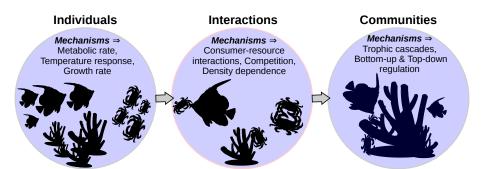
# Week 6: Mechanistic Models in Ecology and Evolution

CMEE Masters 2015-16

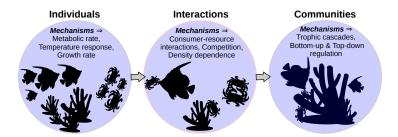
Samraat Pawar

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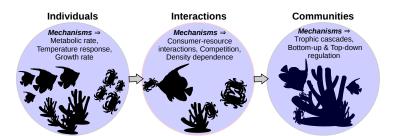
November 10, 2015



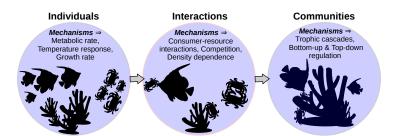
- Mechanistic models aim to explain the PROCESSES underlying observed patterns
- Empirical or phenomenological models show relationships between observed data (e.g. population size as a function of temperature or rainfall), but provide no insights into why they are related



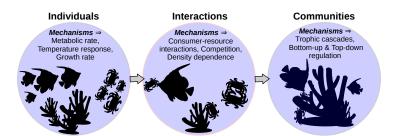
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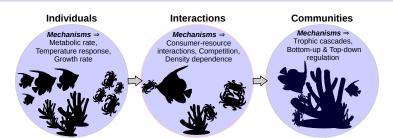
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  - Why the cycles?, Why the travelling waves? What mechanisms operate? (budmoth/parasitoid interaction? (budmoth/food quality interaction?)
- Another example, measles outbreaks (Papers in your Readings directory)

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• For example, the Ricker model can be thought of as mechanistic:

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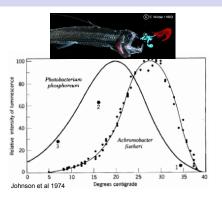
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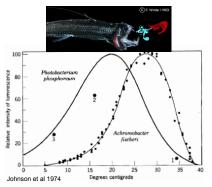
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- Many (including yours truly!) now argue that we have not progressed far enough because the first level has been ignored!







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T = temperature (K)

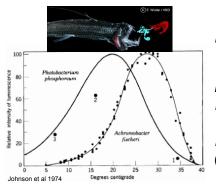
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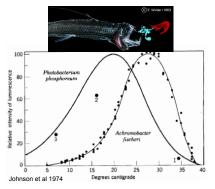
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- What about alternative models?



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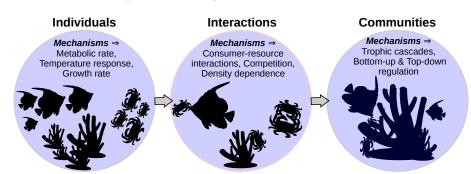
But first: A preview of the long practical

## MECHANISTIC MODELLING: WHAT'S THE BIG IDEA?

- Use biological knowledge to construct models
- See if the models "agree well" with data
- Whichever model "agrees best" is most likely to have the right mechanisms
- That's the one that's best for predictions (e.g. population cycles), estimating rates (e.g. growth rates), etc.
- Don't use models you already know have the wrong mechanisms!

## MECHANISTIC MODELLING: HOW TO BUILD THEM?

- It's an art, take practice (look at Levins' paper on the strategy of model building in biology)
- Build models one mechanism at a time in biology, it means start at the right level of organization!



## MECHANISTIC MODELLING: HOW TO BUILD THEM?

- For example, the Boltzmann-Arrhenius model is a good first try describe and uncover mechanisms underlying individual level rates
- The next step would be to include high-temperature effects (e.g., the Schoolfield model)
- The next step would be to include species interactions with temperature dependence of individuals (or go in an evolutionary direction!)

### FITTING MODELS TO DATA

#### Two common ways to do it:

- One-step forecasting (appropriate for discrete models)
- Ensemble fitting (appropriate for full time series or responses) this is what you will be doing in NLLS

There include maximum likelihood, bayesian methods, and Non-linear least squares (NLLS) optimization or fitting. You will use NLLS. Basically, this is how it works:

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- Stop simulations when the adjustments make virtually no difference to the rss



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- rss = sum(residuals \*\* 2)
- Then, AIC is n \* log((2 \* pi) / n) + n + 2 + n \* log(rss) + 2 \* k (what is n and k?)
- And BIC is n + n \* log(2 \* pi) + n \* log(rss / n) + (log(n)) \* (k + 1)
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#### Also note that:

 R<sup>2</sup> = 1 - (rss/tss), where tss is total sum of squares: tss = sum((Observations - mean(Predictions)) \*\* 2) (a useful measure of goodness of fit – you should report it)



### READINGS

- Levins, R. 1966 The strategy of model building in population biology. Am. Sci. 54, 421–431.
- Johnson, J. B. & Omland, K. S. 2004 Model selection in ecology and evolution. Trends Ecol. Evol. 19, 101–108.
- Papers in the Temperature\_response\_papers, but especially Schoolfield, R. M., Sharpe, P. J. & Magnuson, C. E. 1981 Non-linear regression of biological temperature-dependent rate models based on absolute reaction-rate theory. J. Theor. Biol. 88, 719–31.