FACULTY OF BIOSCIENCE ENGINEERING

Estimating realistic biological variability in Dynamic Energy Budget model parameters of a copepod

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Introduction

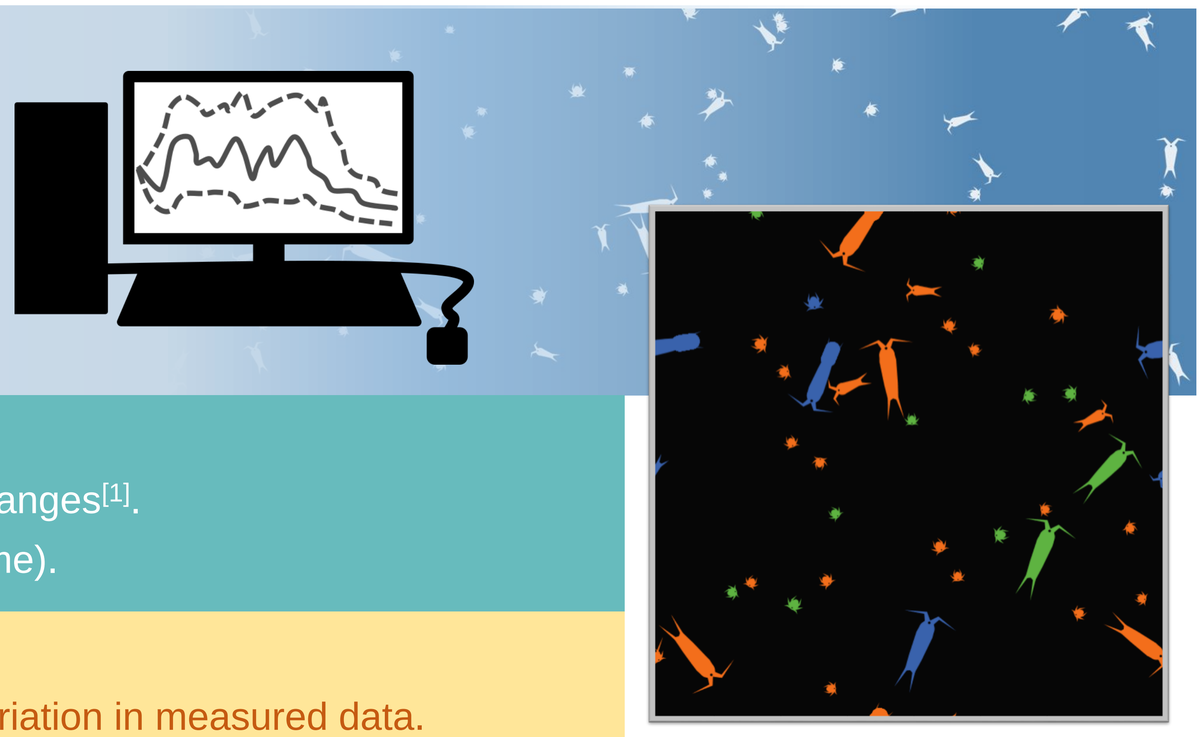
Copepod DEB-IBM

Purpose: Extrapolation of individual-level effects to populations

Species: Harpacticoid copepod *Nitocra spinipes*

Applied concepts:

- Dynamic Energy Budget theory (DEB)
- Individual-Based Modelling (IBM)



DEB-IBM visualisation in NetLogo

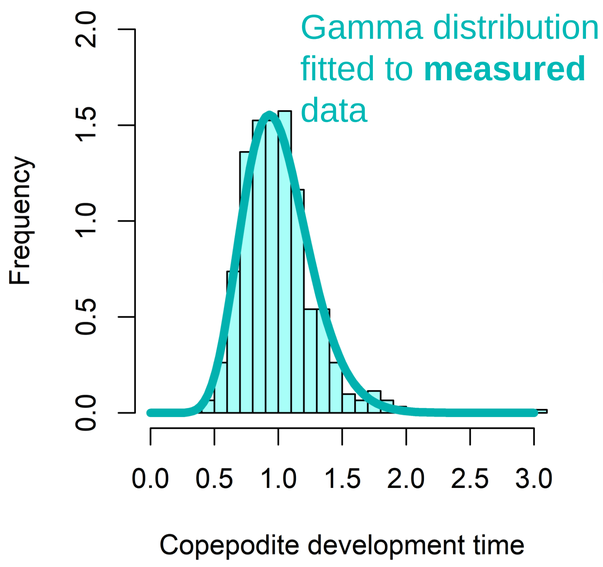
Biological variability

- Makes populations more resilient to stress and environmental changes[1].
- Is key to evolution (not considered in the model at this point in time).

Challenge

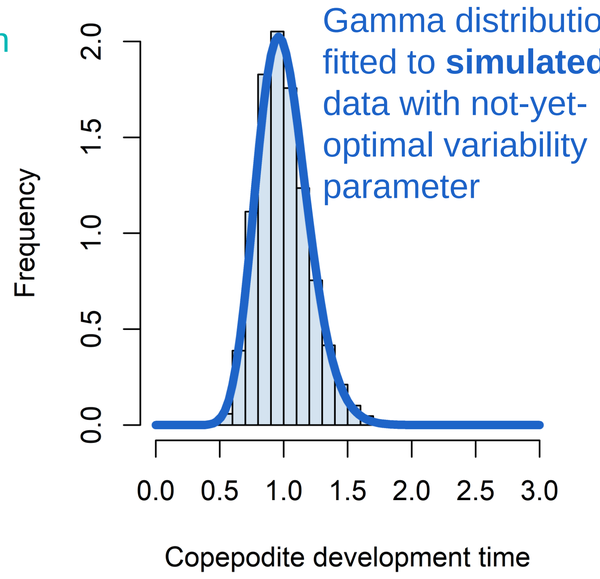
- Make realistic estimates of variability in DEB parameters from variation in measured data.

Material and Methods



1. Development time data were extracted from literature[2] and normalized by dividing all values by the mean development time per data set.

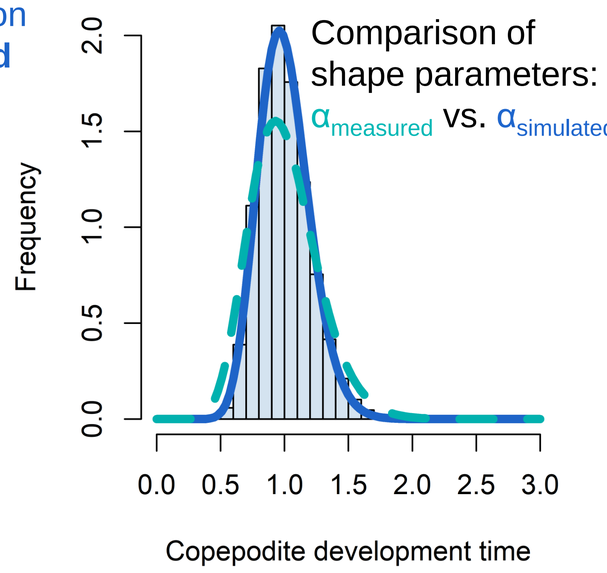
2. A gamma distribution was found to give a good fit with just one **shape parameter α**.



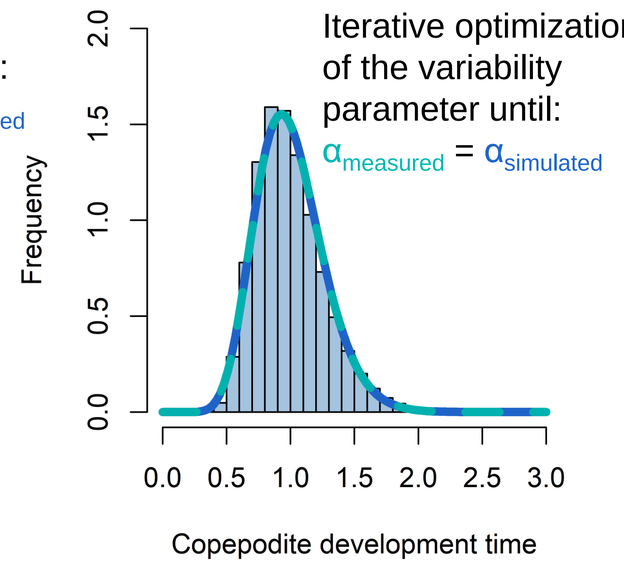
3. Variability was added to one DEB parameter (here *somatic maintenance rate* $[\dot{p}_M]$ drawn from a log-normal distribution).

4. The life histories of 10^7 animals were simulated.

5. A gamma distribution was fitted to the simulated data.



6. The difference between the measured and the simulated data was assessed by the loss function $(\alpha_{measured} - \alpha_{simulated})^2$.



7. The variability parameter (CV of log-normal distribution) was adjusted iteratively to minimize the loss function.

Results and Discussions

DEB parameter	CV log $_{conventional}$	CV log $_{best\ fit}$	KS test p-value meas. vs. sim. data
$[\dot{p}_M]$	-	0.291	0.17
$\{\dot{p}_{Am}\}$	0.05[3] – 0.1[4]	0.184	0.012
κ	-	0.087	1.4×10^{-10}

- Scattering the somatic maintenance rate $[\dot{p}_M]$ around a log-normal distribution resulted in a distribution of development times that resembles the distribution in the measured data the closest.
- Data on further endpoints such as the reproduction rate per female can be included as a next step. It is, however, important that the datasets are big enough to allow for proper analysis of the endpoints' distributions.

Conclusions

- By the use of 10^7 simulations (Monte Carlo method) of individual life histories per iteration step, the variability parameter (CV of log-normal distribution) could be estimated with high accuracy.
- This approach allows us to simulate life histories of copepods with a realistic variation in development time by adding variability to just one DEB parameter.
- Since biological variability affects the resilience of a population, we expect the model to give better predictions of population dynamics at stress conditions.

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References

[1] Oliver, T.H., et al., *Biodiversity and Resilience of Ecosystem Functions*. Trends in Ecology & Evolution, 2015. 30(11): p. 673-684.

[2] Koch, J., et al., *Temperature and Food Quantity Effects on the Harpacticoid Copepod Nitocra spinipes: Combining in Vivo Bioassays with Population Modeling*. PLoS ONE, 2017. 12(3): p. e0174384.

[3] Martin, B.T., et al., *Limitations of extrapolating toxic effects on reproduction to the population level.* Ecological Applications, 2014. 24(8): p. 1972-1983.

[4] Martin, B.T., et al., *Dynamic Energy Budget Theory Meets Individual-Based Modelling: A Generic and Accessible Implementation.* Methods in Ecology and Evolution, 2012. 3(2): p. 445-449.

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