AmP projects: Setting up

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AmP projects

- Set up individual objectives and plan for the „own project" time (14hrs)
(+ DEB in practice)

- Final day: 3 hours total of AmP presentations.
  - Groups of 1-3 people, 7min/person or 10 min/group

Topics and objectives of lecture:

- File descriptions
- Auxiliary theory (know the difference between core DEB theory and auxiliary theory assumptions)
- Know how to navigate AmP database and associated resources

Code structure
Input-Output files
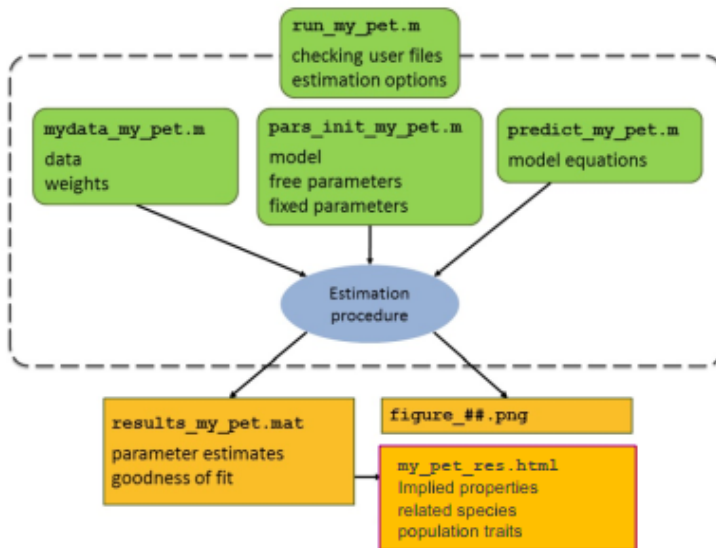
mydata_my_pet
- Sets metaData (classification, eco-codes, links, references etc)
- Sets the data (real data, pseudo data, auxiliary data)
- Sets weight coefficients

predict_my_pet
- Computes the predictions for the data sets in mydata-file given parameter values
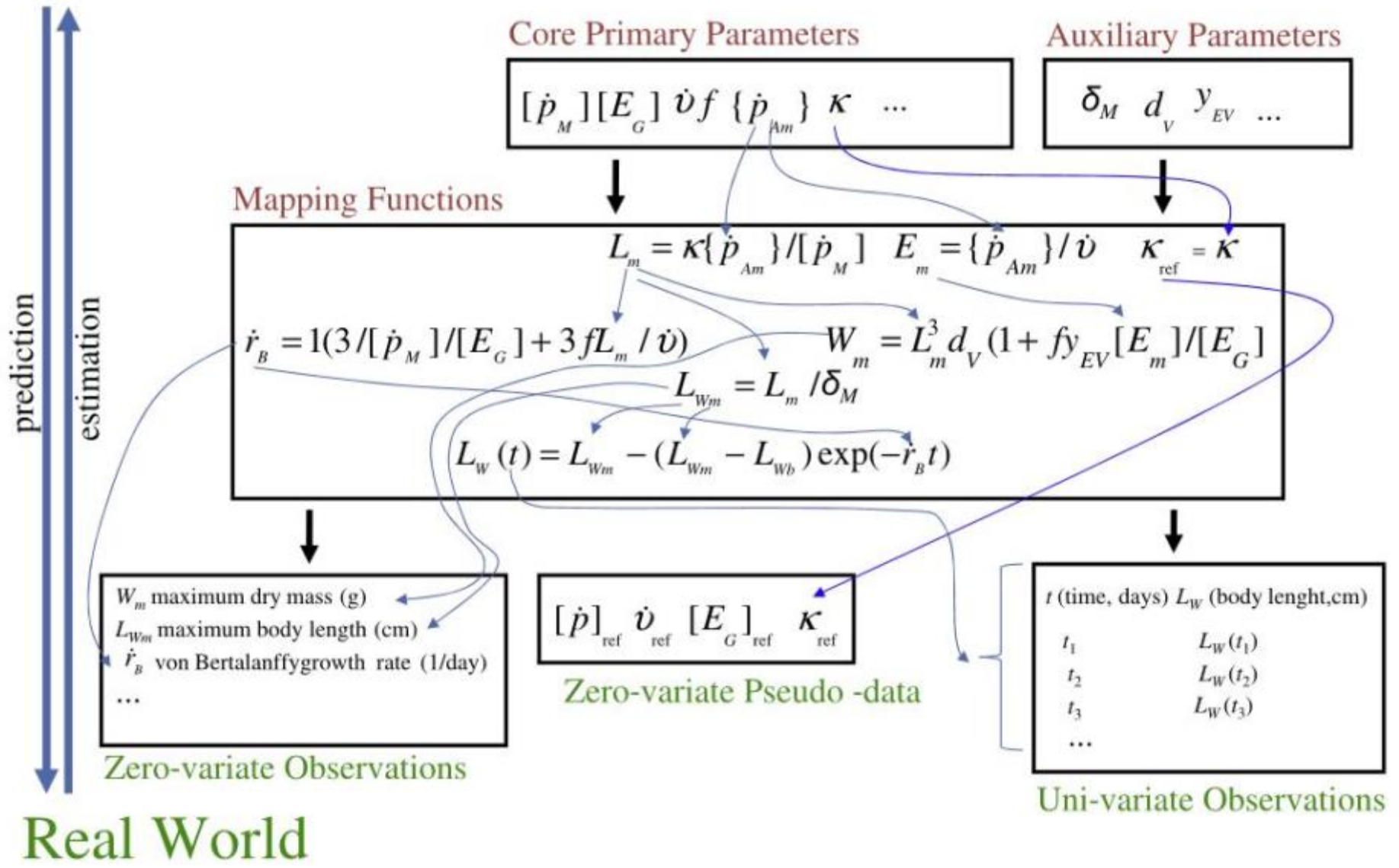
pars_init_my_pet
- Sets the model
- Sets the initial parameter values to start the estimation procedure

run_my_pet
- Checks the user's files
- Sets the estimation options
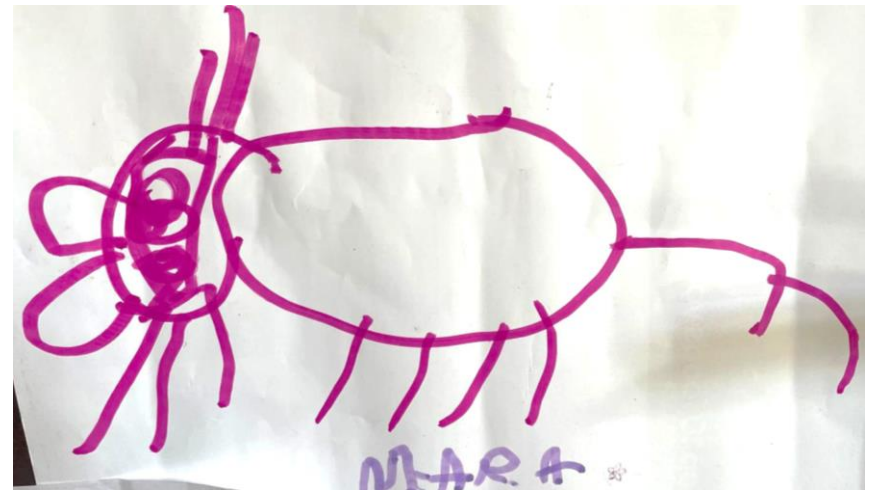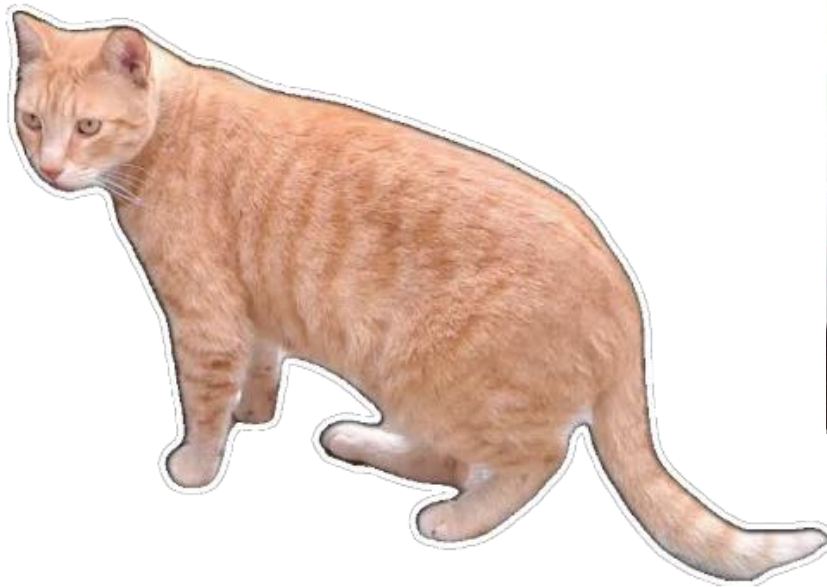- Runs the estimation procedure

IMPORTANT: work in a local (your) folder where only *your species* files are; set paths to DEBtool and AmPtool, which should be somewhere separately

Abstract World

Core Primary Parameters

$$[\dot{p}_M]\ [E_G]\ \dot{v}\ f\ \{\dot{p}_{Am}\}\ \kappa\ \ldots$$

Auxiliary Parameters

$$\delta_M\ d_V\ y_{EV}\ \ldots$$

Mapping Functions

$$L_m = \kappa\{\dot{p}_{Am}\}/[\dot{p}_M] \quad E_m = \{\dot{p}_{Am}\}/\dot{v} \quad \kappa_{ref} = \kappa$$

$$\dot{r}_B = 1(3/[\dot{p}_M]/[E_G] + 3fL_m/\dot{v}) \qquad W_m = L_m^3 d_V (1 + fy_{EV}[E_m]/[E_G]$$

$$L_{Wm} = L_m/\delta_M$$

$$L_W(t) = L_{Wm} - (L_{Wm} - L_{Wb})\exp(-\dot{r}_B t)$$

W_m maximum dry mass (g)

L_{Wm} maximum body length (cm)

$\dot{r}_B$ von Bertalanffygrowth rate (1/day)

...

Zero-variate Observations

$$[\dot{p}]_{ref}\ \dot{v}_{ref}\ [E_G]_{ref}\ \kappa_{ref}$$

Zero-variate Pseudo -data

t (time, days)	L_W (body lenght,cm)
t_1	$L_W(t_1)$
t_2	$L_W(t_2)$
t_3	$L_W(t_3)$
...	

Uni-variate Observations

prediction

estimation

Real World

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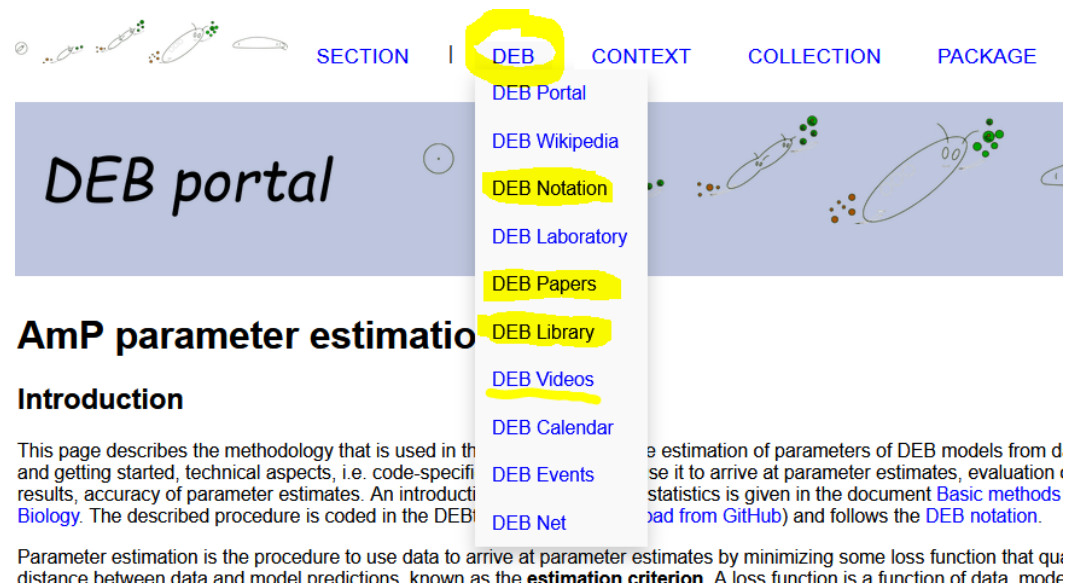# Reality   vs. model

Don't stress!

Some suggestions (data and eqs)

- Zotero DEB library as a resource

- Stay on top of references and units for data

- Make notes of important details to help modeling and interpretation

- Transform data in the mydata files – keep track of transformations in one place and transform into standard DEB units (cm, g, J, etc)

- Always have *DEB notation* handy. Follow the nomenclature in the equations but also how the code relates to the symbols

Work with your own equation notes

$$L(t) = L_\infty - (L_\infty - L_b)\exp(-t\dot{r}_B) \quad \text{or} \quad t(L) = \frac{1}{\dot{r}_B}\ln\frac{L_\infty - L_b}{L_\infty - L}$$

$$\dot{r}_B = \frac{1}{3/\dot{k}_M + 3fL_m/\dot{v}} = \frac{\dot{k}_M/3}{1 + f/g}$$

$$L_\infty = fL_m - L_T$$

```
% time-length
rT_B = kT_M/ 3/ (1 + f_tL/ g); L_i = L_m * f_tL; L_b = L_m * get_lb([g k v_Hb], f_tL);
L = L_i - (L_i - L_b) * exp( - rT_B * tL_f(:,1)); % cm, structural length at time
ELw_f = L/ del_M;                                 % cm, shell length
```

Data and equations - suggestions

- Have handy the papers (or their appendices) with the most useful equations you will be using

- Write units in comments next to quantities in the code

- First change equations and assumptions in your *notes*, only after that change them in your *code* (error in code vs. error in model/assumption)

Work with standardized nomenclature

DEB nomenclature

Standardized link between symbols and **code**

$$E_0 \qquad \text{E\_0}$$

$$a_b, a_p \qquad \text{aT\_b}$$

$$a_m$$

units $\longleftarrow$ L_b, L_p

$$L_\infty$$

$$W_w^b$$

$$W_w^p \qquad \text{Ww\_p}$$

$$W_w^\infty$$

$$N_\infty$$

Calculating quantities with DEBtool

Symbol	Units	Interpretation	
E_0	J	initial energy in egg	initial_scaled_reserve
a_b, a_p	d	age at birth, puberty	get_tj
a_m	d	age at death	get_tm_mod
L_b, L_p	cm	structural length at birth, puberty	get_tj
L_∞	cm	ultimate volumetric length	$s_{\mathcal{M}} f L_m$
W_w^b	g	wet weight at birth	$L_b^3(1 + f\omega)$
W_w^p	g	wet weight puberty	$L_p^3(1 + f\omega)$
W_w^∞	g	ultimate wet weight	$L_\infty^3(1 + f\omega)$
N_∞	#	life time reproductive output	cum_reprod (std-DEB) or cum_reprod_j (abj-DEB)

Notes: some routines are pre-coded, some you will find in other predict files

Completeness score

Table 3

The completeness of available data can be ranked with marks from low to high at the following levels; each level includes previous levels.
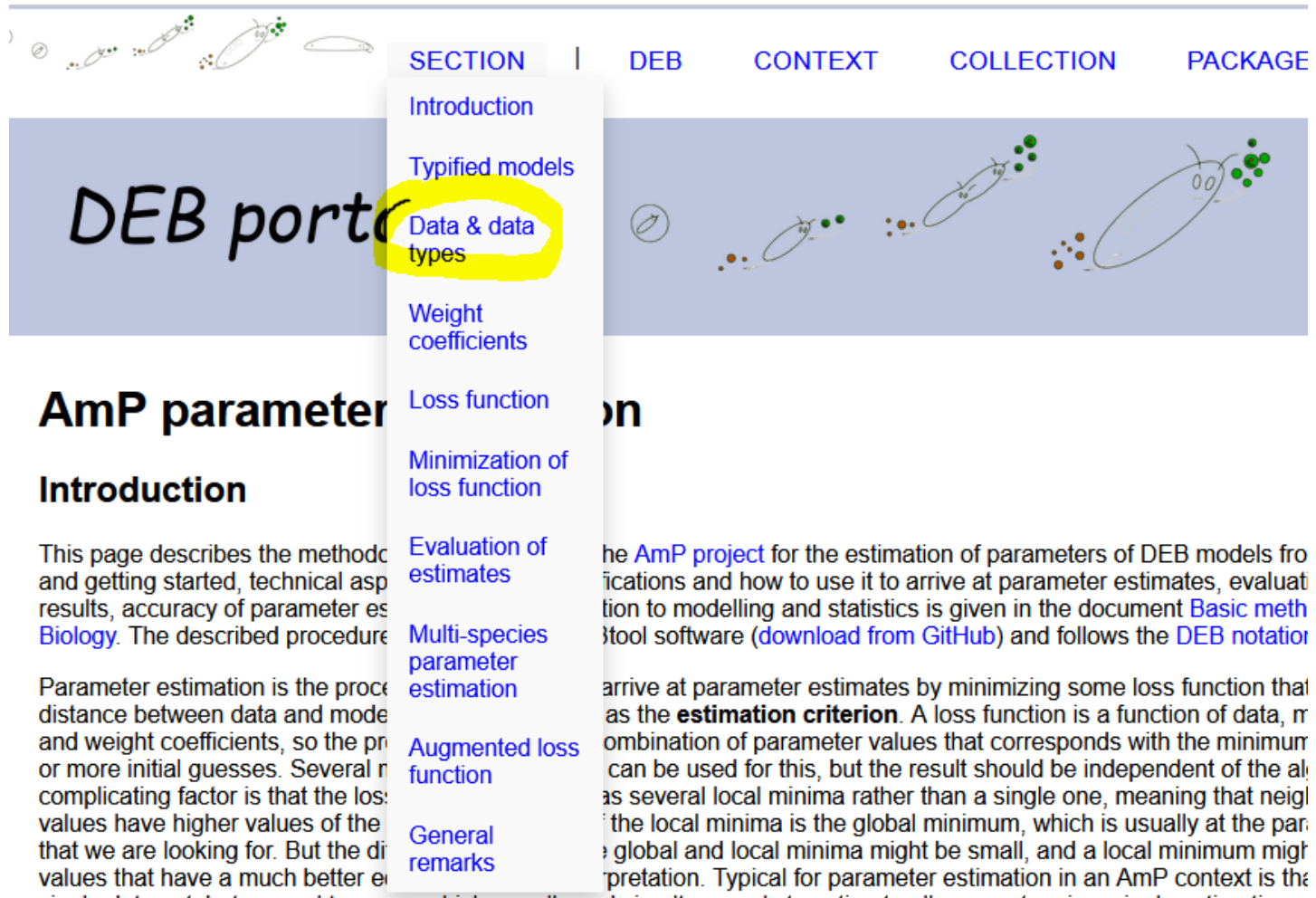
0	Maximum length and body weight; weight as function of length
1	Age, length and weight at birth and puberty for one food level; mean life span (due to ageing)
2	Growth (curve) at one food level: length and weight as functions of age at constant (or abundant) food level
3	Reproduction and feeding as functions of age, length and/or weight at one food level
4	Growth (curve) at several (>1) food levels; age, length and weight at birth and puberty at several food levels
5	Reproduction and feeding as functions of age, length and/or weight at several (>1) food levels
6	Respiration as function of length or weight and life span at several (>1) food levels
7	Elemental composition at one food level, survival due to ageing as function of age
8	Elemental composition at several (>1) food levels, including composition of food
9	Elemental balances for C, H, O and N at several body sizes and several food levels
10	Energy balance at several body sizes and several food levels (including heat)

Notes

- Sometimes your data will 'skip' a level: if you have e.g. data for levels 0-3, and then level 6, this is not 'complete=6' but lower!
- The more data *types* you have, the more information on parameters you have, but data are on different individuals and different conditions, so keep track of maintaining consistency

Check model outputs

```
'results_output':
0      - only saves data to .mat (no printing to html or screen and no figures) - use this for (automatic) continuations
1, -1  - no saving to .mat file, prints results to html (1) or screen (-1), shows figures but does not save them
2, -2  - saves to .mat file, prints results to html (2) or screen (-2), shows figures but does not save them
3, -3  - like 2 (or -2), but also prints graphs to .png files (default is 3)
4, -4  - like 3 (or -3), but also prints html with implied traits
5, -5  - like 4 (or -4), but includes related species in the implied traits
6      - like 5, but also prints html with population traits
```

file:///C:/Users/Nina/Dropbox (Personal)/w_DEB_turtle_MATLAB/deb_Dermochelys_Anna/DEB_Dermoche

Search for symbol .. | Search for units .. | Search for label .. | Short/Medium/Long/Pars

		Dermochelys coriacea		Caretta caretta		Caretta caretta MED		Lepidochelys kempii		Lepidochelys olivacea		Natator depressus		Chelonia mydas		Eretmochelys imbricata		date: 2025/05/27; allStat version: 2025/02/15
symbol	units	value	°C	value	°C	value	°C	value	°C	value	°C	value	°C	value	°C	value	°C	func resp	description
model	-	std	NA	std	NA	std	NA	std	NA	std	NA	std	NA	std	NA	std	NA	NA	typified model
T_typical	°C	21.13	NA	20	NA	21	NA	20	NA	20	NA	25	NA	23	NA	18	NA	NA	typical body temperature
T_A	K	8000	NA	7200	NA	7200	NA	8000	NA	8000	NA	6274	NA	7680	NA	8000	NA	NA	Arrhenius temperature
z	-	51.0009	NA	48.6078	NA	48.6078	NA	25.02	NA	26.839	NA	36.1956	NA	50.4458	NA	26.507	NA	NA	zoom factor
F_m	l/ d.cm^2	6.5	20	6.5	20	6.5	20	6.5	20	6.5	20	6.5	20	6.5	20	6.5	20	NA	{F_m}, max spec searching rate
kap_X	-	0.27883	NA	0.8	NA	0.8	NA	0.8	NA	0.8	NA	0.8	NA	0.8	NA	0.8	NA	NA	digestion efficiency of food to

Know your data labels

- https://debportal.debtheory.org/docs/AmPestimation.html

Finding predictions

Know your labels !!! debportal.debtheory.org/docs/Uni-variate_data.html

Look in species list

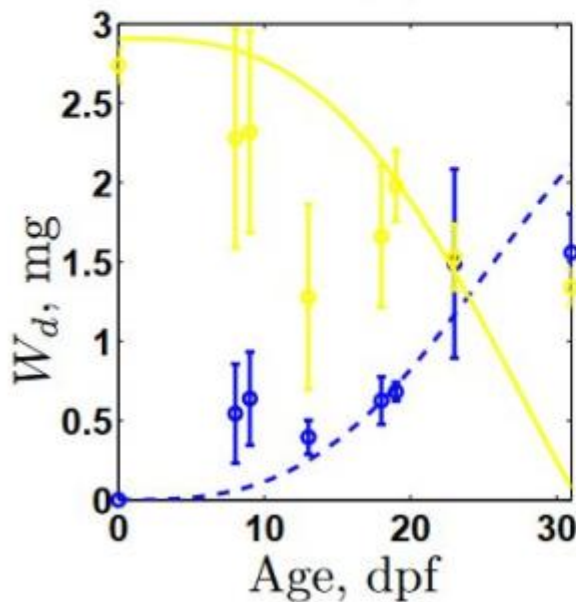Use AmPtool functions **amptool.debtheory.org/docs/**
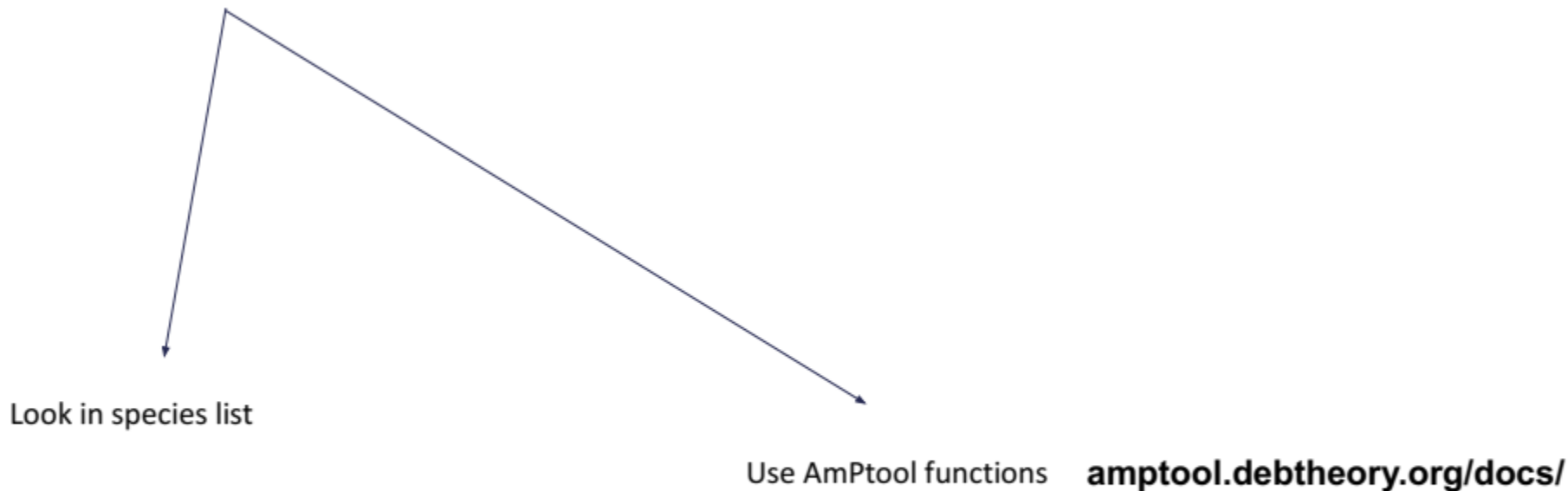
```
select_data({'t-Le','Wwb'},'std')
```

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

Examples of „maps"

Embryo yolk and body:

Abstract World

Model

State Variables
$$V, E, E_R$$

Core Primary Parameters
$$\dot{v}, [\dot{p}_M], \{\dot{p}_{Am}\}, [E_G], \kappa, \dots$$

Auxiliary Parameters
$$\delta_M, \mu_E, w_E, d_V, \dots$$

Mapping Functions

$$e_b = \frac{E_b}{V_b}$$

$$W_{emb} = (w_E - e_b m_{E_m} w_E)[M_V]V$$

$$W_Y = E \frac{w_E}{\mu_E} - e_b m_{E_m} w_E [M_V]V$$

prediction — estimation

Organism data

Real World

time (d)	Yolk dry mass (g)
t_1	$W_Y(t_1)$
t_2	$W_Y(t_2)$
t_3	$W_Y(t_3)$
...	

Uni-variate Observations

time (d)	Embryo dry mass (g)
t_1	$W_{emb}(t_1)$
t_2	$W_{emb}(t_2)$
t_3	$W_{emb}(t_3)$
...	

Uni-variate Observations

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'maps'

Python regius eats mice
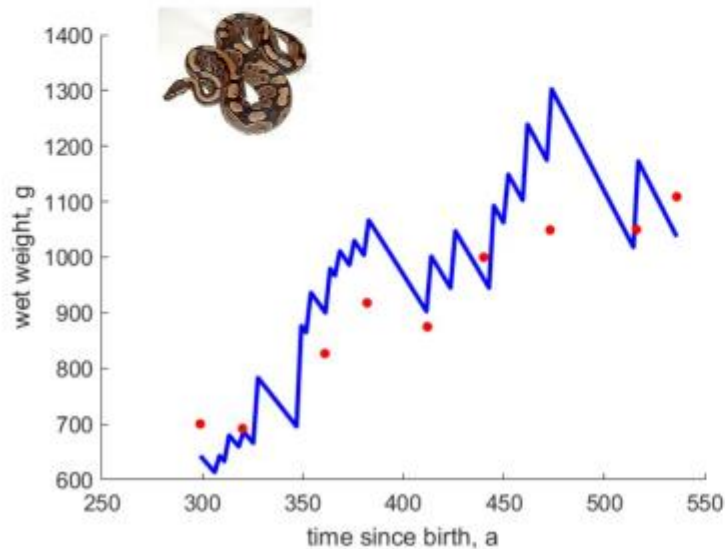
User defined function in the predict file to include weight of gut content:
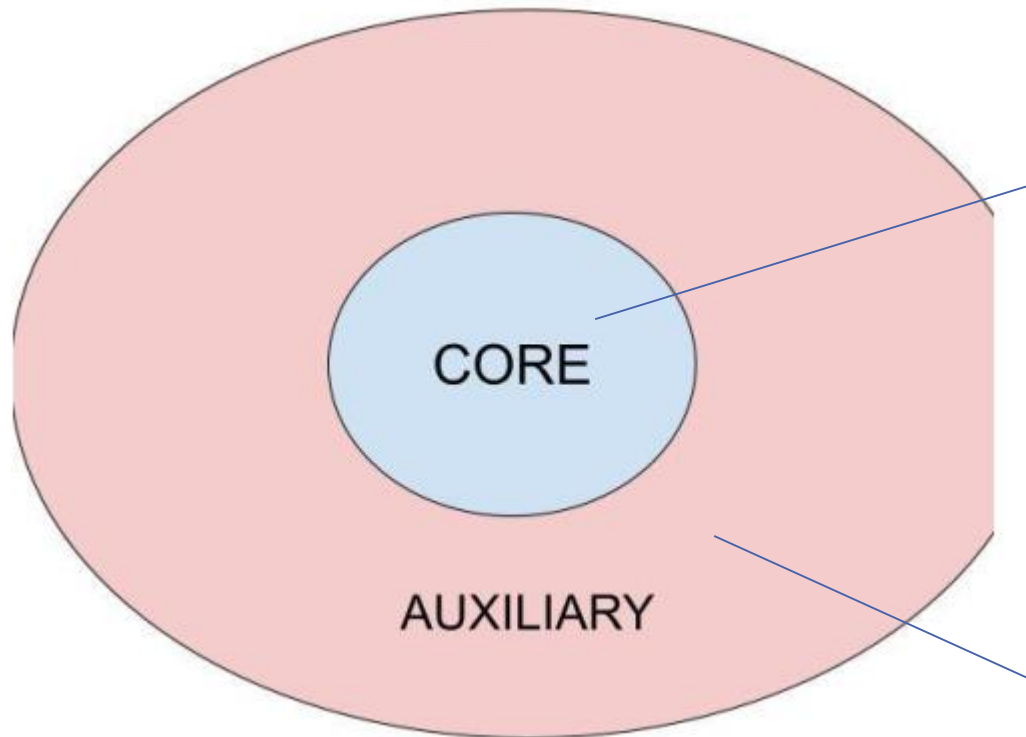
```
function dXeL = dXeL(t,XeL, vT, pT_Am, g, L_m, L_T)
   % routine for predict_Python_regius
   % digestion at max rate

   %unpack state variables
   X = max(0, XeL(1)); e = XeL(2); L = XeL(3);

   dX = - (X > 0) * pT_Am * L^2;
   de = - dX/ L^3 - e * vT/ L;
   r = vT * (e/ L - (1 + L_T/ L)/ L_m)/ (e + g);
   dL = L * r/ 3;

   dXeL = [dX; de; dL];
end
```
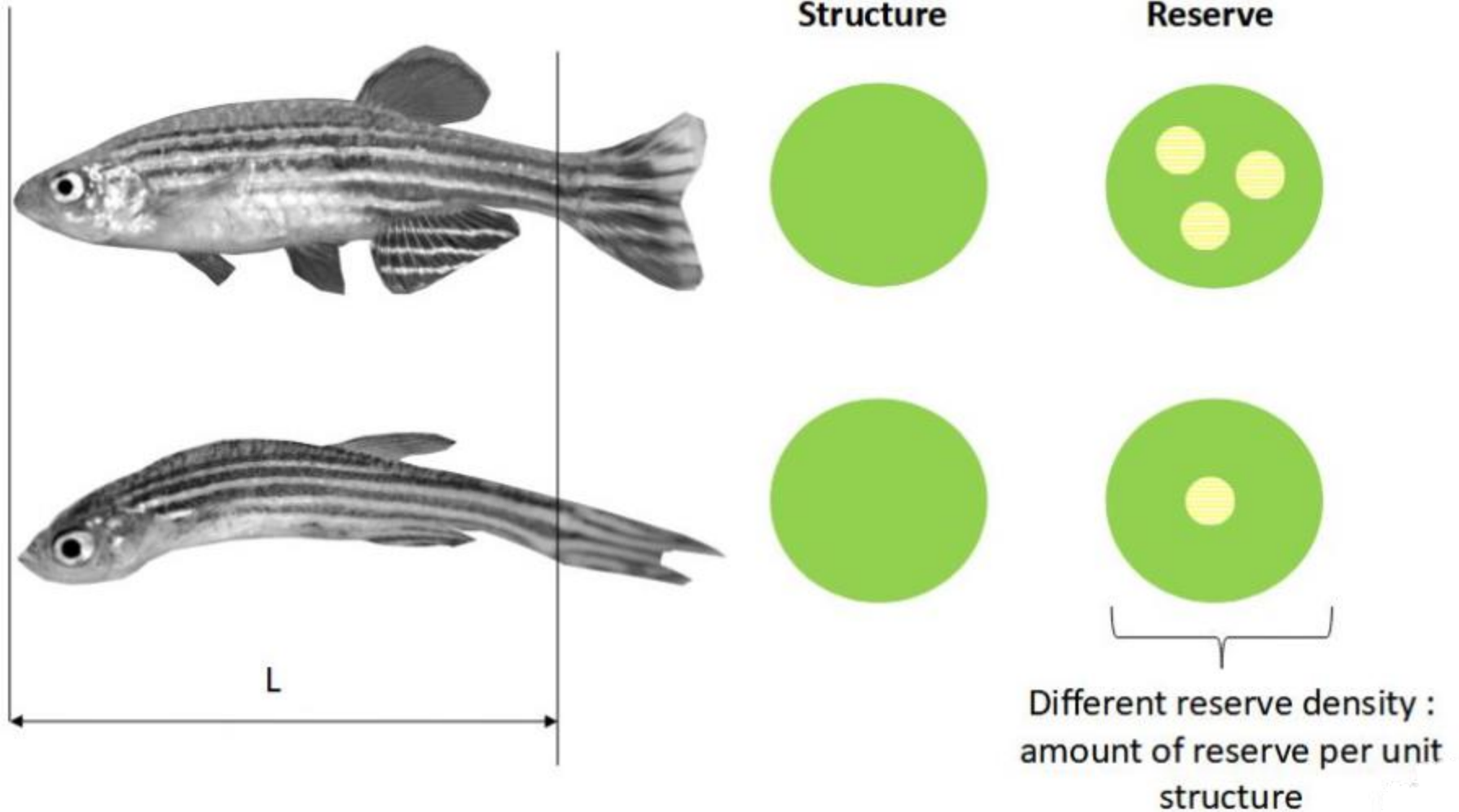
Assumptions..

- Strong homeostasis
- Scaling of metabolism and structure length/volume
- Physical vs structural length
- Length vs weight

Length as quantifier for structure

Structure

Structure + Reserve

L

Different reserve density :
amount of reserve per unit
structure

mydata-file

Set the data
- **metadata** - information about: the species, eco-codes, the types of data, the author, etc
- **data** - value, units, labels, references, temperature (for time and rates)
- **pseudo data** - were set automatically, can be modified

Data

(real)data

Empirical observations of physiological processes
- zero-variate (single measurements)
- uni-variate (lists of values for an independent and an associated dependent variable)
- Read here for more types of data

pseudo-data

Prior knowledge of a selection of parameter values

Fill possible gaps in information in the real data

mydata-file (function*)

```matlab
%% set weights for all real data
weights = setweights(data, []);


%% set pseudodata and respective weights
[data, units, label, weights] = addpseudodata(data, units,
label, weights);


%% pack auxData and txtData for output
auxData.temp = temp;

txtData.units = units;

txtData.label = label;

txtData.bibkey = bibkey;

txtData.comment = comment;
```

Structures in Matlab

- A **Structure** is a collection of data representing a single idea or "object"

- Inside a structure there is a **list of fields** each being a variable name for some sub-piece of data

- Different type of data for each "field"

- Syntax

```
VariableName . Field
```

Structure example

A single variable (named `metaData`) which contains many **fields**. Each field has its own **name** and its own **type**.

```
metaData.phylum     = 'Chordata';
metaData.class      = 'Chondrichthyes';
metaData.order      = 'Squaliformes';
metaData.family     = 'Squalidae';
metaData.species    = 'Squalus_acanthias';
metaData.species_en = 'Spurdog';
```

Structure

Many variables (named `data`, `units`, `label`, `bibkey`, `temp`) which contain many **fields** (e.g. zero-variate data, ab, ap). Variables give different information for a given field.

```
data.ab = 640.5                    data.ap = 2190
units.ab = 'd'                     units.ap = 'd';
label.ab = 'age at birth';         label.ap = 'age at puberty';
bibkey.ab = 'JoneGeen1977';        bibkey.ap = 'Avsa2001'
temp.ab = T_C + 9                  temp.ap = T_C + 9;
```

Pack/unpack variables (DEBtool)

vars_pull : pack & unpack variables into & from structures, according to the syntax and inputs.

Example : unpack variables from data

vars_pull(data**)**

creates or overwrites variables ab and ap in the calling function with the contents of the corresponding named fields

Resources

ξα σου

- AmPestimation:
  https://debportal.debtheory.org/docs/AmPestimation.html

- estim_options function (inputs and outputs):
  https://debtool.debtheory.org/lib/pet/html/estim_options.html

- Plotting **trajectories of states and traits: simu_my_pet**
  https://amptool.debtheory.org/docs/index.html
  https://amptool.debtheory.org/trajectories/html/simu_my_pet.html

- Zotero DEB library:
  https://www.zotero.org/groups/500643/deb_library/

- DEB notation:
  https://www.bio.vu.nl/thb/deb/deblab/bib/Kooy2010_n.pdf

- Summary of concepts:
  https://www.bio.vu.nl/thb/deb/deblab/bib/Kooy2010_i.pdf

- Comments to DEB3:
  https://www.bio.vu.nl/thb/deb/deblab/bib/Kooy2010_c.pdf