procedure



```
function [par, metaPar, txtPar] = pars_init_group(metaData)
```

```
metaPar.model = {'abj', 'abj', 'abj', 'abj'};  
metaPar.cov_rules = ''; % see function parGrp2Pets  
metaPar.weights.E_Hb = 0;  
metaPar.weights.E_Hj = 0;  
metaPar.weights.E_Hp = 0;  
metaPar.weights.h_a = 0;  
metaPar.weights.kap = 0;  
metaPar.weights.p_M = 2;  
metaPar.weights.v = 2;  
metaPar.weights.z = 0;  
metaPar.weights.del_M = 0;  
metaPar.weights.f_tW = 5;
```

$$F_{sb} = \sum_{i=1}^n \sum_{j=1}^{n_i} \frac{w_{ij}}{n_i} \frac{(d_{ij} - p_i)^2}{d_i^2 + p_i^2} + \sum_{k=1}^N \frac{w_k \text{var}(\theta_k)}{\text{mean}(\theta_k)^2}$$

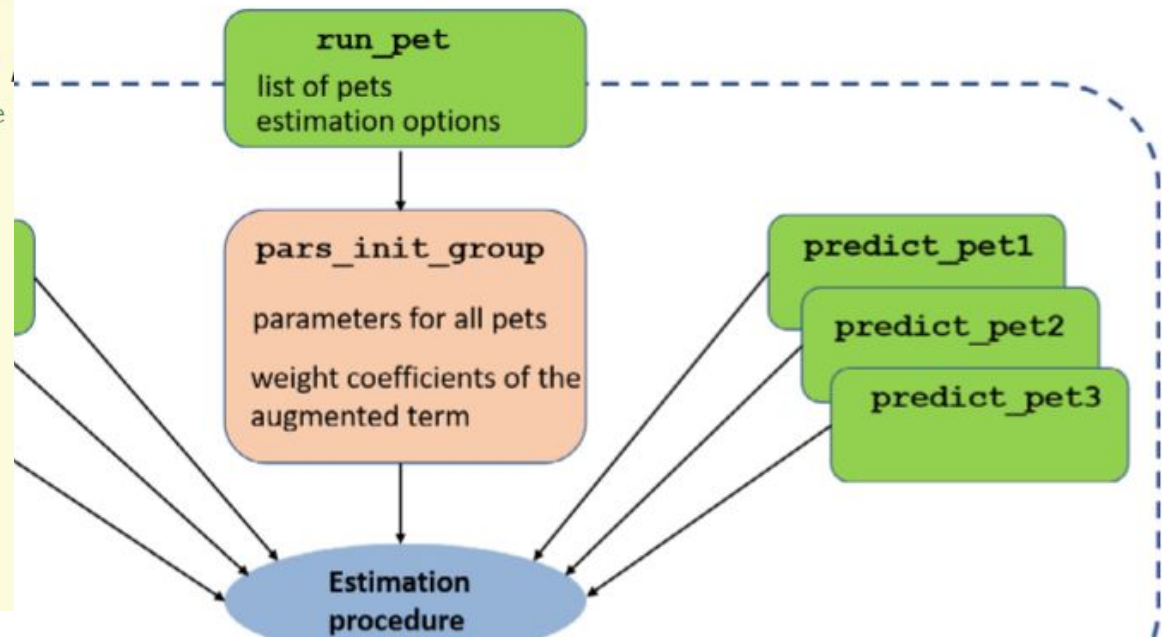
with $d_i = \frac{1}{n_i} \sum_{j=1}^{n_i} d_{ij}$ and $p_i = \frac{1}{n_i} \sum_{j=1}^{n_i} p_{ij}$

$w_k = 0$ parameter θ_k is the same

w_k large parameter θ_k is different


```
function [par, metaPar, txtPar
```

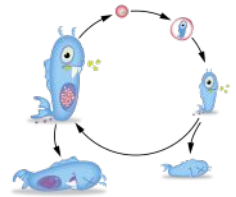
```
metaPar.model = {'abj', 'abj'};
metaPar.cov_rules = ''; % see
metaPar.weights.E_Hb = 0;
metaPar.weights.E_Hj = 0;
metaPar.weights.E_Hp = 0;
metaPar.weights.h_a = 0;
metaPar.weights.kap = 0;
metaPar.weights.p_M = 2;
metaPar.weights.v = 2;
metaPar.weights.z = 0;
metaPar.weights.del_M = 0;
metaPar.weights.f_tW = 5;
```



```
%% core primary parameters
```

```
par.E_G = 5224.8351; free.E_G = 1; units.E_G = 'J/cm^3'; label.E_G = '[E_G], spec cost for st
par.E_Hb = [ 3.923e-02 1.895e-03 1.571e-02 2.708e-03]; free.E_Hb = [1 1 1 1]; units.E_Hb = 'J';
par.E_Hj = [ 4.526e-02 1.659e-02 6.274e-02 3.675e-02]; free.E_Hj = [1 1 1 1]; units.E_Hj = 'J';
par.E_Hp = [ 3.024e+04 5.980e+03 1.252e+05 4.548e+03]; free.E_Hp = [1 1 1 1]; units.E_Hp = 'J';
par.F_m = [6.5 6.5 6.5 6.5]; free.F_m = [0 0 0 0]; units.F_m = '1/d.cm';
par.T_A = [9000 9000 9000 9000]; free.T_A = [0 0 0 0]; units.T_A = 'K'; label.T_A =
par.h_a = [ 3.376e-10 1.838e-10 3.989e-10 4.166e-10]; free.h_a = [1 1 1 1]; units.h_a = '1/d^2';
par.k_J = 0.002; free.k_J = 0; units.k_J = '1/d'; label.k_J = 'maturity maint rate coef
par.kap = [0.94169 0.99889 0.98615 0.9977]; free.kap = [1 1 1 1]; units.kap = '-';
par.kap_P = 0.1; free.kap_P = 0; units.kap_P = '-'; label.kap_P = 'faecation efficiency c
par.kap_R = 0.95; free.kap_R = 0; units.kap_R = '-'; label.kap_R = 'reproduction efficienc
par.kap_X = 0.8; free.kap_X = 0; units.kap_X = '-'; label.kap_X = 'digestion efficiency c
par.p_M = [169.1637 163.4297 173.5294 164.2649]; free.p_M = [1 1 1 1]; units.p_M
par.p_T = 0; free.p_T = 0; units.p_T = 'J/d.cm^2'; label.p_T = '{p_T}, surf-spec somatic
par.s_G = 0.0001; free.s_G = 0; units.s_G = '-'; label.s_G = 'Gompertz stress coeffic
par.v = [0.074841 0.09047 0.089094 0.084718]; free.v = [1 1 1 1]; units.v = 'cm/d';
par.z = [17.2809 10.9743 12.9022 11.952]; free.z = [1 1 1 1]; units.z = '-';
```

Application of the augmented loss function to understand differences in morphotypes



Ecological Modelling 430 (2020) 109088

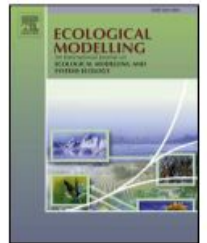


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Ecological Modelling

journal homepage: www.elsevier.com/locate/ecolmodel



Can DEB models infer metabolic differences between intertidal and subtidal morphotypes of the Antarctic limpet *Nacella concinna* (Strebel, 1908)?



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^a Laboratoire de Biologie Marine, Université Libre de Bruxelles, Avenue F.D.Roosevelt, 50. CP 160/15. 1050 BRUXELLES, BELGIUM

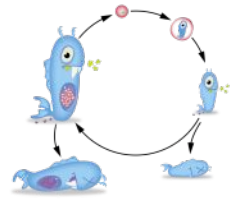
^b UMR 6282 Biogéosciences, Univ. Bourgogne Franche-Comté, CNRS, EPHE, 6 bd Gabriel F-21000 Dijon, France

^c British Antarctic Survey, Natural Environment Research Council, Cambridge, CB30ET UK

^d Kvaplan-Niva, Fram High North Research Centre for Climate and the Environment, 9296 Tromsø, Norway

^e Department of Theoretical Biology, VU University Amsterdam, de Boelelaan 1087, 1081 HV Amsterdam, The Netherlands

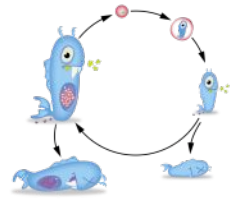
Application of the augmented loss function to understand differences in morphotypes



Some overall results:

- Minor differences in temperature-corrected parameter values between both populations
- Despite the known morphological difference between the populations, the difference in shape coefficients was small

Application of the augmented loss function to understand differences in morphotypes



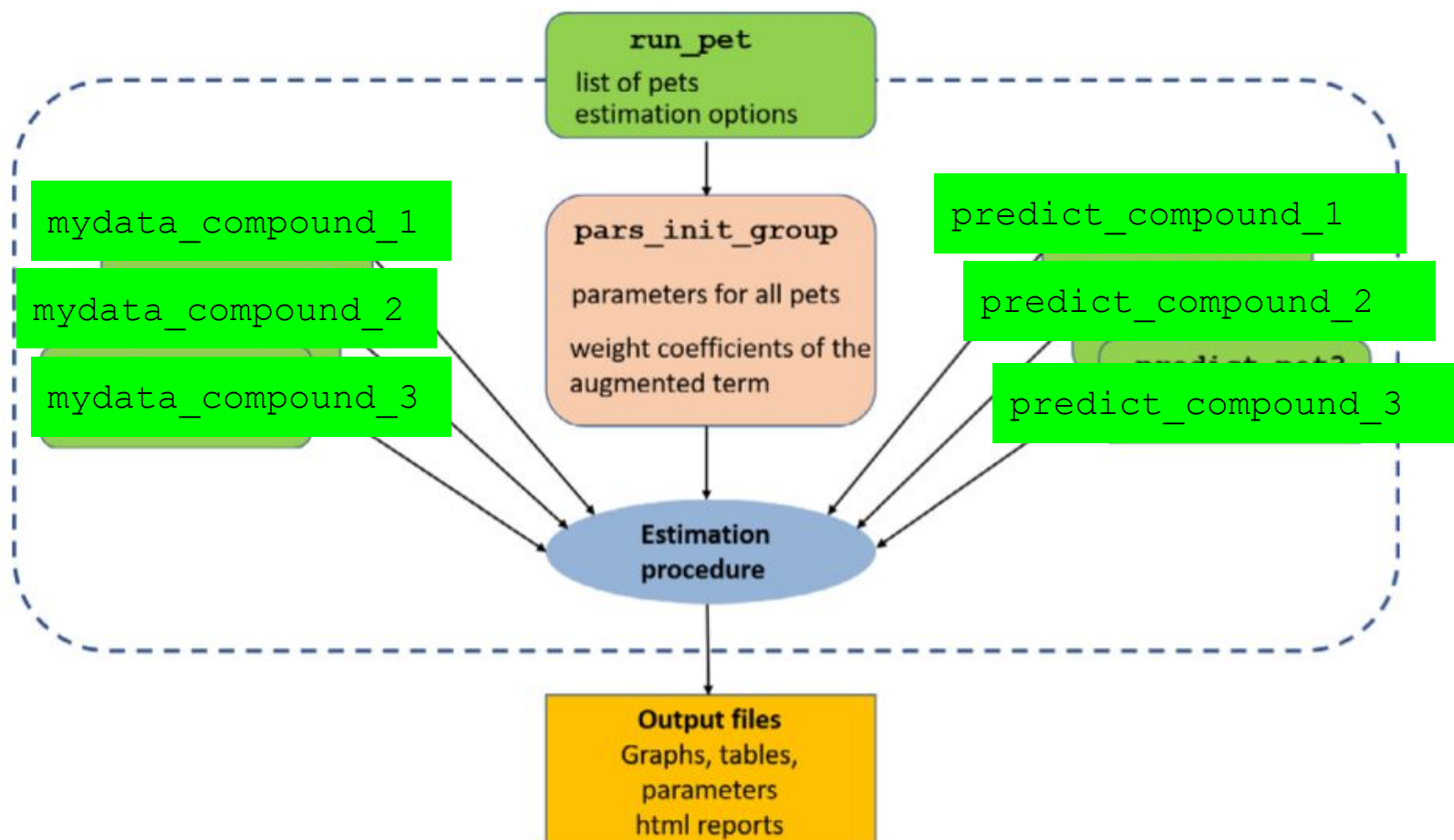
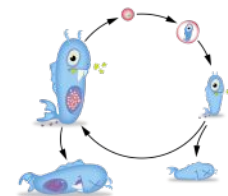
Authors ran “merging trials” gradually increasing the weight of the parameter:

they tried to merge the models into a single one, parameter by parameter, to evaluate the contrasts in parameters between the types

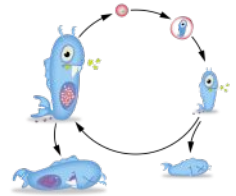
models were merged without generating significant changes in MRE and loss function values

=> There is still a lot to understand with this approach

Augmented loss function in the context of multiple compounds



OECD guidelines 232 Collembolan Reproduction Test in Soil



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0730-7268/07 \$12.00 + .00

MODELING THE EFFECTS OF BINARY MIXTURES ON SURVIVAL IN TIME

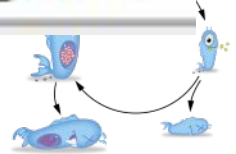
JAN BAAS,^{*†} BART P.P. VAN HOUTE,[‡] CORNELIS A.M. VAN GESTEL,[§] and SEBASTIAAN A.L.M. KOOIJMAN[†]

[†]Vrije Universiteit Amsterdam, Department of Theoretical Biology, De Boelelaan 1085, 1081 HV, Amsterdam, The Netherlands

[‡]Vrije Universiteit Amsterdam, Department of Molecular Cell Physiology, De Boelelaan 1085, 1081 HV, Amsterdam, The Netherlands

[§]Vrije Universiteit Amsterdam, Department of Animal Ecology, De Boelelaan 1085, 1081 HV, Amsterdam, The Netherlands

(Received 25 August 2006; Accepted 8 January 2007)



mydata_OECD232_Cd_Pb.m

mydata_OECD232_Cd_Zn.m

mydata_OECD232_Cu_Cd.m

mydata_OECD232_Cu_Pb.m

mydata_OECD232_Zn_Cu.m

mydata_OECD232_Zn_Pb.m

predict_OECD232_Cd_Pb.m

predict_OECD232_Cd_Zn.m

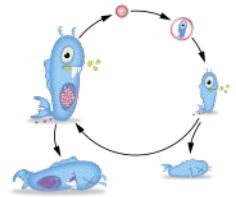
predict_OECD232_Cu_Cd.m

predict_OECD232_Cu_Pb.m

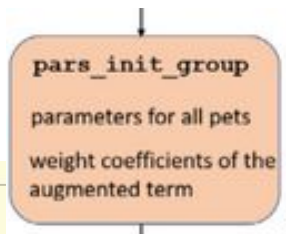
predict_OECD232_Zn_Cu.m

predict_OECD232_Zn_Pb.m

Modeling effects of mixtures. For the exposure to two compounds simultaneously, the effects are described by the toxicity parameters of the individual compounds, extended with an interaction parameter called d_{AB} , which is expressed as



$$\text{Effect} \sim [A] + [B] + d_{AB}[A][B]$$



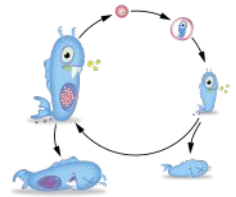
```
%% parameters
```

```
% stress
```

```
par.c_0Cd = 1.0929; free.c_0Cd = 1; units.c_0Cd = 'mg/g'; label.c_0Cd = 'No-Ef
par.c_0Cu = 3.0546; free.c_0Cu = 1; units.c_0Cu = 'mg/g'; label.c_0Cu = 'No-Ef
par.c_0Pb = 0.00029355; free.c_0Pb = 1; units.c_0Pb = 'mg/g'; label.c_0Pb = 'N
par.c_0Zn = 4.0419; free.c_0Zn = 1; units.c_0Zn = 'mg/g'; label.c_0Zn = 'No-Ef
par.b_Cd = 0.044493; free.b_Cd = 1; units.b_Cd = 'g/d.mg'; label.b_Cd = 'killi
par.b_Cu = 0.21539; free.b_Cu = 1; units.b_Cu = 'g/d.mg'; label.b_Cu = 'killin
par.b_Pb = 0.085115; free.b_Pb = 1; units.b_Pb = 'g/d.mg'; label.b_Pb = 'killi
par.b_Zn = 0.4856; free.b_Zn = 1; units.b_Zn = 'g/d.mg'; label.b_Zn = 'killing
par.k_eCd = 56.0527; free.k_eCd = 1; units.k_eCd = '1/d'; label.k_eCd = 'elimi
par.k_eCu = 442.5756; free.k_eCu = 1; units.k_eCu = '1/d'; label.k_eCu = 'elim
par.k_ePb = 0.0054207; free.k_ePb = 1; units.k_ePb = '1/d'; label.k_ePb = 'eli
par.k_eZn = 569.9706; free.k_eZn = 1; units.k_eZn = '1/d'; label.k_eZn = 'elim
par.d_xy = [7.1001e-06 0.0064216 0.074399 0.00085962 0.00047524 0.001
% other
```

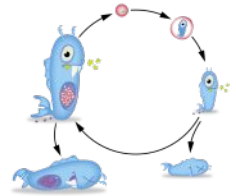
```
par.h = 0.01277; free.h = 1; units.h = '1/d'; label.h = 'hazard rate in the bl
```


More generally, for mixtures the model contains three parameters per compound describing the effect of the individual compound, a control mortality rate for the experiment, and one interaction parameter for each pair of compounds. So for a mixture of k compounds, a total of 1 (control mortality) + $3k$ (effect parameters for the three compounds) + $k(k - 1)/2$ interaction parameters are required.



```
%% parameters
% stress
par.c_0Cd = 1.0929; free.c_0Cd = 1; units.c_0Cd = 'mg/g'; label.c_0Cd = 'No-Ef
par.c_0Cu = 3.0546; free.c_0Cu = 1; units.c_0Cu = 'mg/g'; label.c_0Cu = 'No-Ef
par.c_0Pb = 0.00029355; free.c_0Pb = 1; units.c_0Pb = 'mg/g'; label.c_0Pb = 'N
par.c_0Zn = 4.0419; free.c_0Zn = 1; units.c_0Zn = 'mg/g'; label.c_0Zn = 'No-Ef
par.b_Cd = 0.044493; free.b_Cd = 1; units.b_Cd = 'g/d.mg'; label.b_Cd = 'killi
par.b_Cu = 0.21539; free.b_Cu = 1; units.b_Cu = 'g/d.mg'; label.b_Cu = 'killin
par.b_Pb = 0.085115; free.b_Pb = 1; units.b_Pb = 'g/d.mg'; label.b_Pb = 'killi
par.b_Zn = 0.4856; free.b_Zn = 1; units.b_Zn = 'g/d.mg'; label.b_Zn = 'killing
par.k_eCd = 56.0527; free.k_eCd = 1; units.k_eCd = '1/d'; label.k_eCd = 'elimi
par.k_eCu = 442.5756; free.k_eCu = 1; units.k_eCu = '1/d'; label.k_eCu = 'elim
par.k_ePb = 0.0054207; free.k_ePb = 1; units.k_ePb = '1/d'; label.k_ePb = 'eli
par.k_eZn = 569.9706; free.k_eZn = 1; units.k_eZn = '1/d'; label.k_eZn = 'elim
par.d_xy = [7.1001e-06 0.0064216 0.074399 0.00085962 0.00047524 0.001
% other
par.h = 0.01277; free.h = 1; units.h = '1/d'; label.h = 'hazard rate in the bl
```

Binary compound alone:



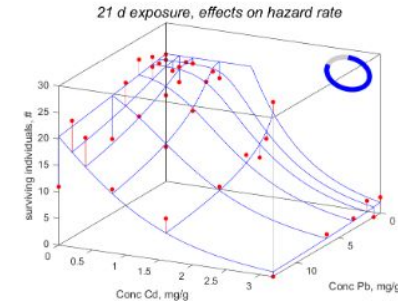
OECD232_Cd_Pb

author: Bas Kooijman
institution: VU University Amsterdam
email: bas.kooijman@vu.nl
date: 2022 3 1
toxTest: OECD232
species: Folsomia candida
casno: 7440-43-9 & 7439-92-1
compound: Cd & Pb
endpoint: # surviving individuals
target: hazard rate
DEBpars: NA
DEBmodel: [NA](#)

[results](#)

[elasticities](#)

[bibliography](#)



[TKTD model](#)

Toxicokinetic assumptions

- The temperature, food density and external concentrations (i.e. in the water) are constant
- The uptake rates are proportional to the external concentrations
- The elimination rates k_e are proportional to the internal concentrations

Toxicodynamic assumptions

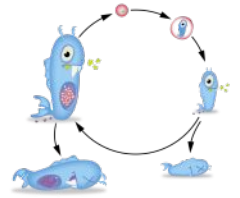
- Effects are linked to the internal concentrations c_x and c_y , scaled such that they have the dimension of external concentrations
- The hazard rate equals $h + b_x \cdot \max(0, c_x - c_{0x}) + b_y \cdot \max(0, c_y - c_{0y}) + d_{xy} \cdot \max(0, c_x - c_{0x}) \cdot \max(0, c_y - c_{0y})$ for no-effect concent

Discussion

- Growth is neglected

Facts

“Philosophy of modelling effects”

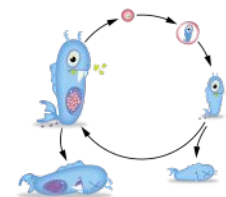


Choose your reference model and parameters

Effects modelled as a change in a well chosen parameters

Goal: understanding instead of describing data

AmP procedure can be used to obtain control model and parameters.



RESEARCH

Open Access



Modelling effects of time-variable exposure to the pyrethroid beta-cyfluthrin on rainbow trout early life stages

Elke I. Zimmer^{1*} , Thomas G. Preuss², Steve Norman³, Barbara Minten⁴ and Virginie Ducrot²

AmP entry for
rainbow trout
Control model
and parameters

Availability of data and materials

All data generated or analysed during this study are included in this published article and its Additional file.

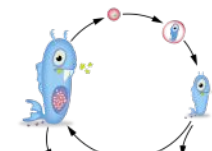
The physiological model for rainbow trout and the data used for its parameterization are available from: https://www.bio.vu.nl/thb/deb/deblab/add_my_pet/entries_web/Oncorhynchus_mykiss/Oncorhynchus_mykiss_res.html, Version: 20170527.



Contents lists available at ScienceDirect

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Prediction of long-term variation in offspring metabolism due to BPA in eggs in rainbow trout using the DEB model

B. Sadoul^{a,b,*,1}, S. Augustine^{c,1}, E. Zimmer^d, M.-L. Bégout^e, M.M. Vijayan^a

Table 1

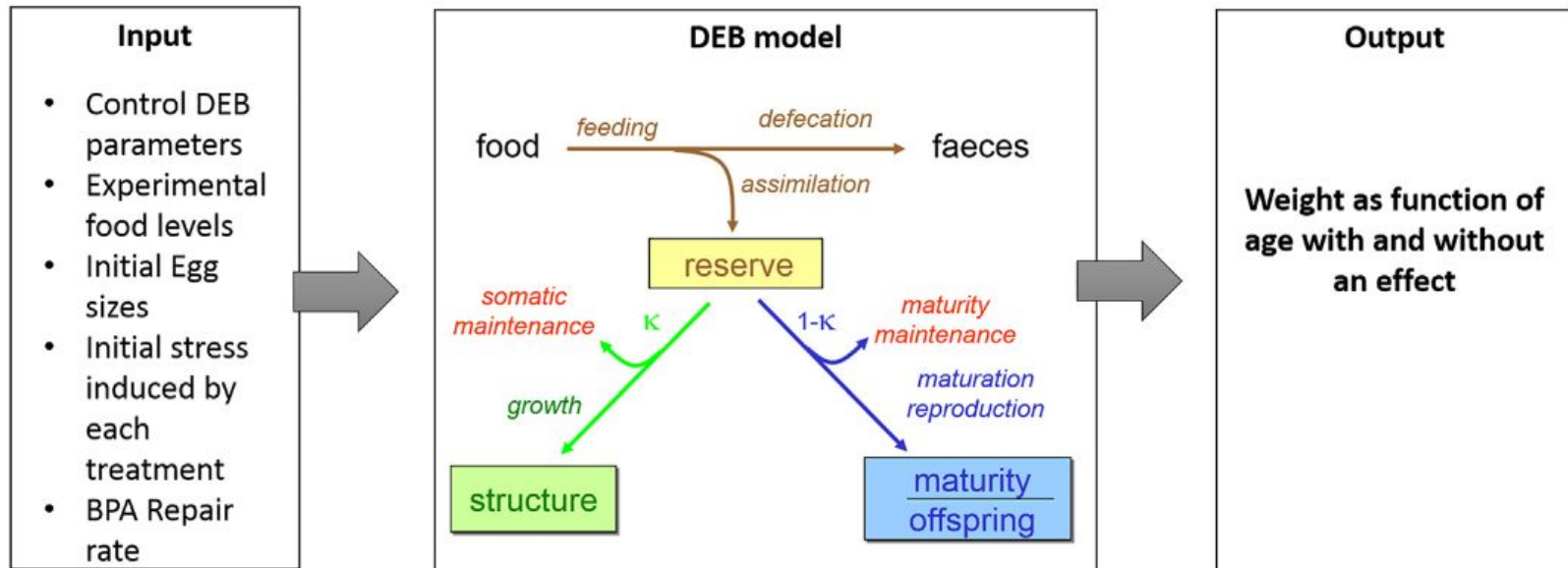
Primary parameter values estimated in this study at reference temperature (20 °C) and uploaded online ([AmP version 20171030](#)).

Symbol	Value	Unit	Description
$\{\dot{p}_{Am}\}$	2512	J/d/cm ²	Maximum surface area specific assimilation rate
$\{\dot{f}_m\}$	6.5	l/d/cm ²	Maximum specific searching rate
κ_X	0.8	–	Digestion efficiency of food to reserve
κ_P	0.1	–	Faecation efficiency of food to faeces
$\dot{v}$	0.03	cm/d	Energy conductance
κ	0.62	–	Allocation fraction to soma
κ_R	0.95	–	Reproduction efficiency
$[p_M]$	344	J/d/cm ³	Volume specific somatic maintenance
$\dot{k}_J$	0.002	1/d	Maturity maint rate coefficient
$[E_G]$	5268	J/cm ³	Specific cost for structure
E_H^b	43	J	Maturity at birth
E_H^j	854	J	Maturity at metamorphosis
E_H^p	388 10 ⁴	J	Maturity at puberty
$\dot{h}_a$	3.004 10 ⁻²⁴	1/d ²	Weibull aging acceleration
s_G	10	–	Gompertz stress coefficient

Parameters $\{\dot{f}_m\}$, κ_X , κ_P , κ_R , $\dot{k}_J$, $\dot{h}_a$ and s_G were fixed.

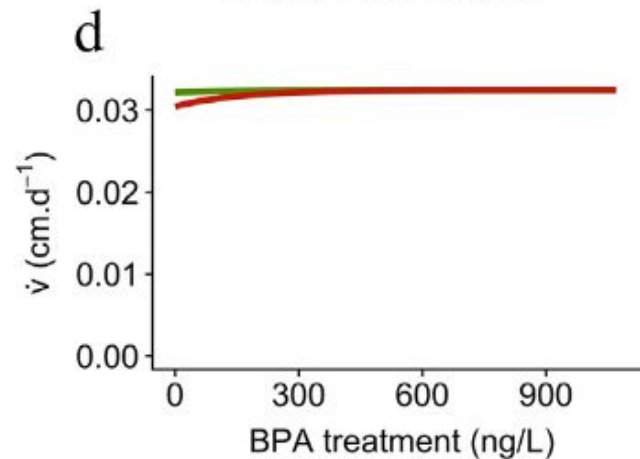
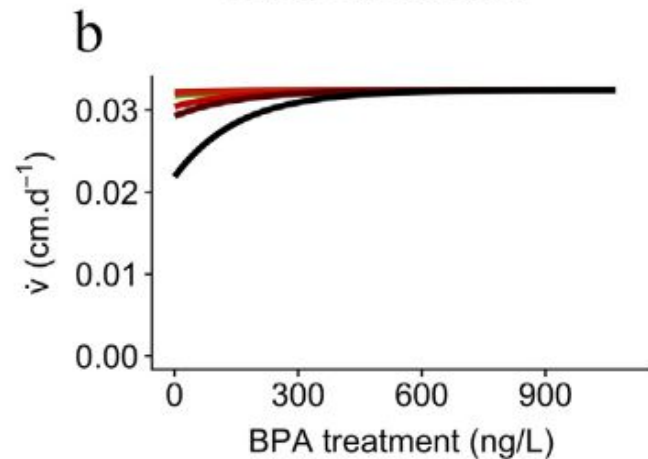
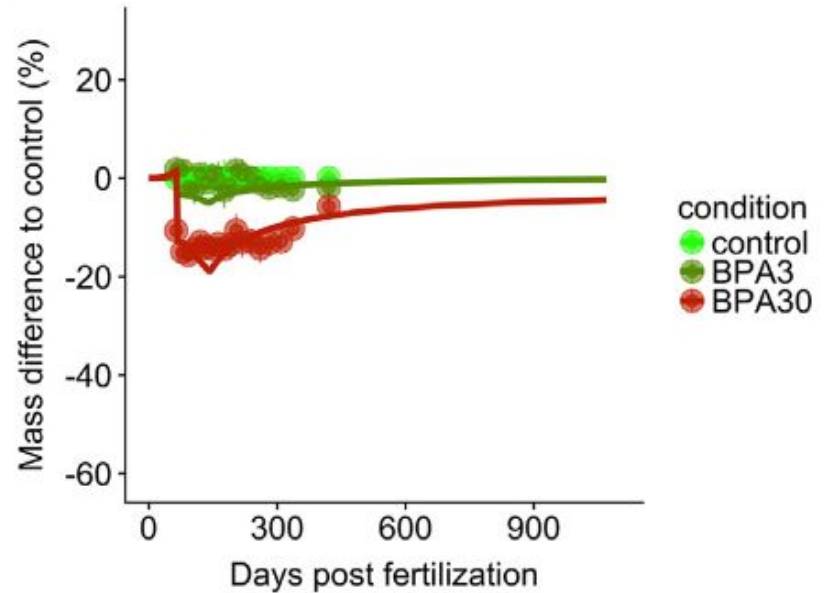
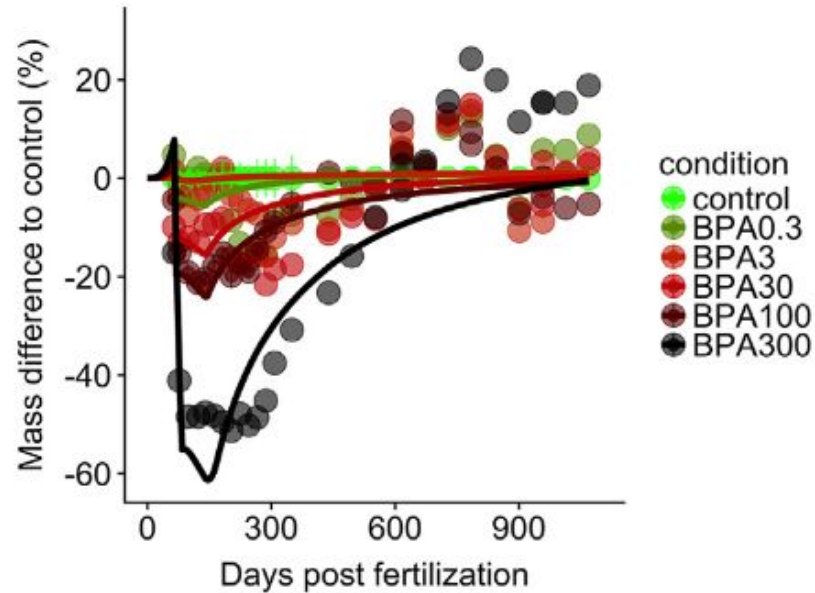
Prediction of long-term variation in offspring metabolism due to BPA in eggs in rainbow trout using the DEB model

B. Sadoul^{a,b,*,1}, S. Augustine^{c,1}, E. Zimmer^d, M.-L. Bégout^e, M.M. Vijayan^a

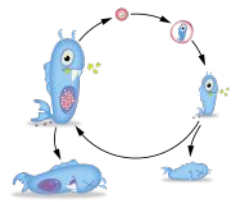


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Regulation of reproductive processes with dynamic energy budgets



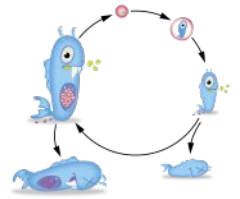
Erik B. Muller^{1,2}  | Konstadia Lika³ | Roger M. Nisbet⁴ | Irvin R. Schultz⁵ | Jérôme Casas⁶ | André Gergs⁷ | Cheryl A. Murphy⁸ | Diane Nacci⁹ | Karen H. Watanabe¹⁰

2.2 | Dynamic energy budget theory

This study uses the standard model of dynamic energy budget (std-DEB) theory as a reference. Since Kooijman (2010) has described

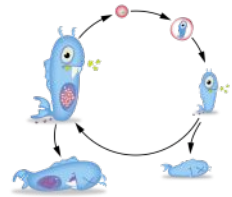
Interpretation		Value	Source
(c) Fixed parameters (T = 11°C)			
d_M	C-mole to dry weight conversion	24.6 g/C-mole	AmP ^a
d_W	Wet weight to dry weight conversion	0.2	AmP
f	Scaled food density	0.9	See text ^b
j_M	Specific maintenance rate	0.025/day	AmP
k_j	Maturity maintenance coefficient	0/day	See text
m_{FO}	Initial density of reproductive matter (stdDEB+)	0 ^c	See text
m_{GM}	Maximum density of reproductive matter (stdDEB+)	6.60	See text
M_{Vm}	Maximum structural biomass	1.12 C-mole	AmP
y_F	Conversion efficiency general reserve to reproductive buffer	0.95	AmP
y_G	Conversion efficiency reproductive reserve to gonads (stdDEB+)	1	See text
y_{RE}	Conversion efficiency general to reproductive reserve	0.95	AmP
y_V	Conversion efficiency general reserve to structure	0.88	AmP
κ	Fraction reserves allocated to soma (stdDEB+)	0.56	AmP

“Effects” as deviations from a well chosen reference



Here the strategy is to have some parameters fixed because estimated from data, and then estimate parameters from modules which can be removed.

Trajectory reconstruction

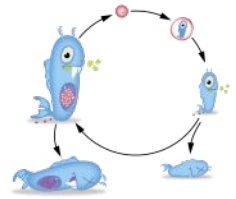


Option 1 : Adopt the same strategy outlined before.
Choose a reference set of parameters, and back
estimate past food and temperature conditions:

in the reference growth is a function of food

for the trajectory reconstruction : write out food as a function of growth. Treat growth parameters as “given”. Estimate the food parameters.

Option 1 : Adopt the same strategy outlined before.
Choose a reference set of parameters, and back
estimate past food and temperature conditions:



Journal of Sea Research

journal homepage: www.elsevier.com/locate/seares

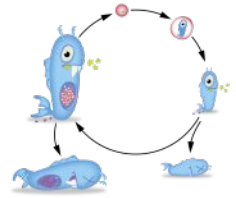


What can the shell tell about the scallop? Using growth trajectories along
latitudinal and bathymetric gradients to reconstruct physiological history
with DEB theory



Romain Lavaud^{a,b,*}, Aurélie Jolivet^b, Eric Rannou^c, Fred Jean^b, Øivind Strand^d,
Jonathan Flye-Sainte-Marie^b

Step 1: “reference parameters”



DEB CONTEXT COLLECTION PACKAGE USE

Pecten_maximus (Great scallop):

Results

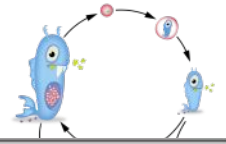
Code

Links



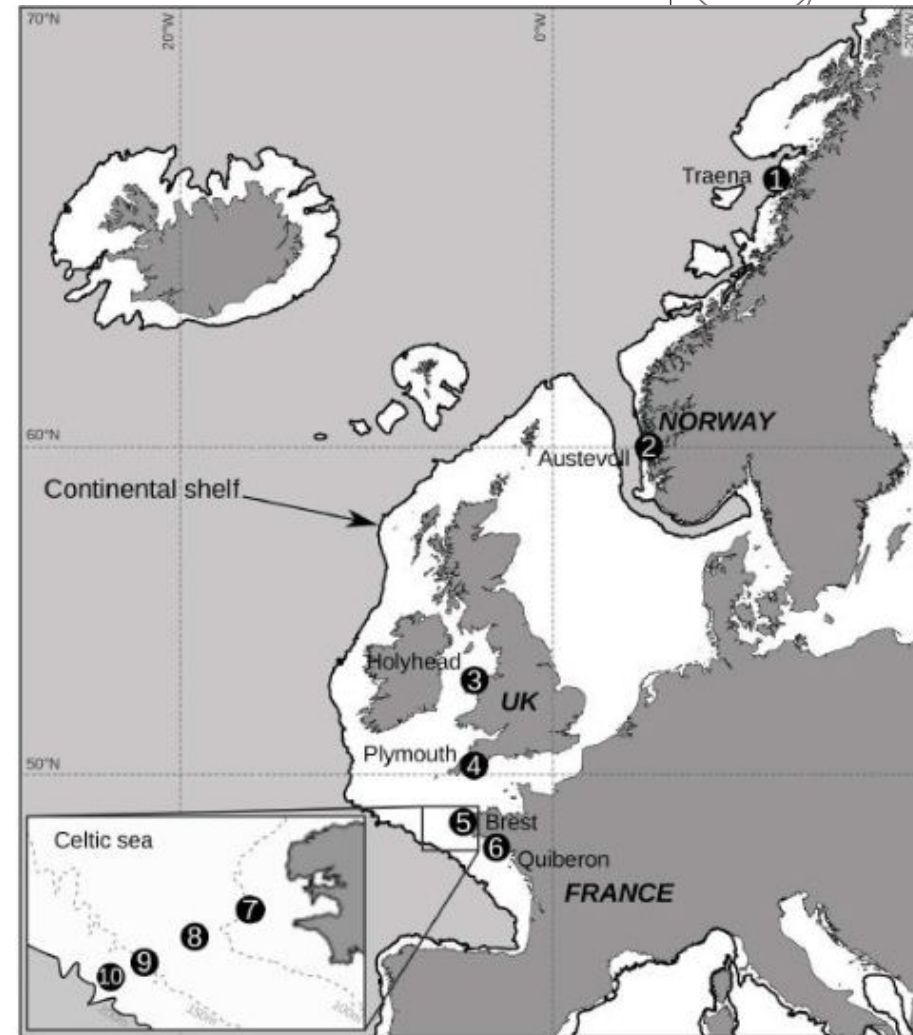
Predictions & Data for this entry

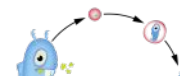
Model: abj	climate: MC	migrate:	phylum: Mollusca
COMPLETE = 2.5	ecozone: MANE	food: biPp	class: Bivalvia
MRE = 0.047	habitat: 0jMp, jiMb	gender: D	order: Ostreoida
SMSE = 0.009	embryo: Mp	reprod: O	family: Pectinidae



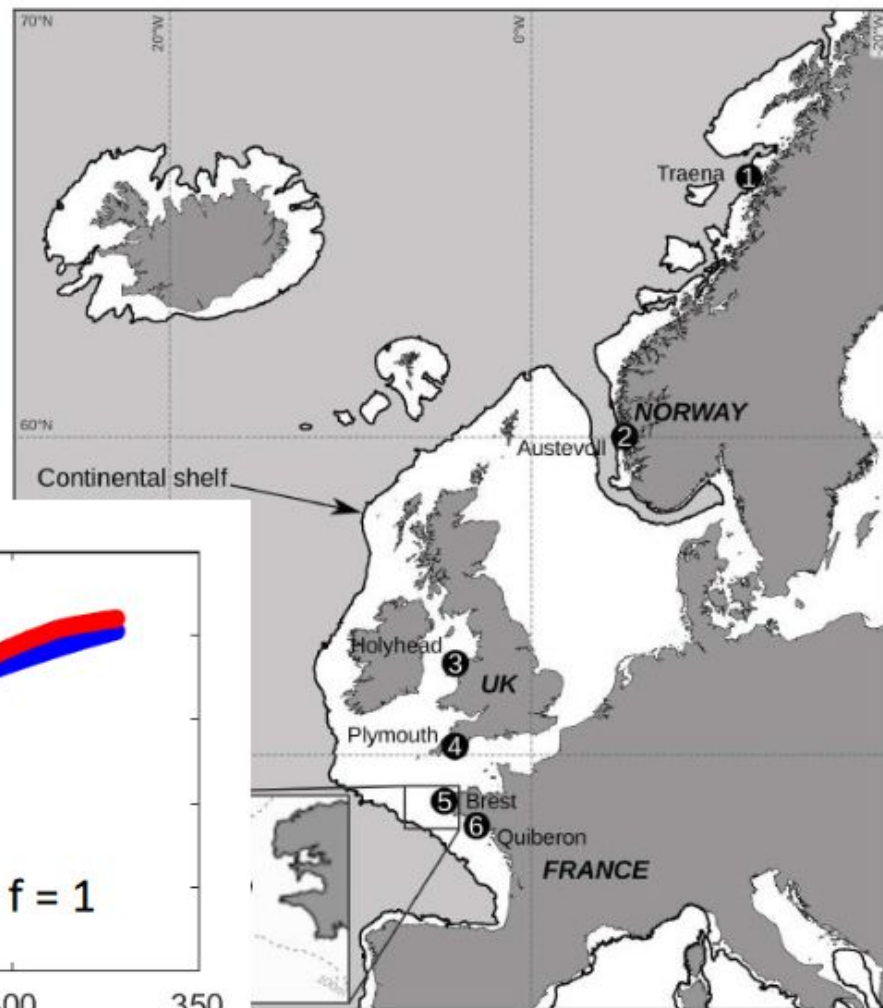
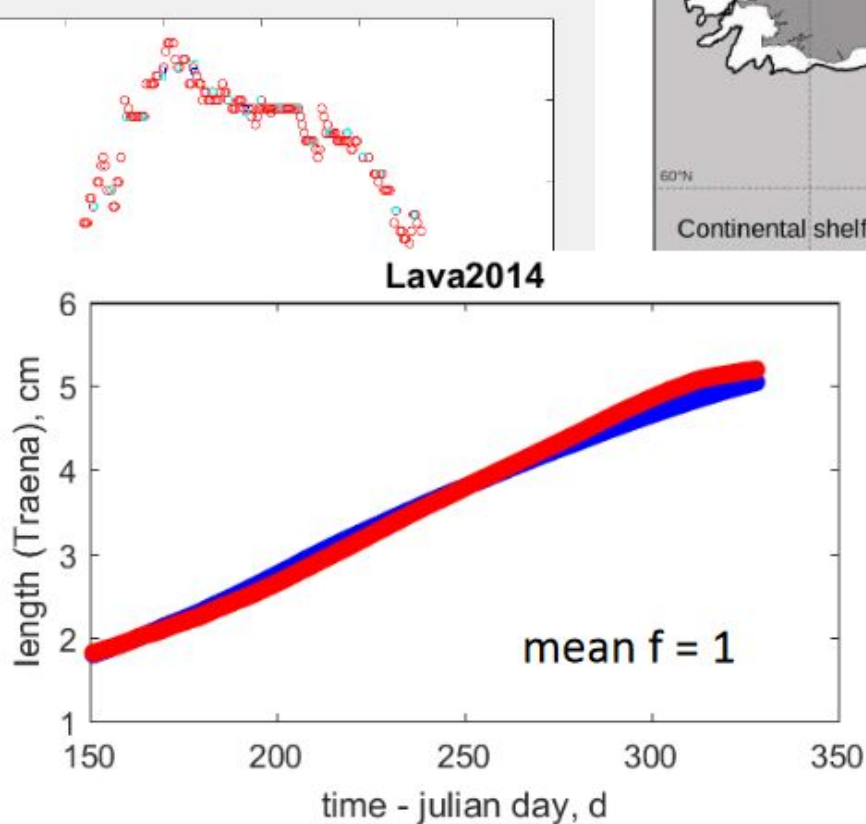
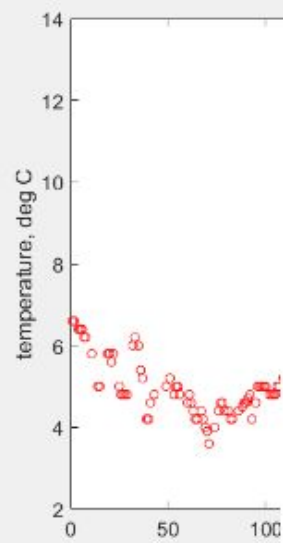
Three sites:

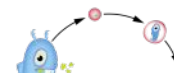
Brest
Celtic Sea
Træna



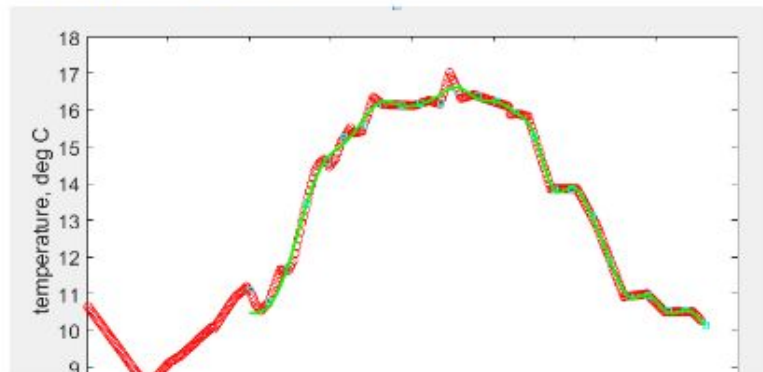


Traena

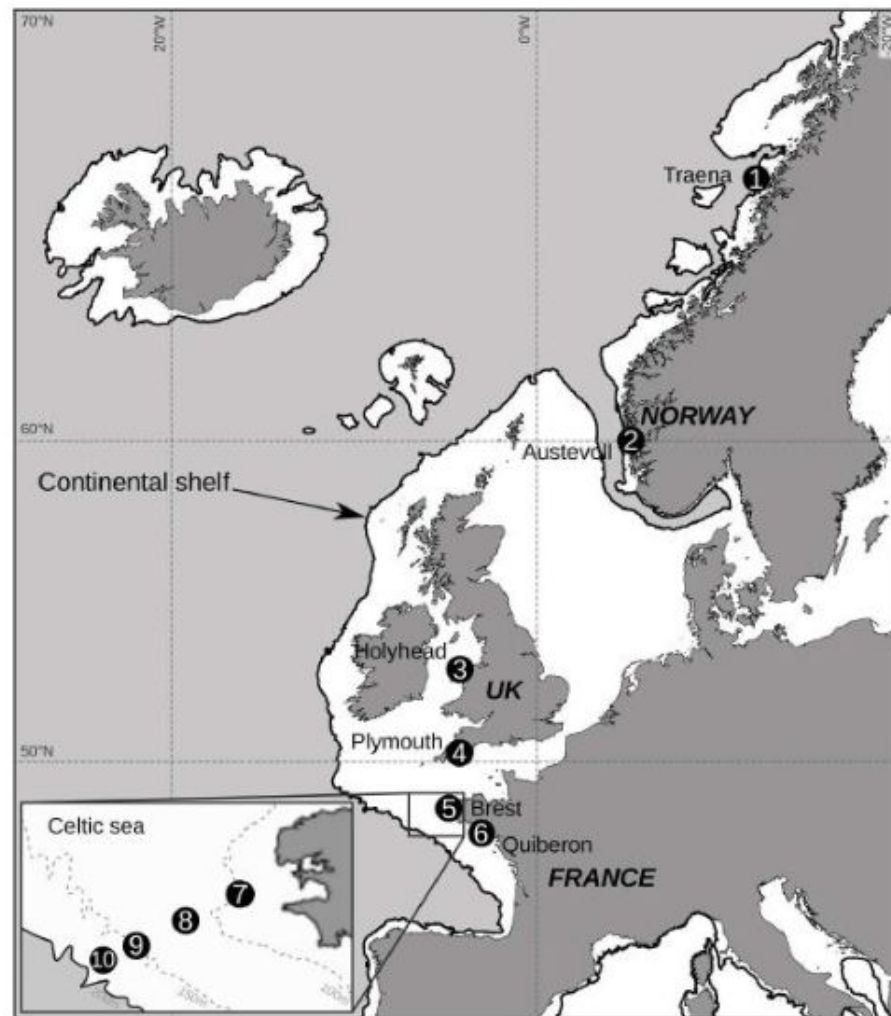
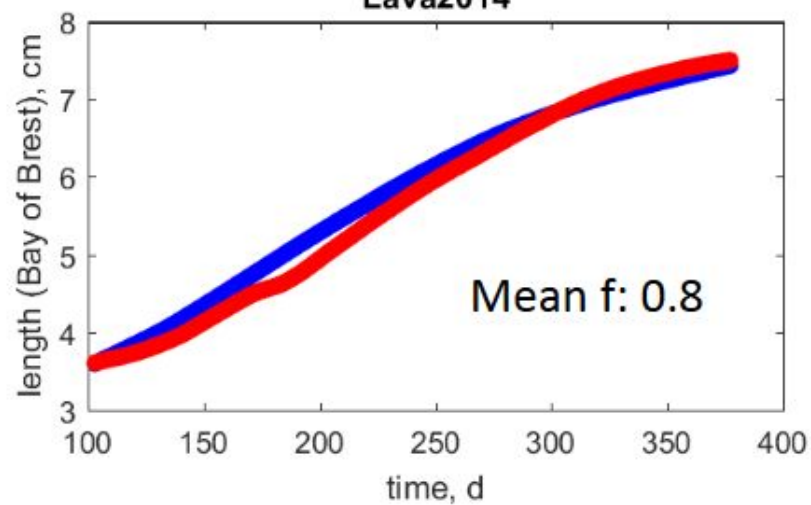


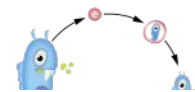


Brest



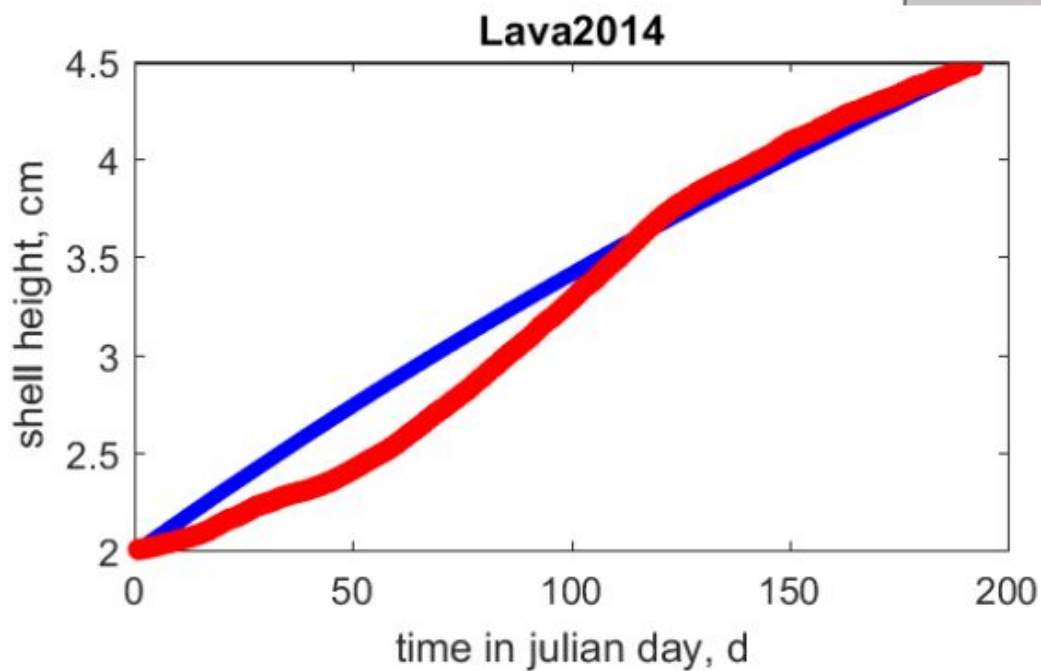
Lava2014

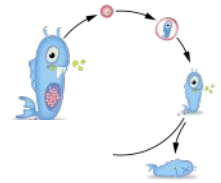




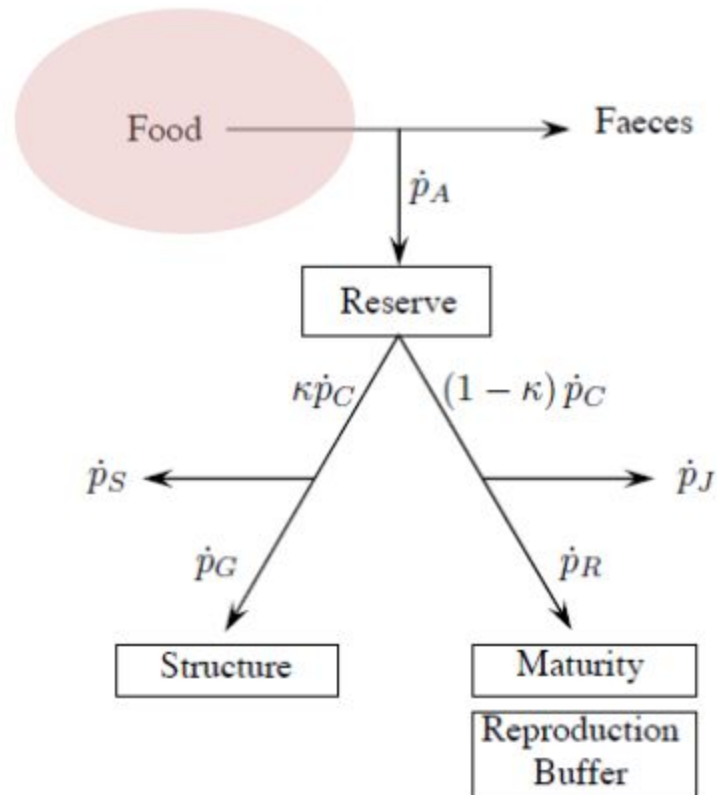
Celtic Sea

Constant 12 degrees mean f: 0.66





Problem formulation



$\dot{p}_A$: Assimilation

$\dot{p}_C$: Mobilization

κ : Fraction of $\dot{p}_C$ mobilized towards growth and somatic maintenance

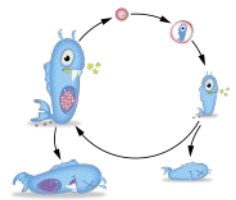
$\dot{p}_S$: Somatic maintenance

$\dot{p}_J$: Maturity maintenance

$\dot{p}_G$: Growth

$\dot{p}_R$: Maturity then Reproduction

The DEB parameters are treated as known – they are the reference



Energy fluxes:

Energy fluxes:

$$\dot{p}_A = f(X) \{ \dot{p}_{Am} \} V^{2/3}$$

$$\dot{p}_C = E \left(\frac{[E_G] \dot{v} V^{2/3} + \dot{p}_S}{\kappa E + [E_G] V} \right)$$

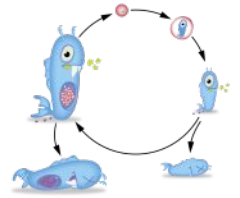
$$\dot{p}_S = [\dot{p}_M] V + \{ \dot{p}_T \} V^{2/3}$$

$$\dot{p}_G = \kappa \dot{p}_C - \dot{p}_S$$

$$\dot{p}_J = \dot{k}_J E_H$$

$$\dot{p}_R = (1 - \kappa) \dot{p}_C - \dot{p}_J$$

Reconstruct the past food level



Energy fluxes:

$$\dot{p}_A = f(X) \{ \dot{p}_{Am} \} V^{2/3}$$

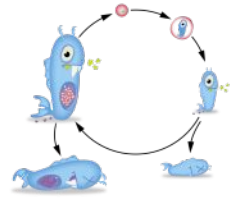
$$\dot{p}_C = E \left(\frac{[E_G] \dot{v} V^{2/3} + \dot{p}_S}{\kappa E + [E_G] V} \right)$$

$$\dot{p}_S = [\dot{p}_M] V + \{ \dot{p}_T \} V^{2/3}$$

$$\dot{p}_G = \kappa \dot{p}_C - \dot{p}_S$$

$$\dot{p}_J = \dot{k}_J E_H$$

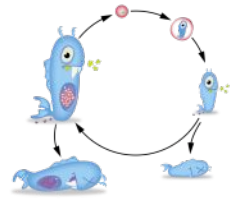
$$\dot{p}_R = (1 - \kappa) \dot{p}_C - \dot{p}_J$$



Approach

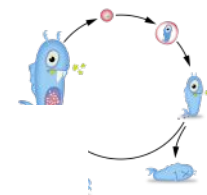
Growth is a function of food

Food is a function of growth

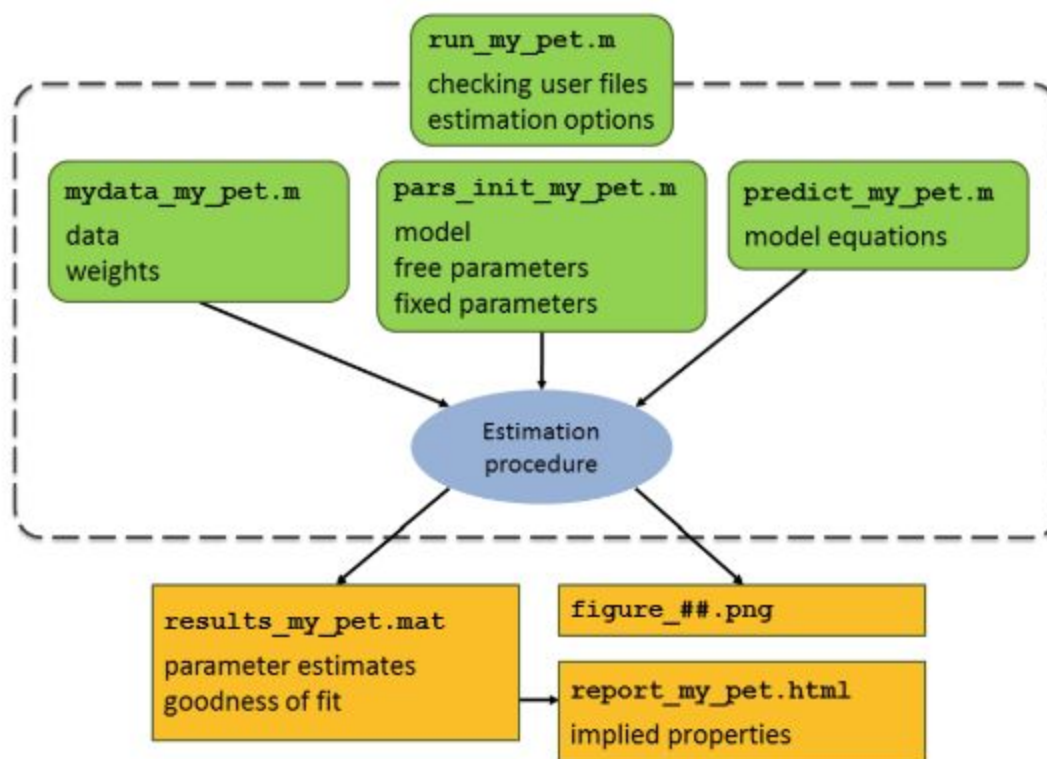


Approach:

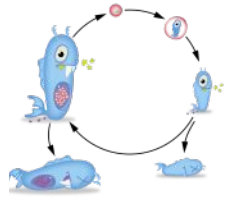
- Step 1: download parameter values
- Step 2: modify the 4-user defined files
- Step 3: Estimate



Adapt the AmP code

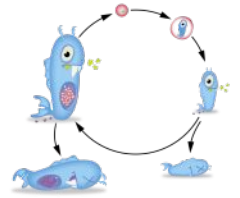


Steps for making your code



- **Step 1**: create folder with the 4-user defined files
- **Step 2**: edit the run file – (define the knot-abscissa for the f that is being estimated - pass the knot abscissa as globals)
- **Step 3**: edit the pars_init file: fix the core DEB parameters, auxiliary parameters, and insert an f parameter for each of the knot abscissa defined in the run file (hint: pass the knot abscissa as a global)
- **Step 4**: modify the predict: remove unnecessary predictions, put prediction for length as function of time-varying food and temperature
- **Step 5**: create additional plots at the end of the run-file

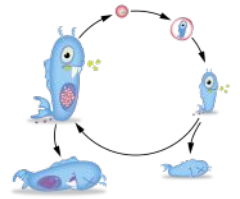
Step 3: edit the pars_init file:



Put results_Pecten_maximus.mat in your working directory

```
mat2pars_init('Pecten_maximus', 1)
```

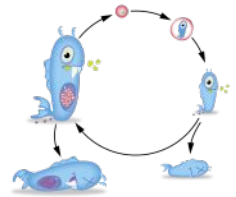
insert an f parameter for each of the knot abscissa defined in the run file (hint: pass the knot abscissa as a global)



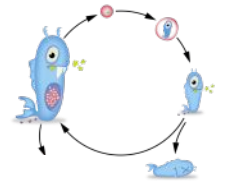
Questions to explore:

- Interval of knot functions
- Interpolation of temperature and food
- Initial conditions
- Starting values for free parameters
- Comparing across sites

add-my-pet/AmPtox

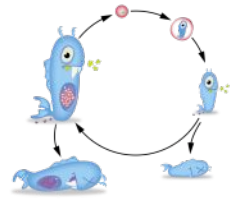


DEB2023_reconstruction	6/7/2023 11:02 PM	File folder
docs	3/13/2023 3:53 AM	File folder
no_pet	6/7/2023 8:03 PM	File folder
OECD201_LAS	6/7/2023 8:04 PM	File folder
OECD202_dichromate	6/7/2023 8:05 PM	File folder
OECD203_dieldrin	5/23/2023 4:57 AM	File folder
OECD210_PAH	5/23/2023 4:57 AM	File folder
OECD221_Cd	3/13/2023 3:53 AM	File folder
OECD222_Cu	3/13/2023 3:53 AM	File folder
OECD232_Cd_Cu_Pb_Zn	5/23/2023 4:57 AM	File folder
OECD232_Cd_Pb	6/7/2023 8:59 PM	File folder
OECD232_Cd_Zn	3/13/2023 3:53 AM	File folder
OECD232_Cu_Cd	3/13/2023 3:53 AM	File folder
OECD232_Cu_Pb	5/10/2023 4:25 AM	File folder
OECD232_Zn_Cu	3/13/2023 3:53 AM	File folder
OECD232_Zn_Pb	5/23/2023 4:57 AM	File folder



 Pecten_maximus	6/7/2023 11:02 PM	File folder
 reconstruction_brest	6/7/2023 11:02 PM	File folder
 reconstruction_celtic	6/7/2023 11:02 PM	File folder
 reconstruction_traena	6/7/2023 11:02 PM	File folder

Start with Celtic



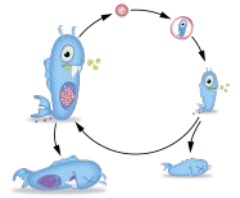
What can the shell tell about the scallop? Using growth trajectories along latitudinal and bathymetric gradients to reconstruct physiological history with DEB theory

Romain Lavaud^{a,b,*}, Aurélie Jolivet^b, Eric Rannou^c, Fred Jean^b, Øivind Strand^d,
Jonathan Flye-Sainte-Marie^b



For full discussion. This was just to illustrate.

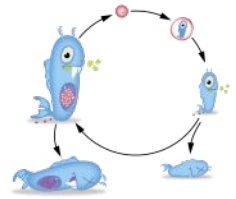
Options:



Option 1 : Adopt the same strategy outlined before.
Choose a reference set of parameters, and back
estimate past food and temperature conditions:

Option 2 : Integrate your reconstruction directly into
the “main” estimation

Many examples in collection of option 2:



https://amptool.debtheory.org/docs/index.html

SECTION | DEB | CONTEXT | COLLECTION | PACKAGE | USE | SERVER

VU

the data time length for embryos as well as wet weight at birth.

Selection on strings in mydata and predict files

A motivation for this type of selection could be the question 'which entries have a changing (scaled) function response in time' and which of these entries have males and females with different parameters)? The answer involves `select_predict`, using the knowledge that such predict files make use of the string 'f = spline1(t, tf)' and 'male', respectively. The required code is

```
[species, nm] = select_predict('f = spline1(t, tf)'); select_predict(nm, 'males')
```

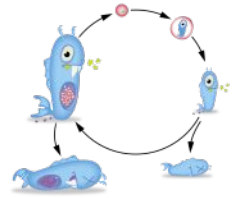
Notice that the default first argument of `select_predict` is absent in the first call (so 'Animalia' is assumed), but present in the second call. Similarly, `select_mydata` can be used for mydata files, e.g. to search for particular authors in references.

Selection in general

you can find a list in the collection by looking for predict files where food level is splined.

often knots are chosen within the predict, and the knot abscissa (parameters) are defined in `pars_init`.

Data: types



Different “nomenclatures” - statistical nomenclature is followed here

zero-
uni-
bi-
tri-

of independent variables !

multi-

more than 1 dependant variables !

Final slide



Questions?