



# Intraspecific variation in a DEB framework

Charlotte Récapet

[charlotte.recapet@univ-pau.fr](mailto:charlotte.recapet@univ-pau.fr)

University Pau Pays de l'Adour

INRAE (National Research Institute for Agriculture, Food and the Environment)

INRAE



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*University of Crete, Heraklion, Greece*

[deb2025.sciencesconf.org](http://deb2025.sciencesconf.org)

A domestic dog



wirestock/freepik C0

An Atlantic salmon



© Anna Löff



A wall lizard



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A grove snail



Angus Davison/Wikimedia CC BY-SA 4.0

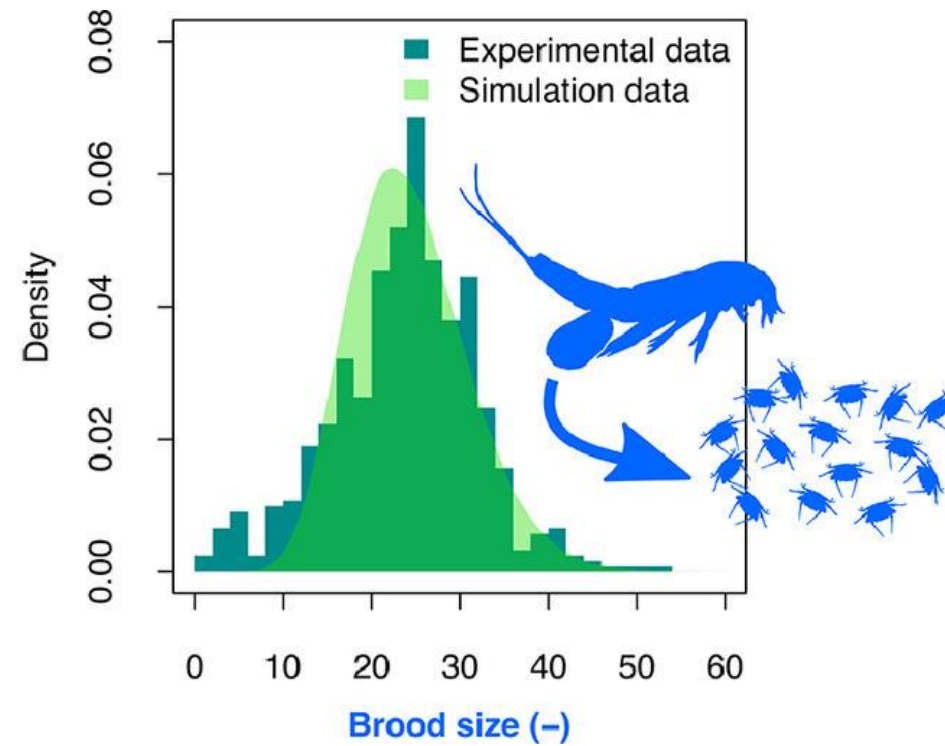
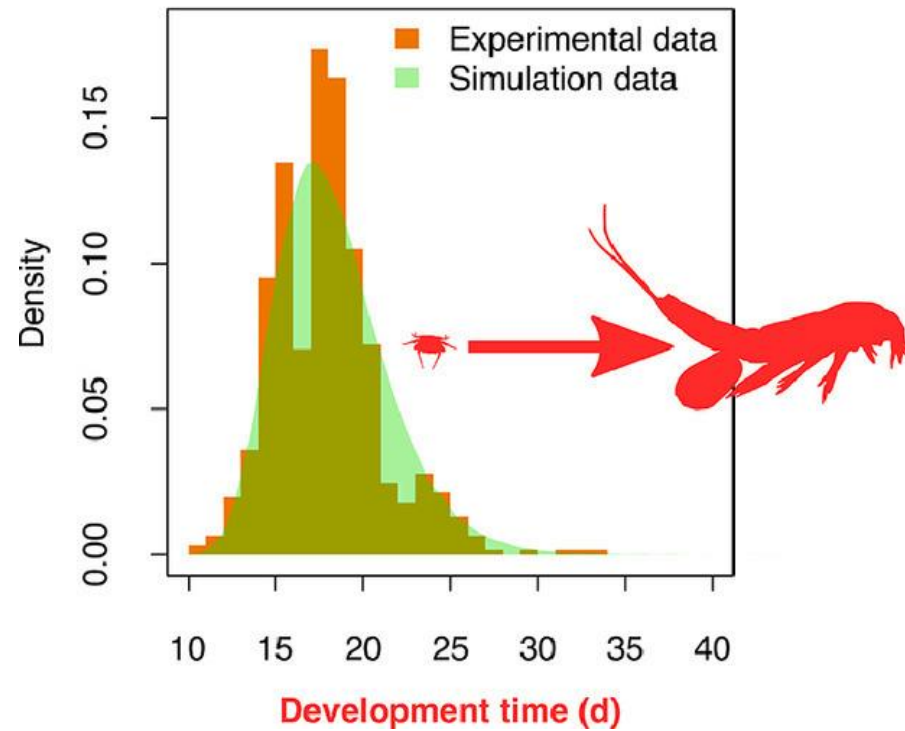
1.

Why bother about  
intraspecific  
variation?



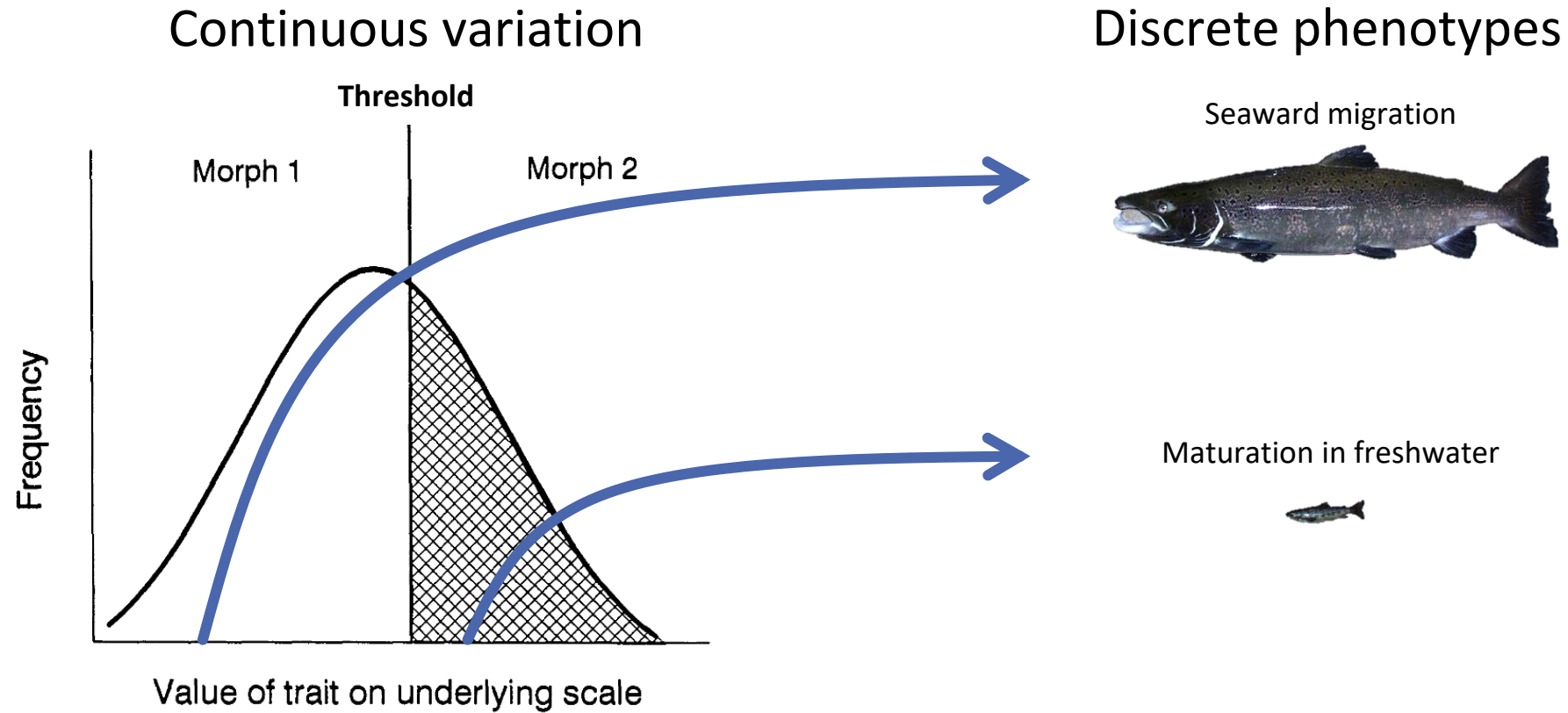


# Impact on individual traits



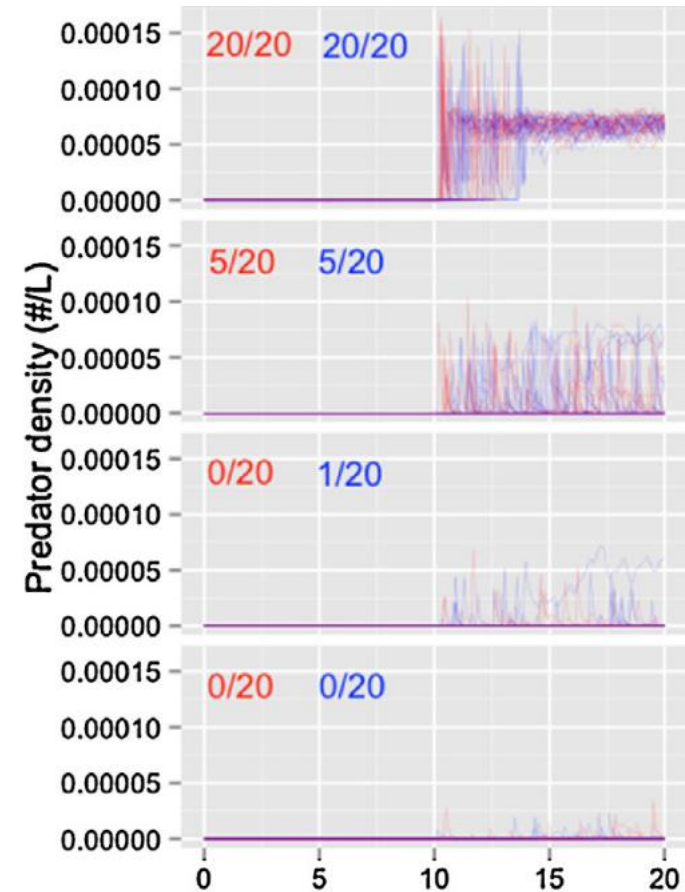
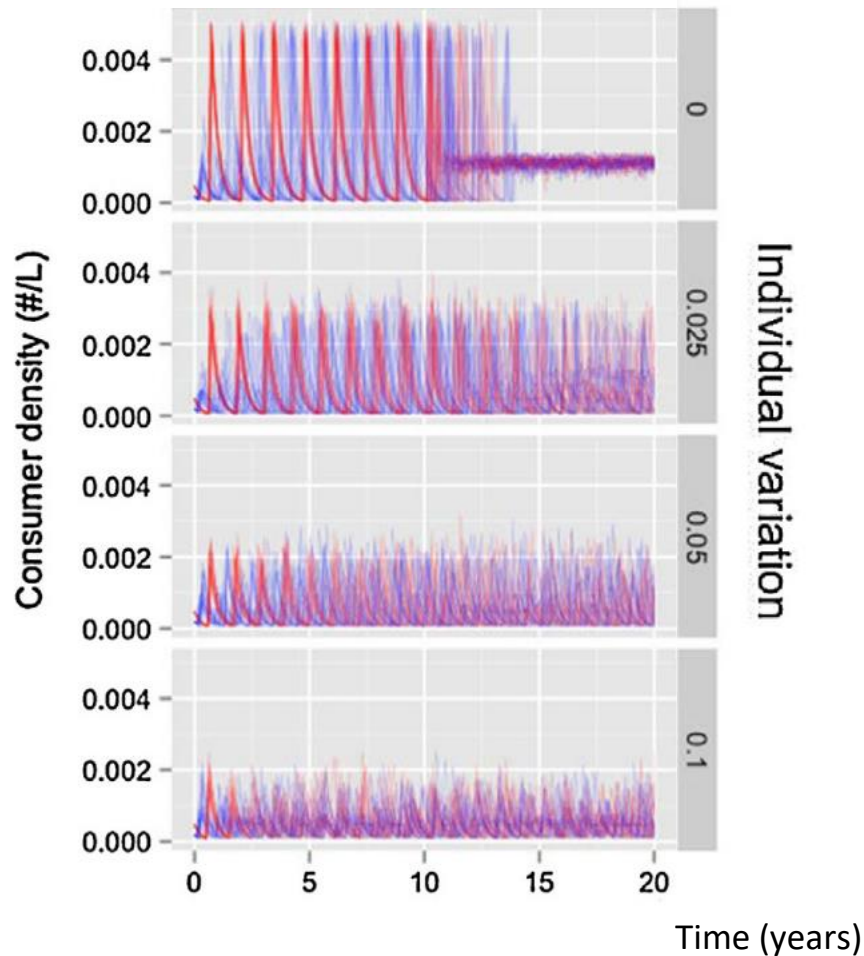
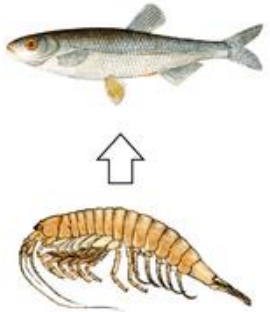
Simulated variation  
in  $\{\dot{p}_{Am}\}$

# Threshold traits



# Impact on demographic processes

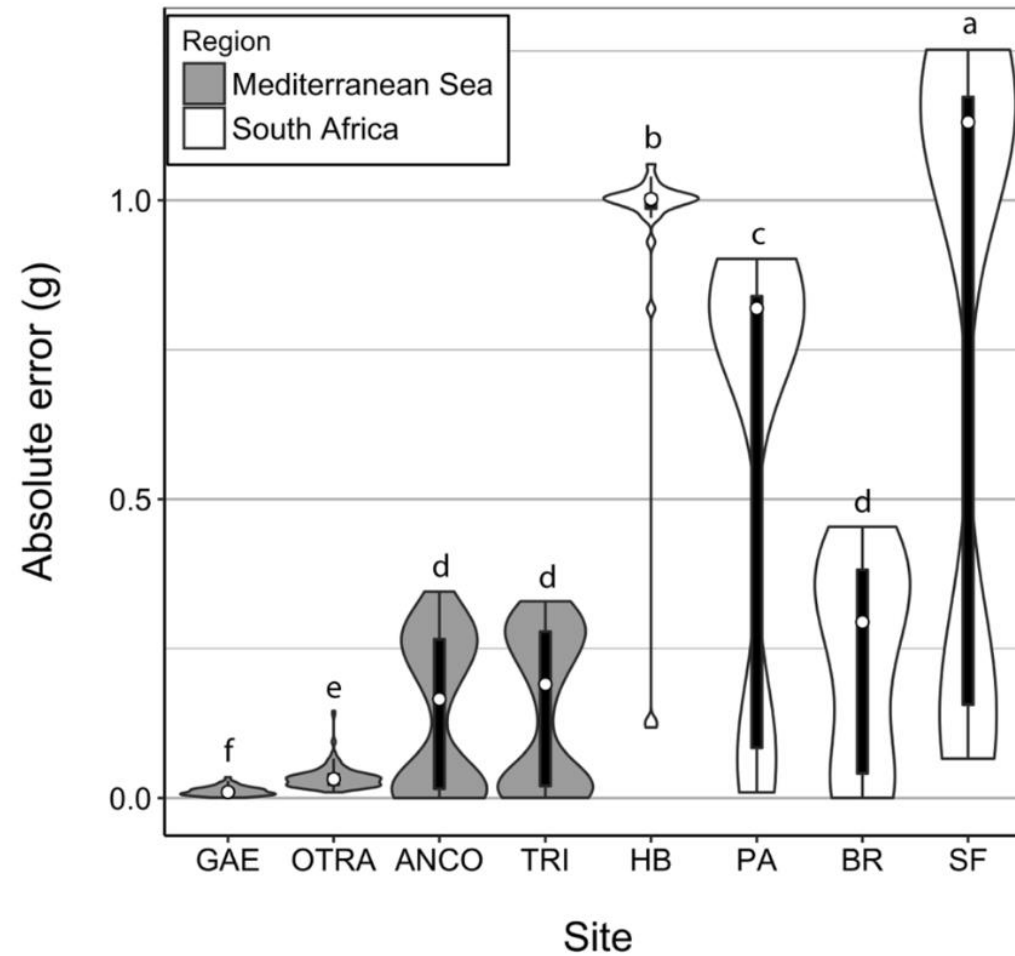
planktivorous fish



piscivorous fish



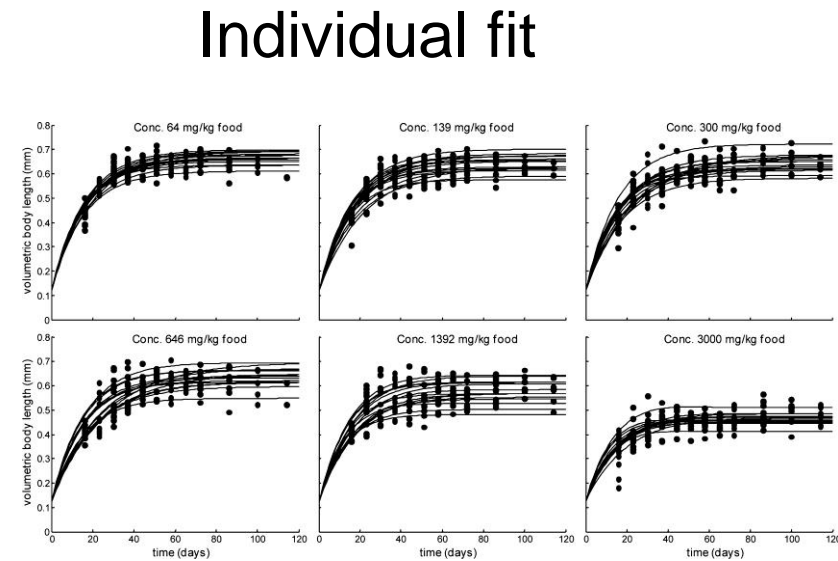
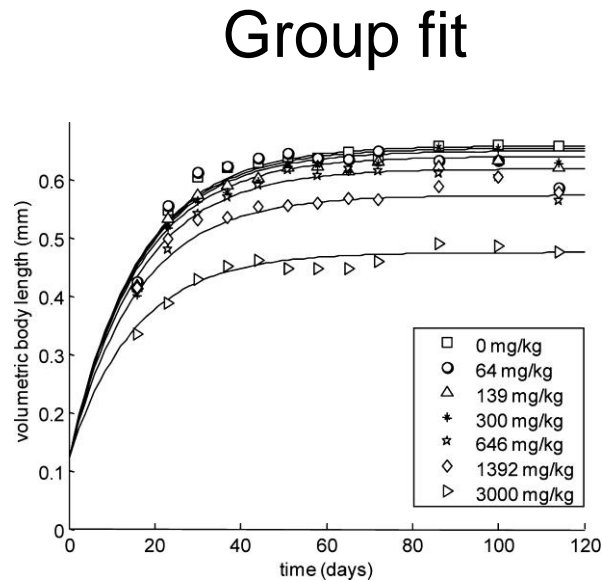
# Poor prediction across populations



# Bias in species parameter estimates



$^{48}\text{Cd}$



**Elimination rate** ( $\text{d}^{-1}$ )

1.62 ( $>0.310$ )

$\neq$

0.139 (0.100–0.235)

**Tolerance** (mg/kg food)

10.8 (10.0–11.5)  $10^3$

$\neq$

8.99 (8.41–9.69)  $10^3$

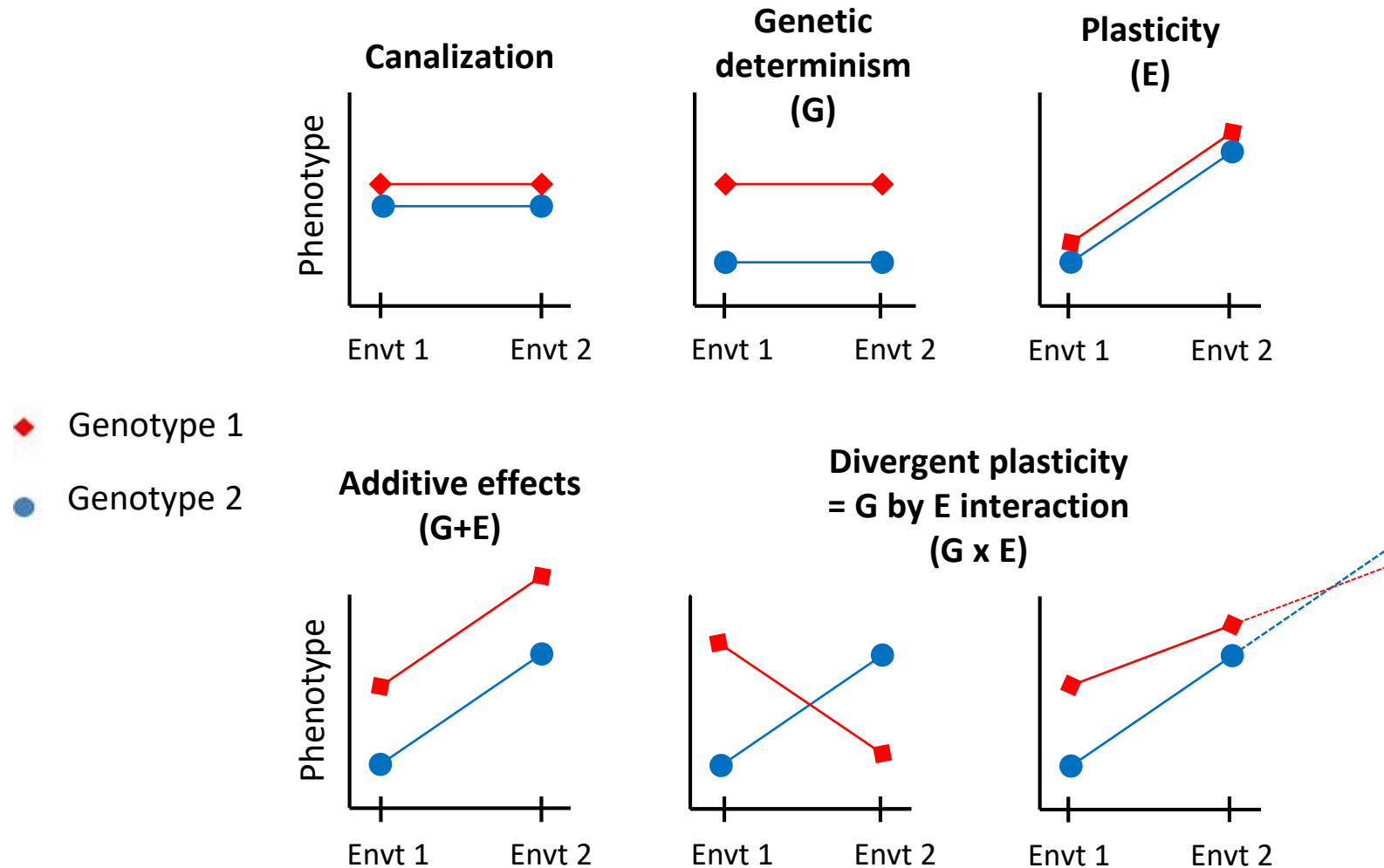


# 2.

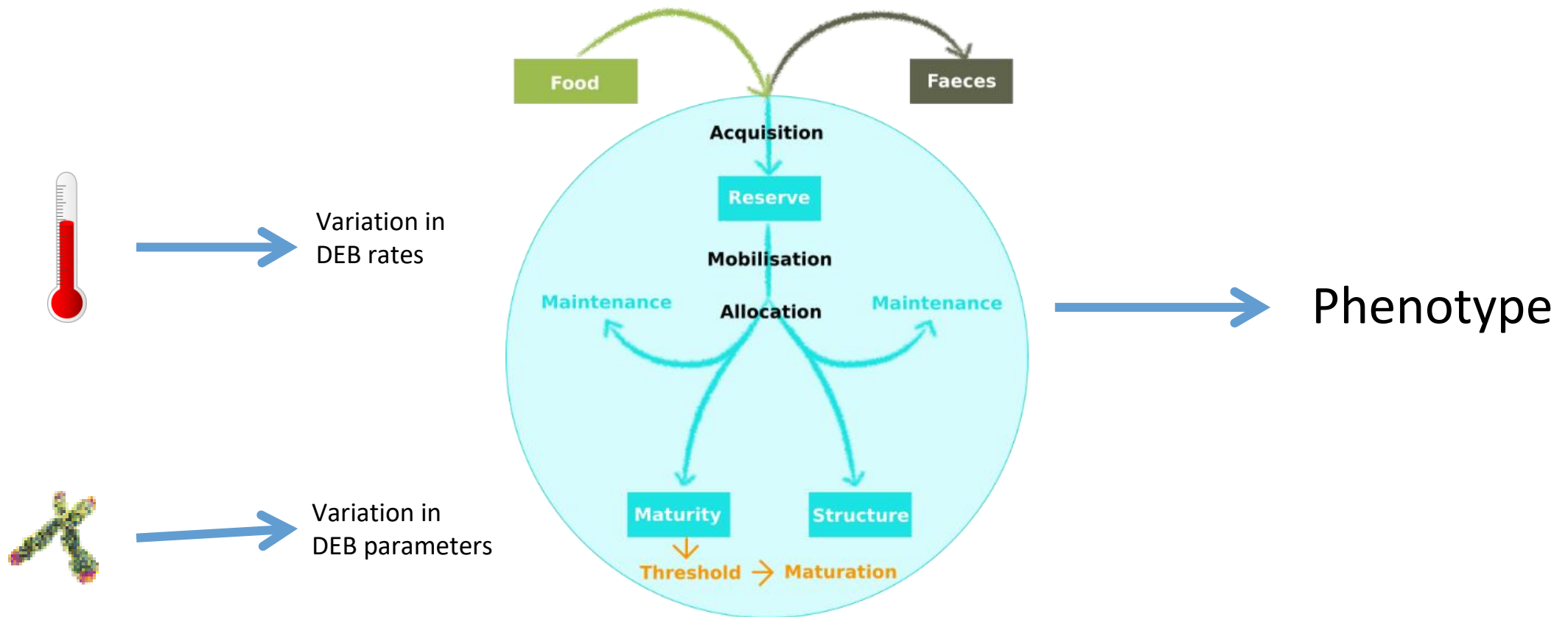
Physiology  
integrates  
genes and the  
environment



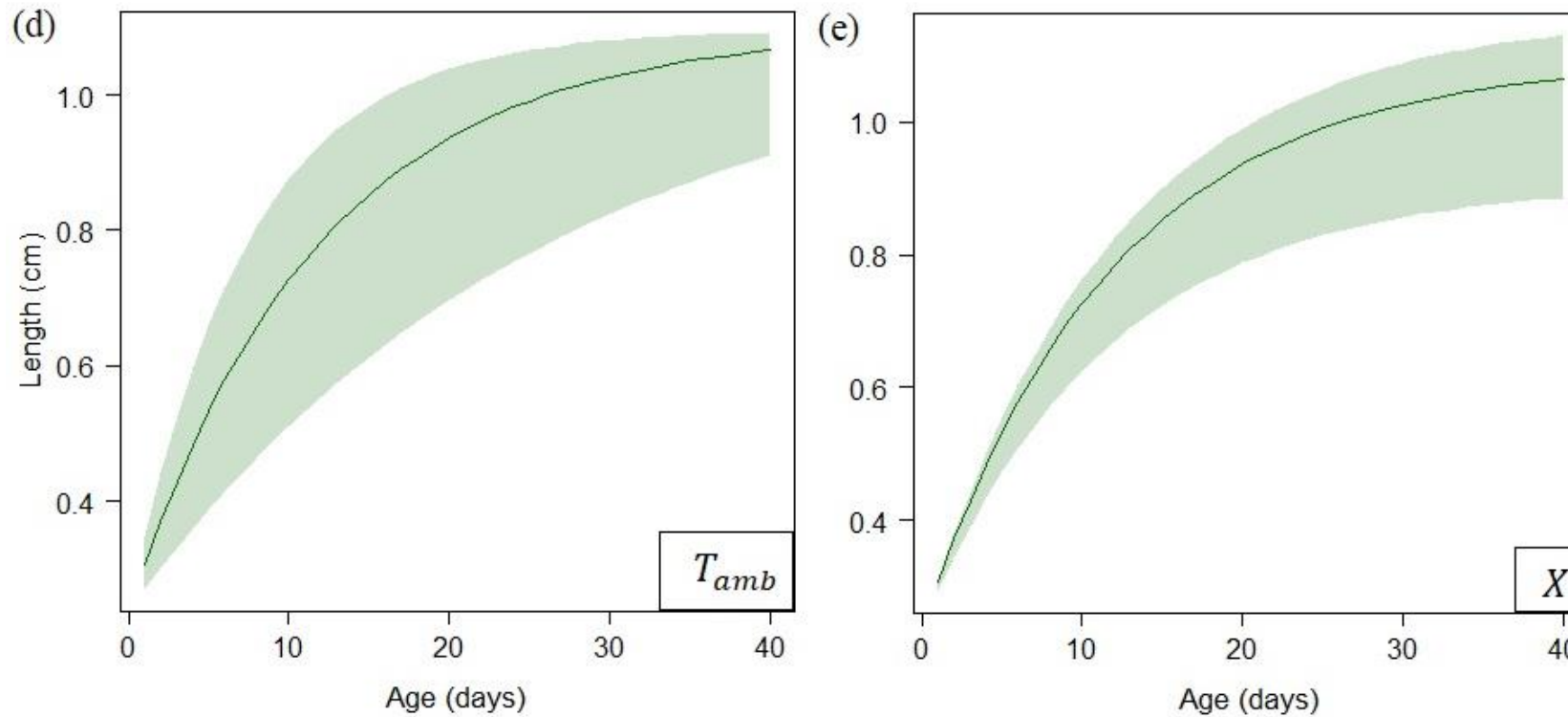
# Sources of individual variation



# But not genetic variation, yet...

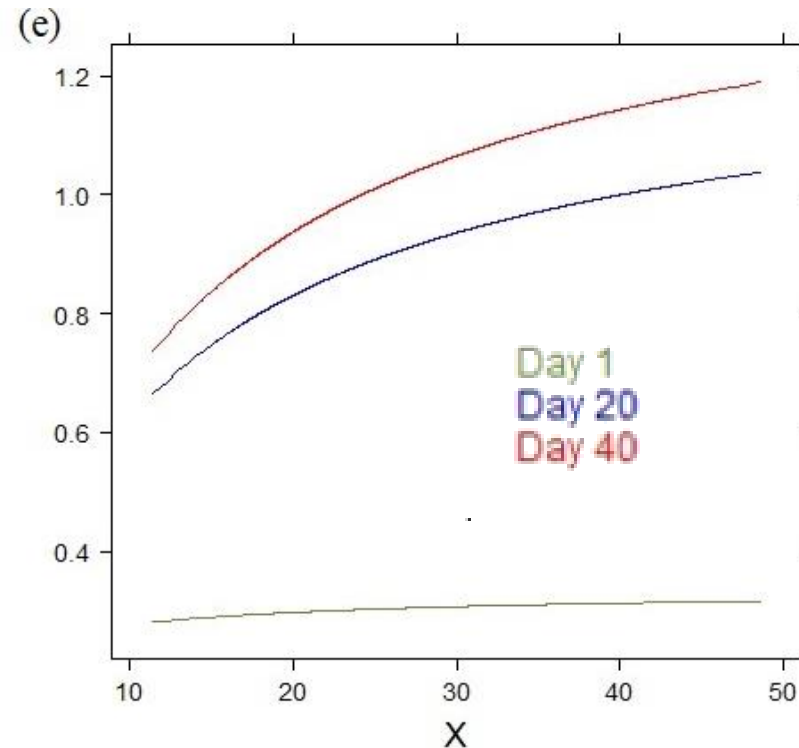
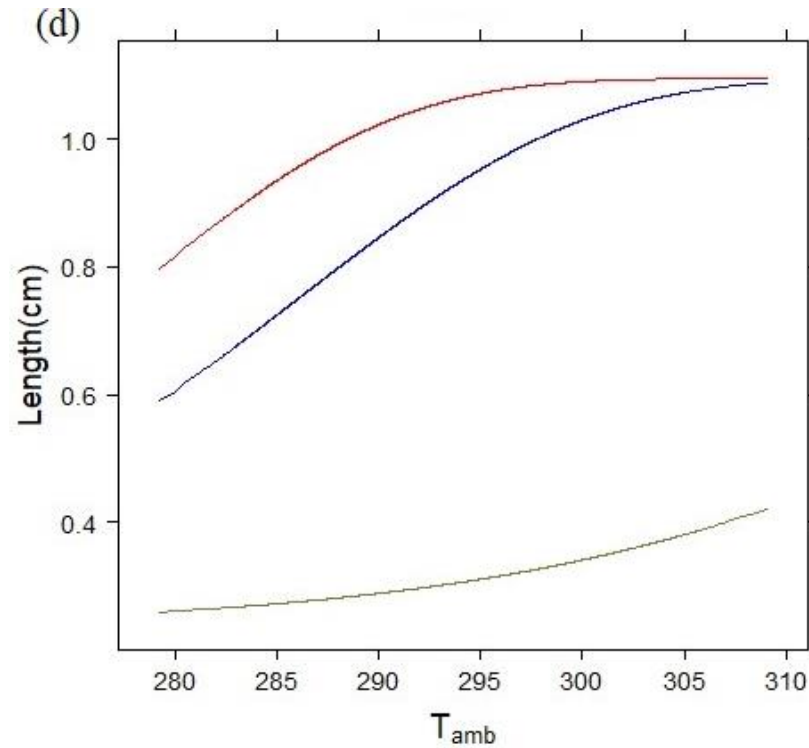


# Plasticity is built within DEB models.





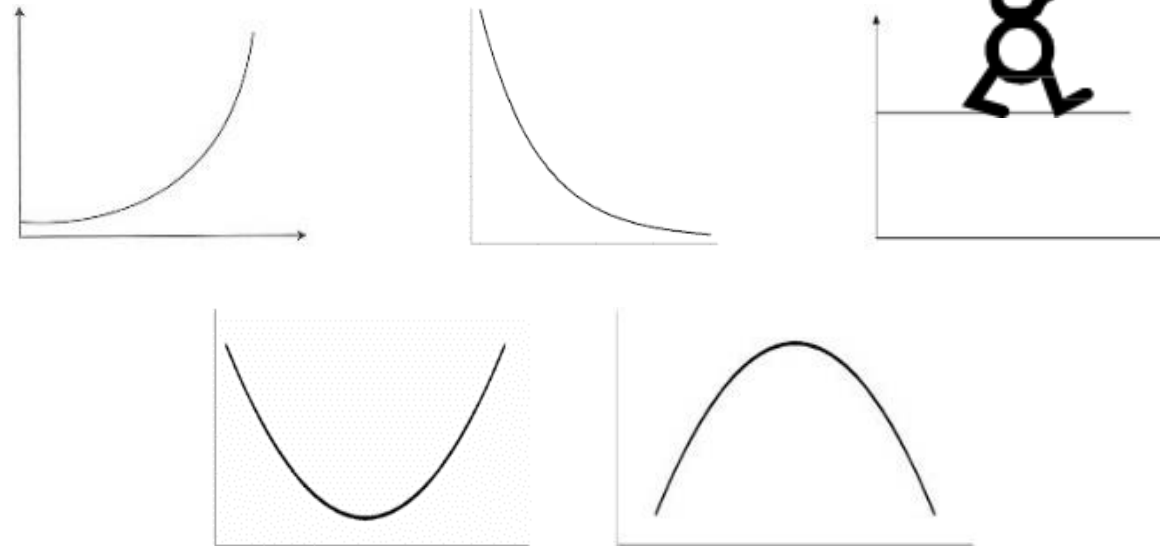
# Plasticity is built within DEB models.



# Exercise: Guess the reaction norms

## Traits

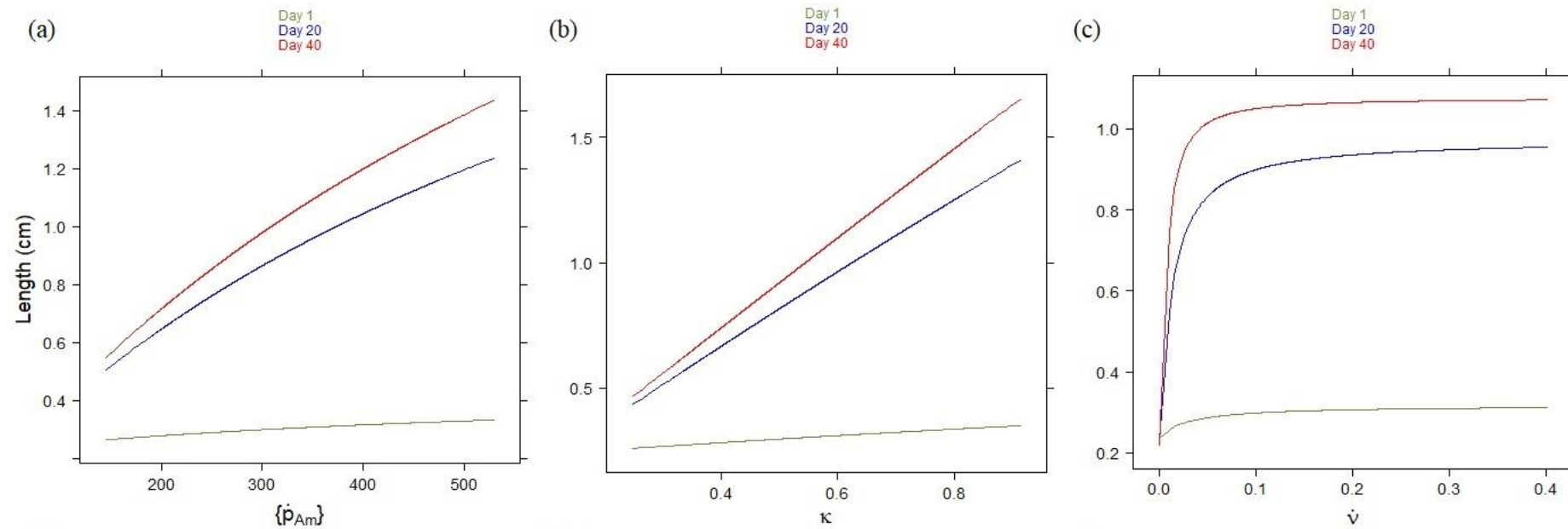
Size (length)  
Reproductive output  
Developmental time



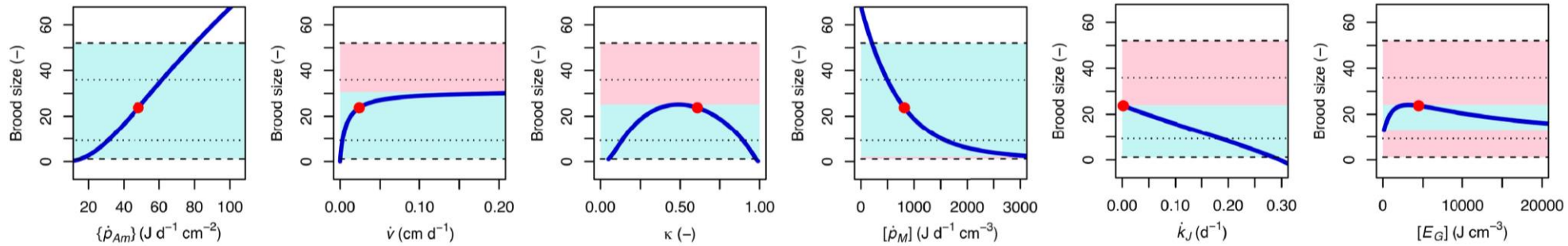
## Parameters

$\{\dot{p}_{Am}\}, \dot{v}$   
 $\kappa, E_H^b, E_H^p$   
 $[\dot{p}_M], \dot{k}_J$

# Size (physical length)

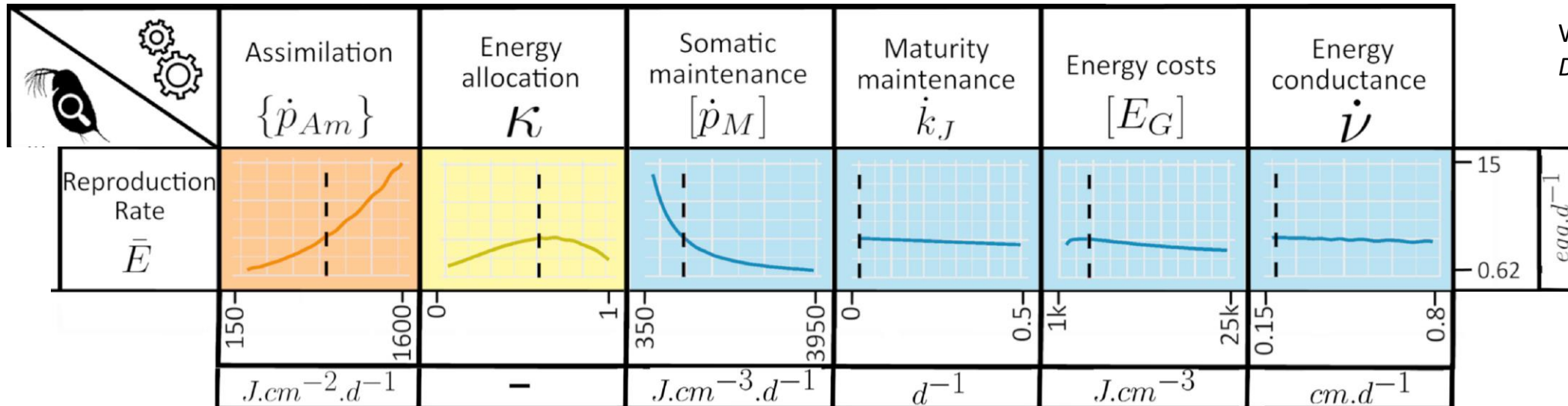


# Reproductive output



Copepod  
*Nitocra spinipes*

Koch & De Schampelaere 2020. *Ecol. Model.* 431, 109091

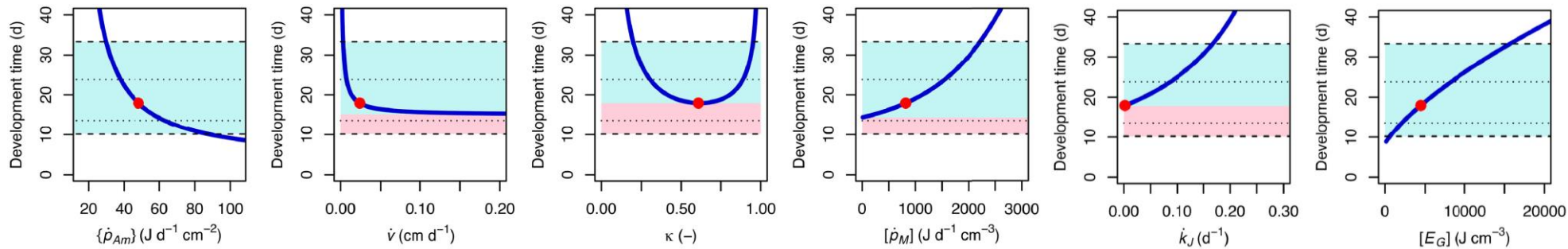


Water flea  
*Daphnia magna*

Debelgarric & Récapet 2025. *Ecol. Model.* 501, 110993

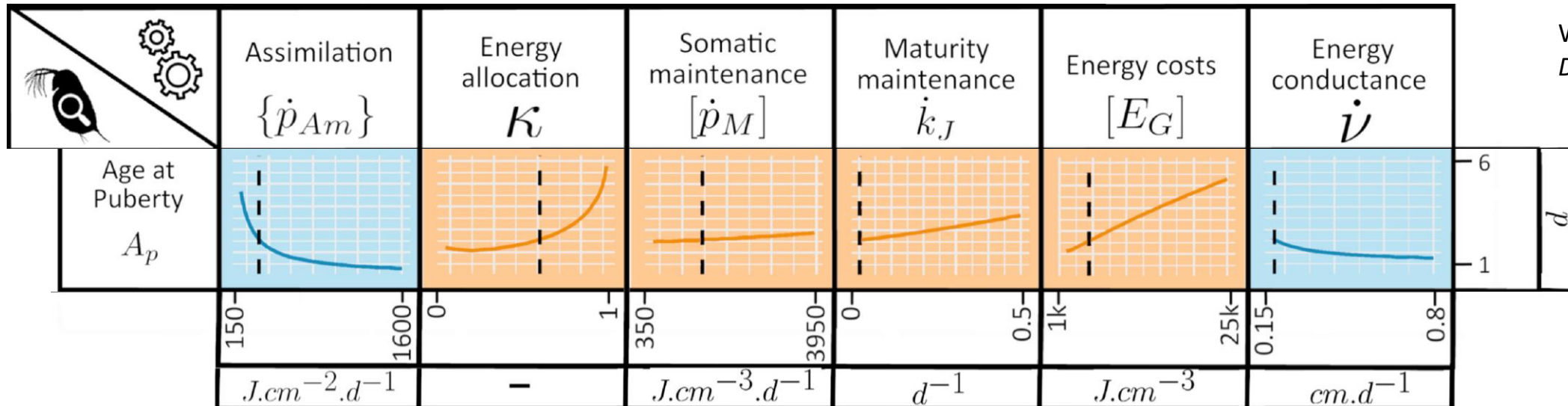


# Development time (hatching → puberty)



Copepod  
*Nitocra spinipes*

Koch & De Schampelaere 2020. *Ecol. Model.* 431, 109091



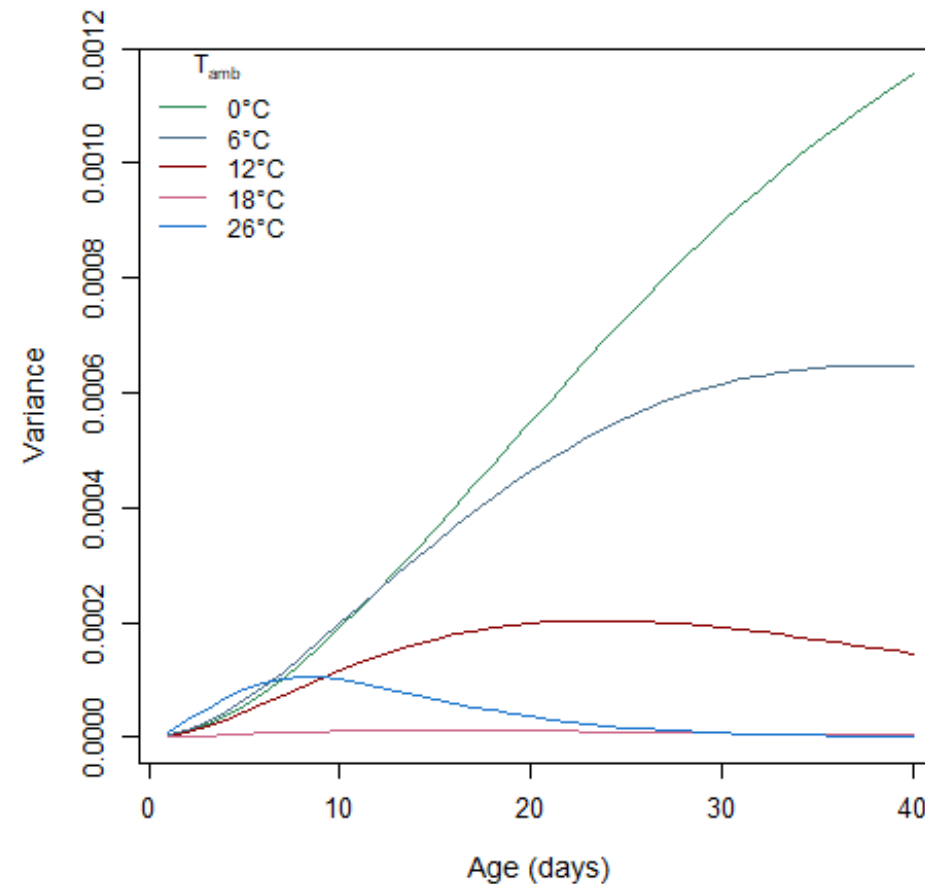
Water flea  
*Daphnia magna*

Debelgarric & Récapet 2025. *Ecol. Model.* 501, 110993

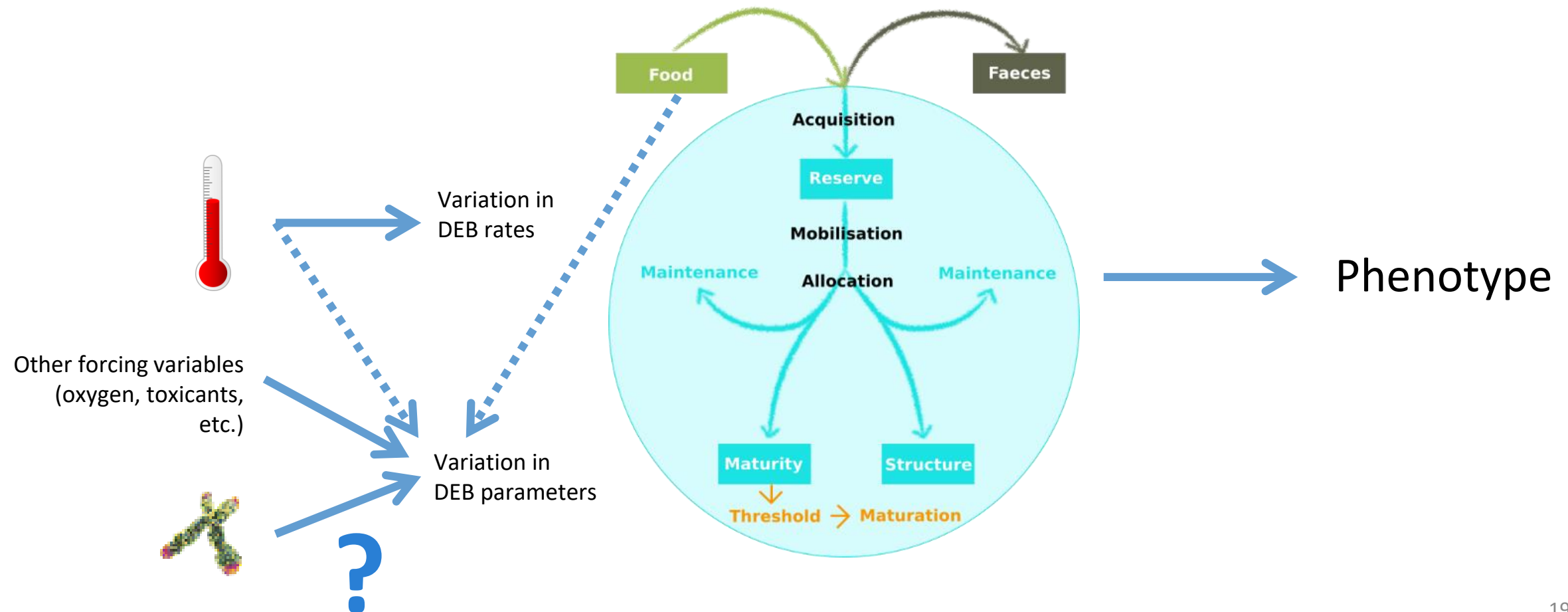
# Interaction between G and E

Inherent to the model

Variance in  
body size due to  
variation in  $T_A$   
at different  $T$



# G x E interactions on DEB parameters?

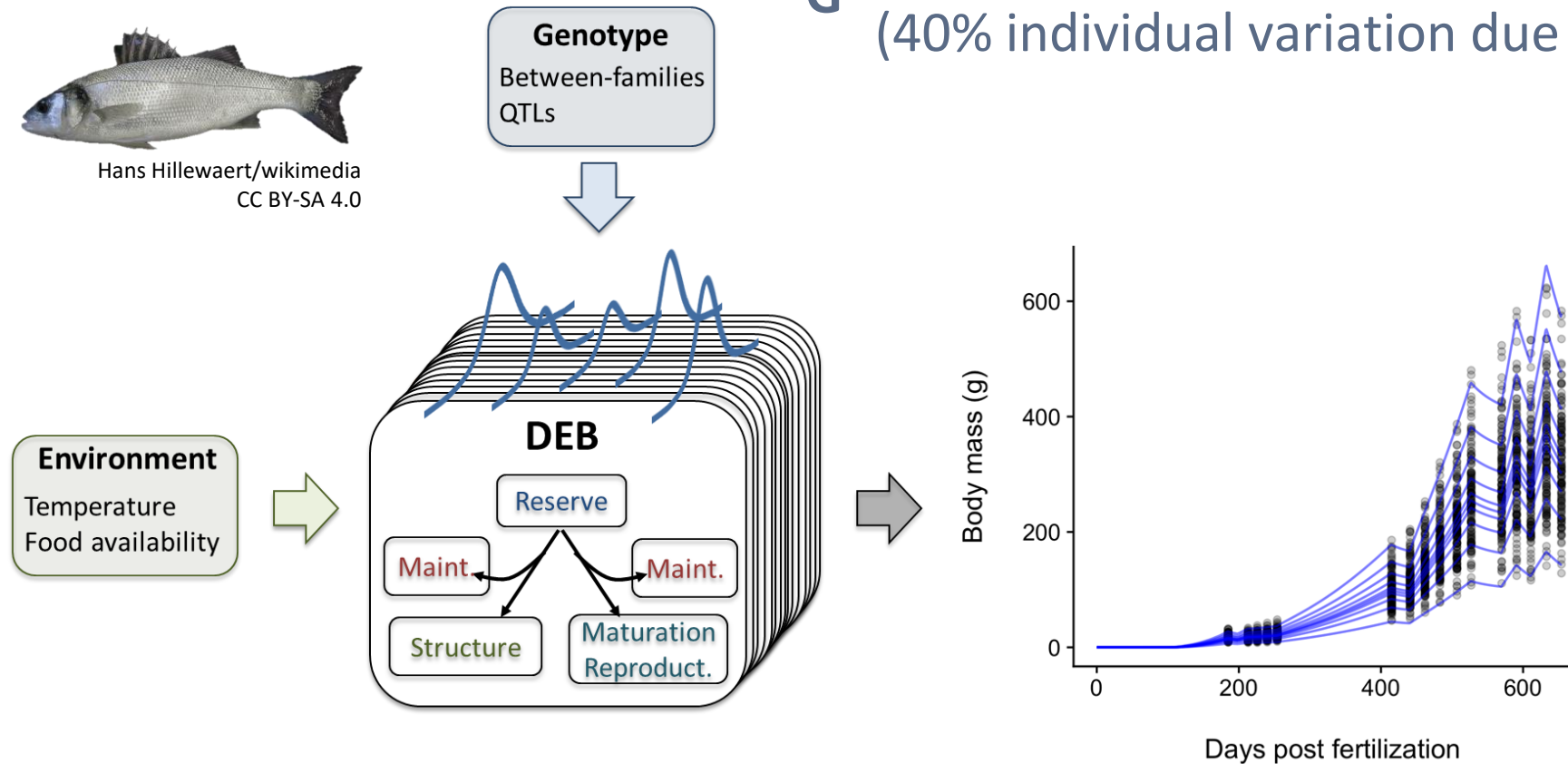


# Heritable variation in DEB parameters



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$E_G$  Heritability = 0.4  
(40% individual variation due to genetic variation)





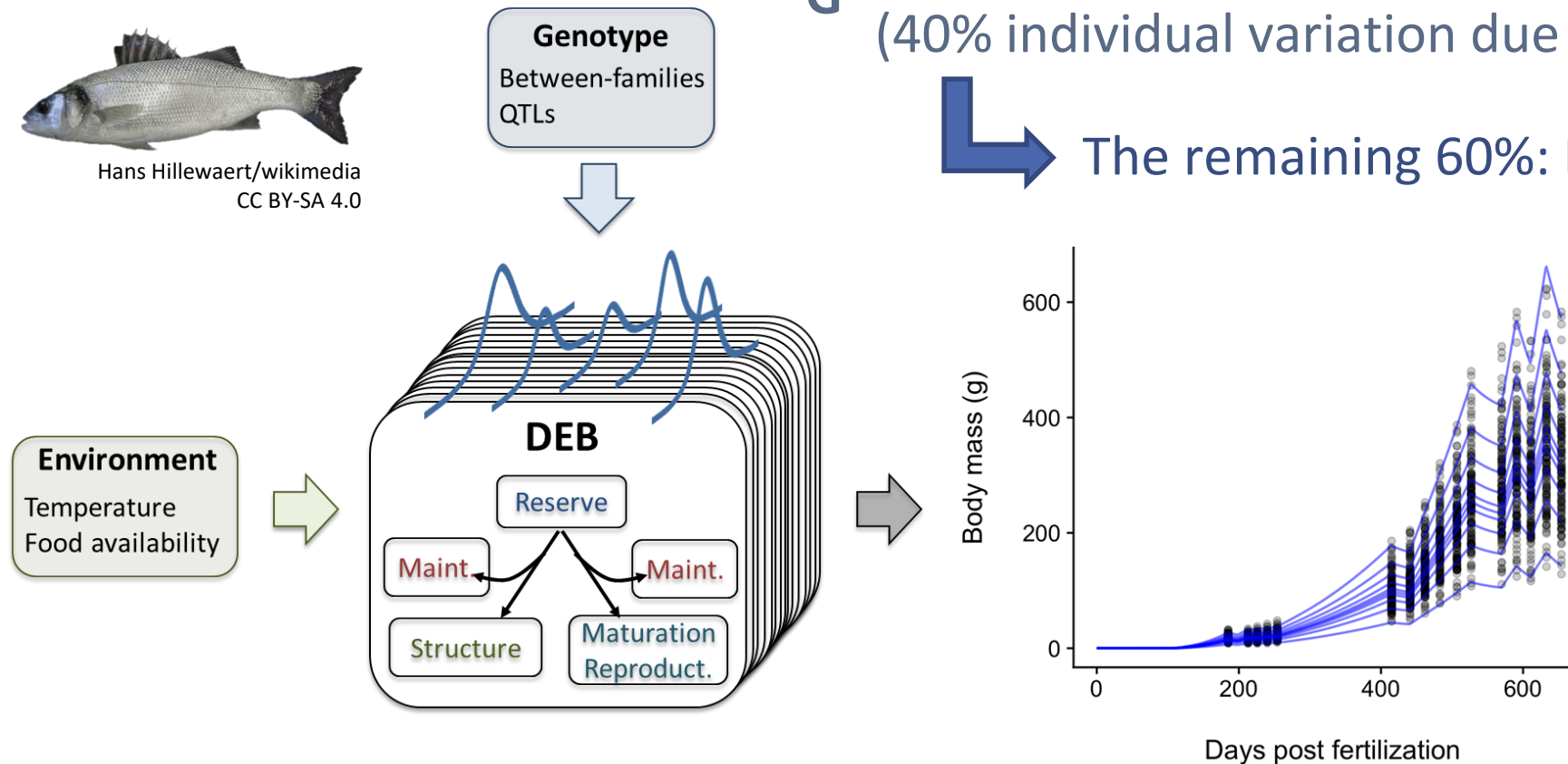
# Interaction between G and E



Hans Hillewaert/wikimedia  
CC BY-SA 4.0

$E_G$  Heritability = 0.4  
(40% individual variation due to genetic variation)

↳ The remaining 60%: Error? Plasticity?



# 3.

## Estimating subspecies variation in DEB parameters



# Each group separately

+

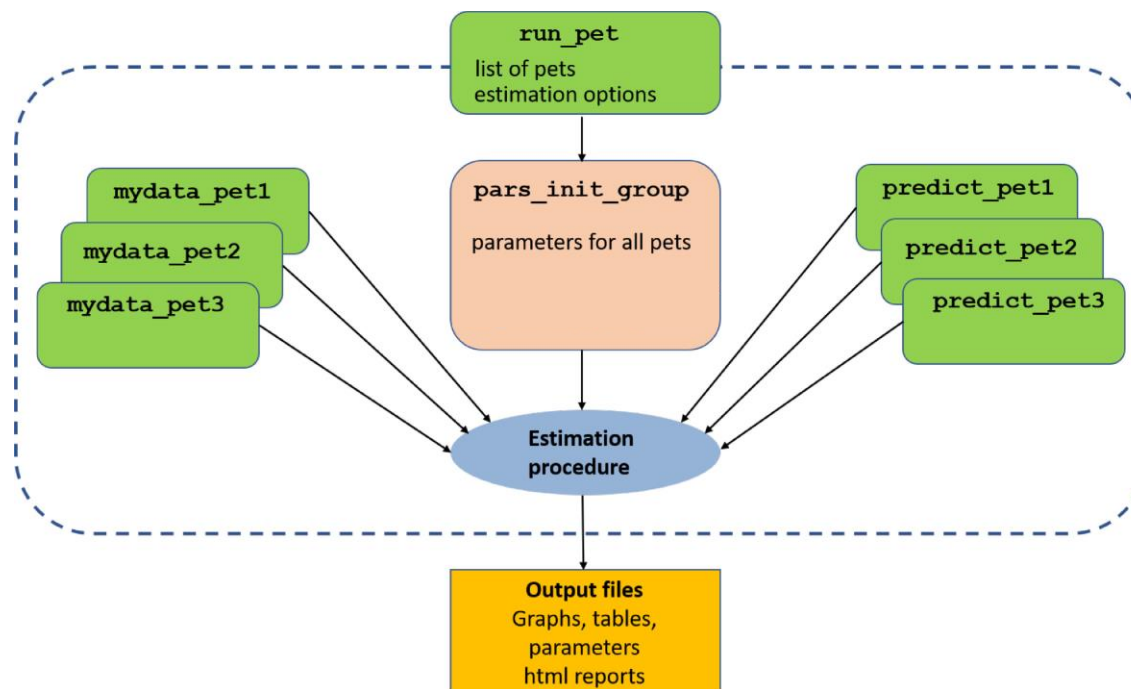
- No assumptions on constant/variable parameters

–

- Sensitive to differences in data completeness
- Difficult to identify biologically significant differences (no credibility interval for  $\Delta$ )

# Joint estimation

## All-or-nothing parameter differences



- Parameters are either equals or different between groups.
- Covariation rules may constrain the parameter space (e.g. between maturity levels and zoom factor).

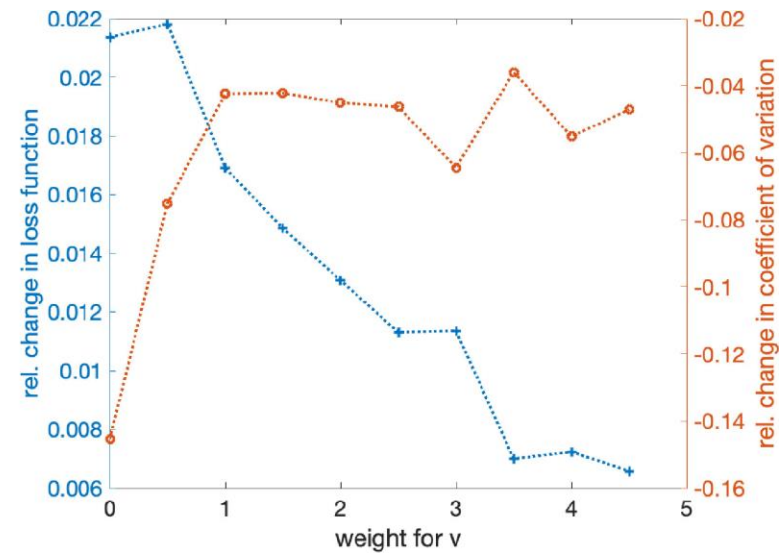
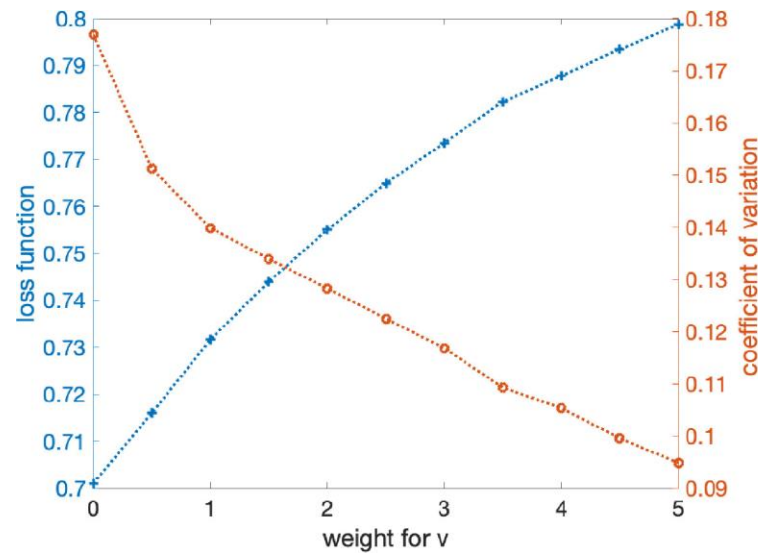




Recall:  
What is a loss function?

# Joint estimation

## Using an augmented loss function



Variation between groups  
not penalized

Variation between groups  
increasingly penalized

# Joint estimation



- Possibility to estimate  $\Delta$  as a parameter  $\rightarrow$  credibility interval
- Use information from data-rich groups to improve estimation in data-poor groups



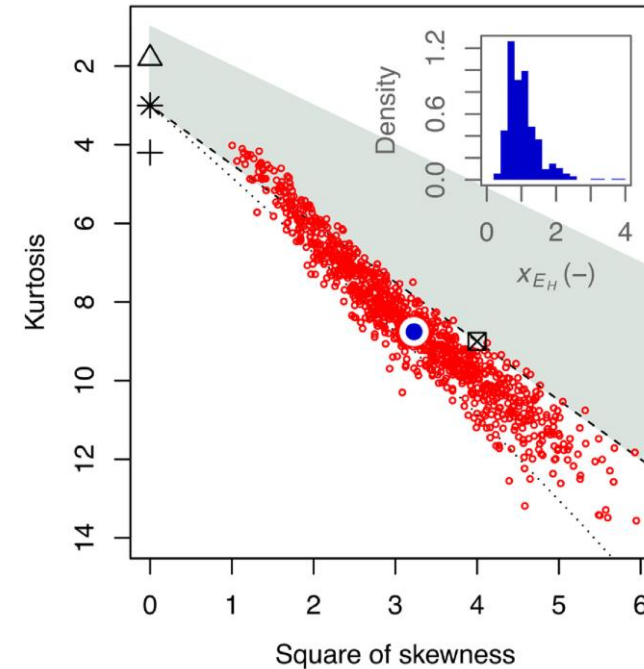
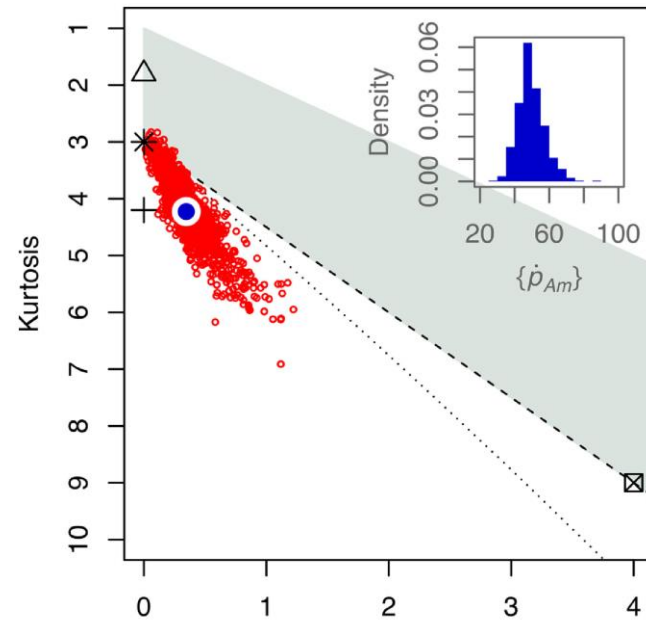
- Requires assumptions on constant/variable parameters

# 4.

## Estimating individual variation in DEB parameters



# Distribution of one trait (OAT)



- Observation      ● Bootstrapping
- Theoretical distributions
- \* Normal      □ Beta
- △ Uniform      ..... Log-normal
- ⊠ Exponential      --- Gamma
- + Logistic

(Weibull is close to gamma and log-normal)

# Distribution of one trait (OAT)

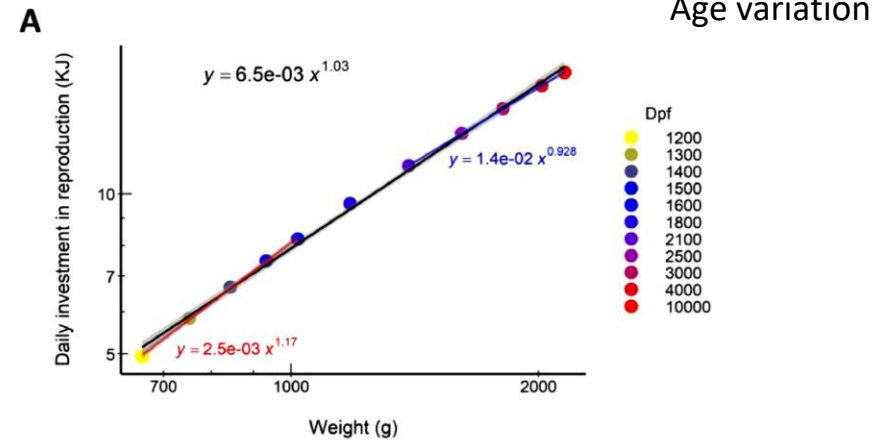
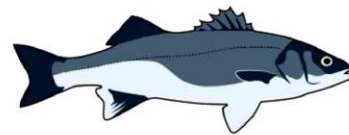


- Possible without longitudinal data (distribution only)
- Help identify most relevant parameters

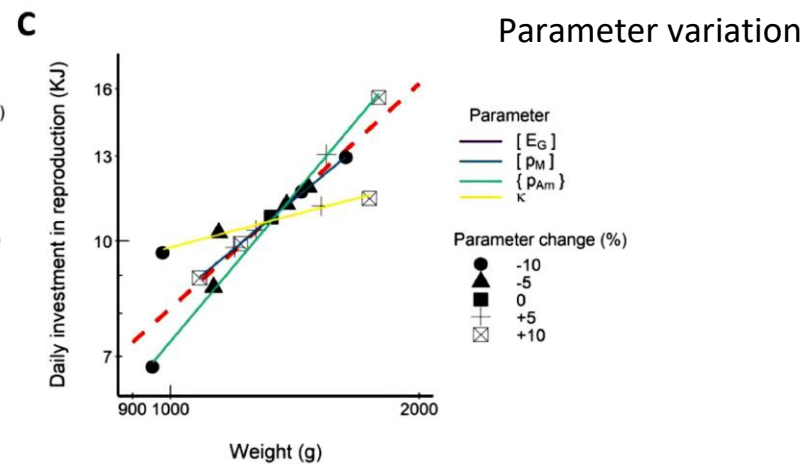
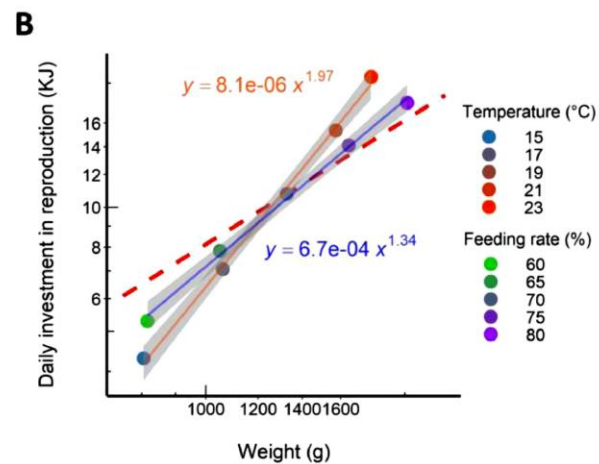


- Assumes one parameter explains all variation
- Rely on only one source of information (trait)

# Relationship between traits (OAT)



Environmental  
variation





# Relationship between traits (OAT)



- Possible without longitudinal data (relationship only)
- Helps identify most relevant parameters

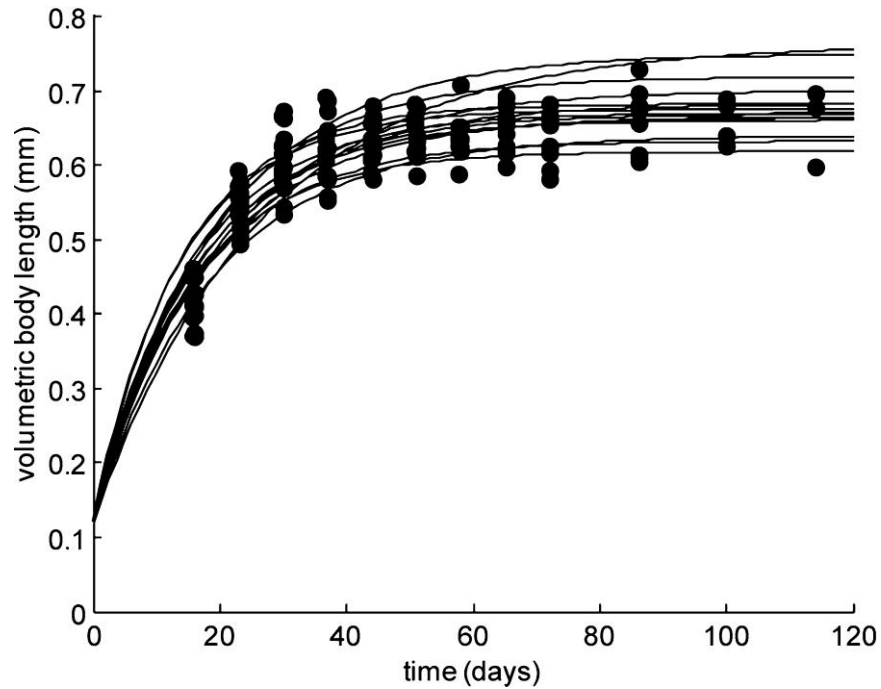


- Assumes one parameter explains all variation
- Does not estimate parameter distribution

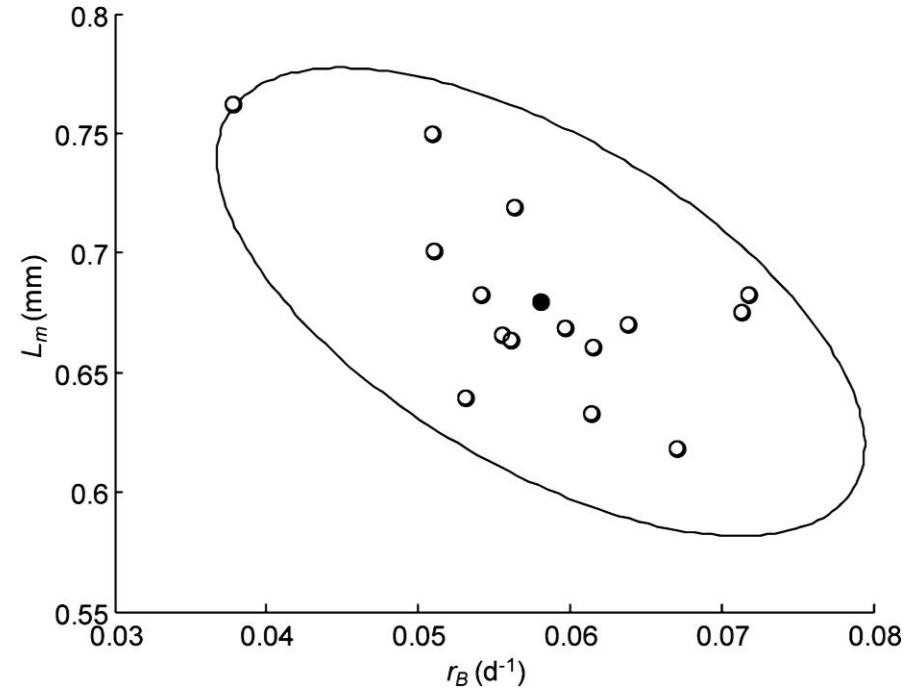
# Individual fit (covariation)



Individual fit

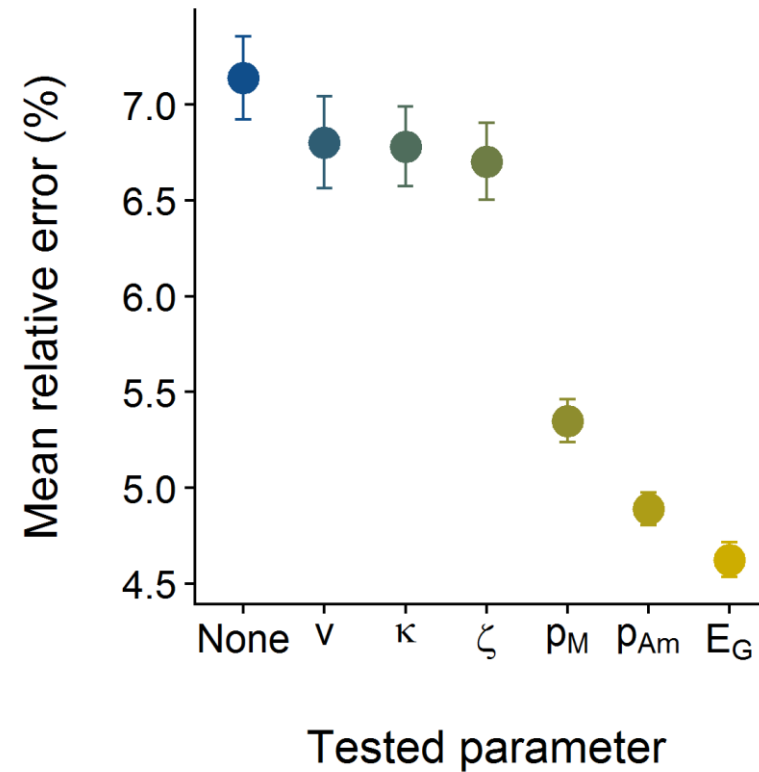
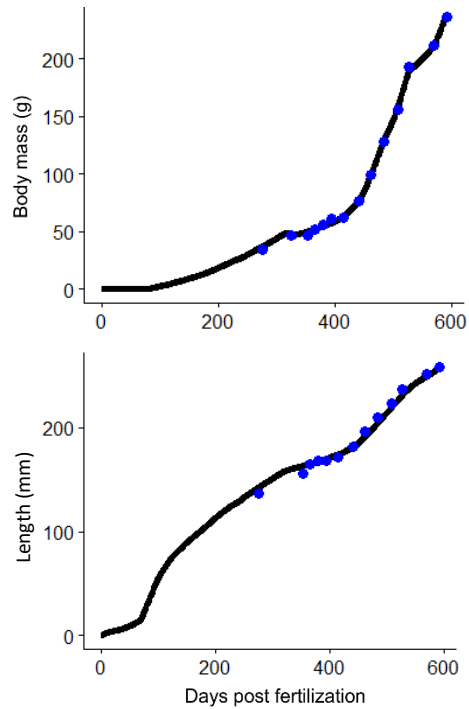


Parameters' distribution



# Individual fit (OAT)

Model fit with one variable parameter



# Many traits – one individual (covariation)

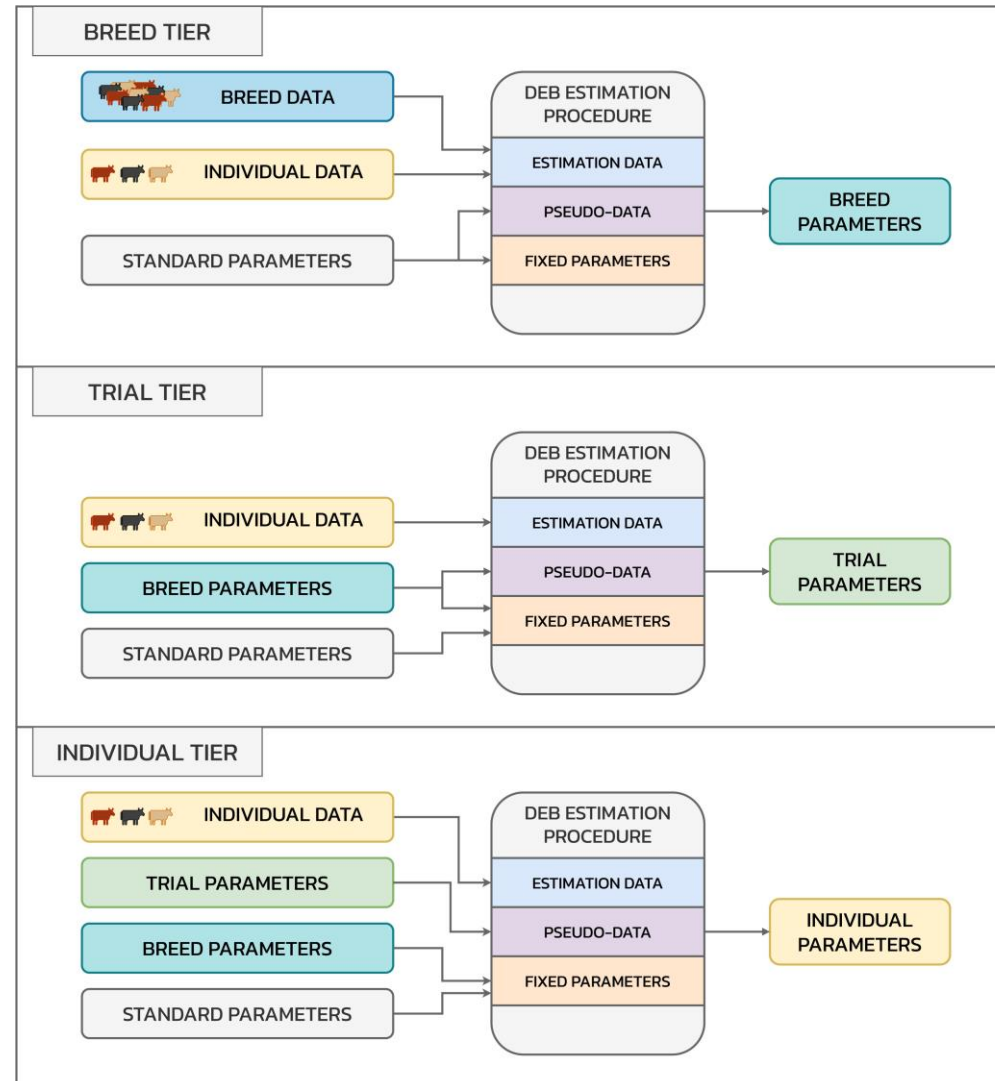


- Can estimate variation in several parameters
- Does not need any assumption on parameter or error (trait) distributions



- Requires longitudinal data
- Sensitive to error in individual data
- Sensitive to identifiability issues (→ OAT)

# Combining estimations at several levels



# Using assumptions on parameters' distribution?



- Each parameter variance (and even covariance) is directly estimated as a new parameter
- Accounts for error in individual data



- Requires individual data on several traits
- Requires assumption on parameter and error distributions
- Number of estimated parameters may increase rapidly!
- Still sensitive to identifiability issues



Let's sum up!



# What should we keep in mind?

- ✓ Risks of ignoring intraspecific variation :
  - poor predictions for some populations
  - biased species-level estimates and predictions
- ✓ DEB-based models can combine environmental and genetic sources of variation.
- ✓ Estimating intraspecific variation :
  - Assumptions on variable parameters may help improve identifiability, but increase risk of error.
  - Measurement errors and intraspecific variation remain difficult to tell apart.

Thank you for your attention

[charlotte.recapet@univ-pau.fr](mailto:charlotte.recapet@univ-pau.fr)