Fitting Models to Data in Ecology and Evolution

CMEE Masters

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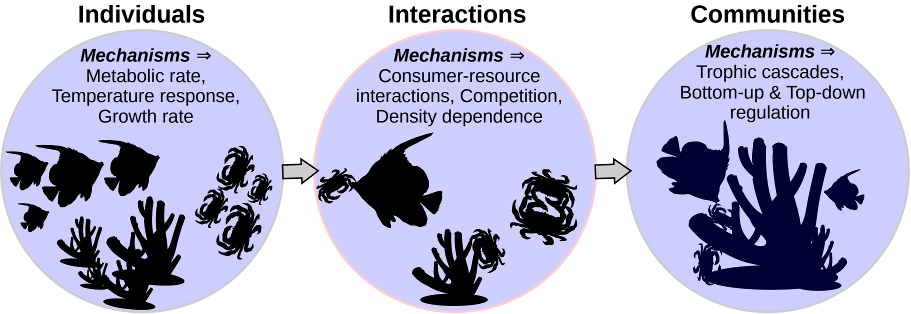

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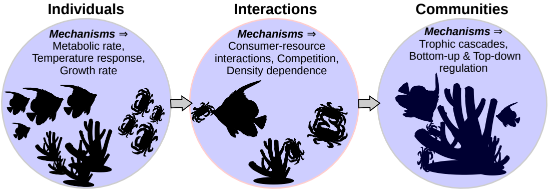

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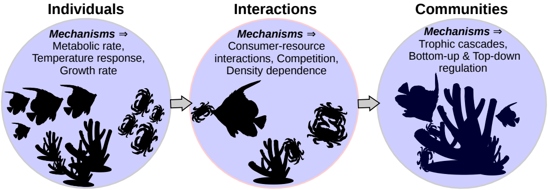

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- For example, insect invasions, outbreaks and spread (http://www.sandyliebhold.com/pubs/science_DC1/) — papers in your `Readings` directory; (http://www.imperial.ac.uk/qmee-cdt/supervisors/)

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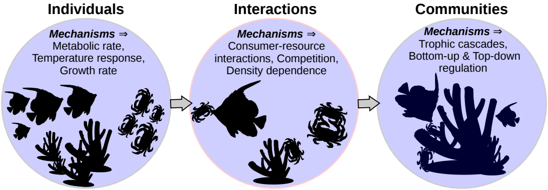

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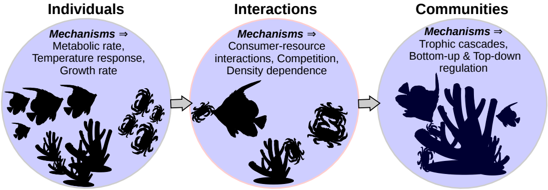

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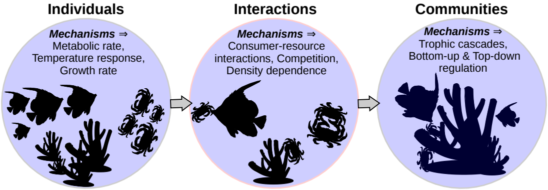

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  - Why the cycles?, Why the travelling waves? What mechanisms operate? (budmoth/parasitoid interaction? (budmoth/food quality interaction?) Are these truly mechanisms?
- Another example, disease outbreaks (Papers in your `Readings` directory)

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- But is this REALLY mechanistic? What are *r* and *k* really?
- Many (including yours truly!) now argue that we have not progressed far enough because the first level has been ignored!

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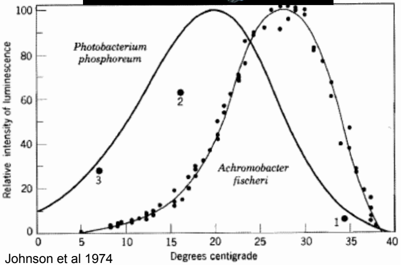

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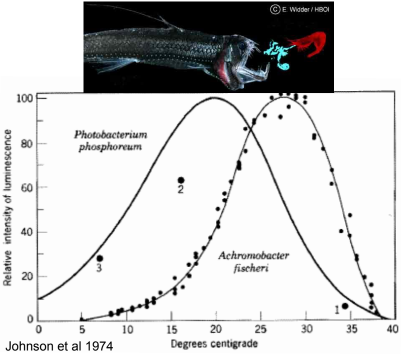

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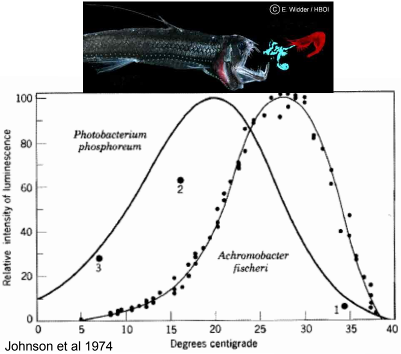

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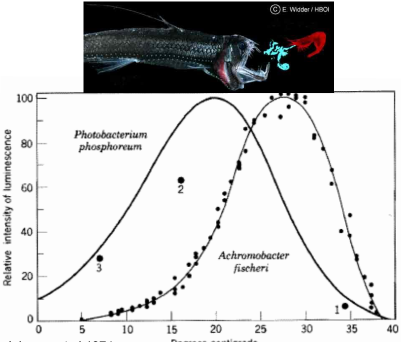

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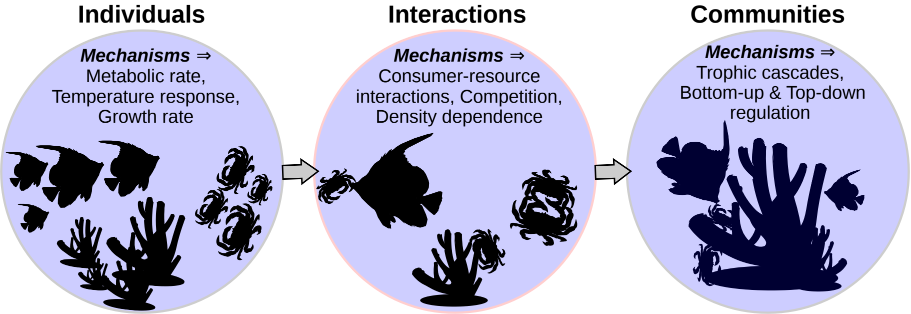
- *What about alternative models?*

MODELLING, AND FITTING MODELS TO DATA: WHAT'S THE BIG IDEA?

- If possible, 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!
- Phenomenological models often perform better than mechanistic ones

MODELS: 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!
- Always consider a alternative that is more parsimonious, even if it is phenomenological (the TPC example: Sharpe-Schoolfield, or Polynomial?)!



MODELS: 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!)

Next: A primer on mechanistic model fitting

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But first: A preview of the Miniproject (back to Notes)

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

ENSEMBLE FITTING

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

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7. Stop simulations when the adjustments make virtually no difference to the rss

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Comparing models

- It's all about the "Likelihood" of a model:
- That is, the likelihood of a set of parameter values (of a model), θ, given outcomes x, equals the probability of those observed outcomes given those parameter values, that is,

$$\mathcal{L}(\theta|x) = P(x|\theta)$$

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- residuals = Observations - Predictions
- 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^2 = 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.
- For the suggested fitting TPCs project: Papers in the `Temperature_response_papers` directory, 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.