

Fitting Models to Data in (VBD) Ecology and Evolution

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MECHANISTIC VS. PHENOMENOLOGICAL MODELS

What does “modelling data” mean to you?

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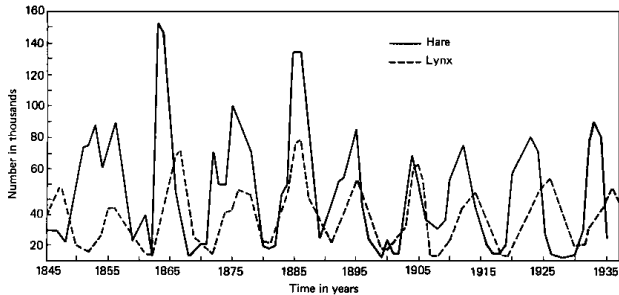
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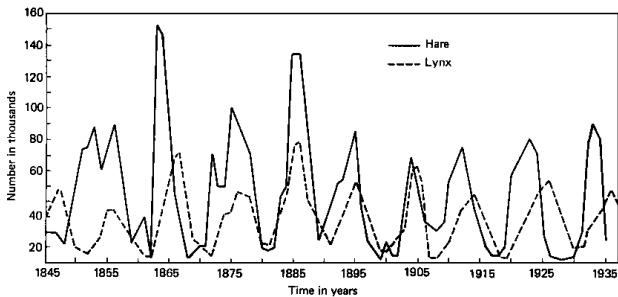
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MECHANISTIC VS. PHENOMENOLOGICAL MODEL FITTING



source: <https://www.cds.caltech.edu/~murray/amwiki/images/8/8f/LHgraph.gif>

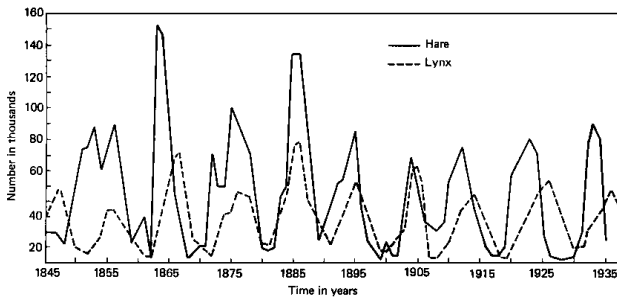
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- **Mechanistic model:** *The Lynx-Hare Cycle is driven by density-dependent population growth in hares*
- **Phenomenological model:** *The Lynx and Hare Cycles have a significant asynchrony (period shift) of x years*

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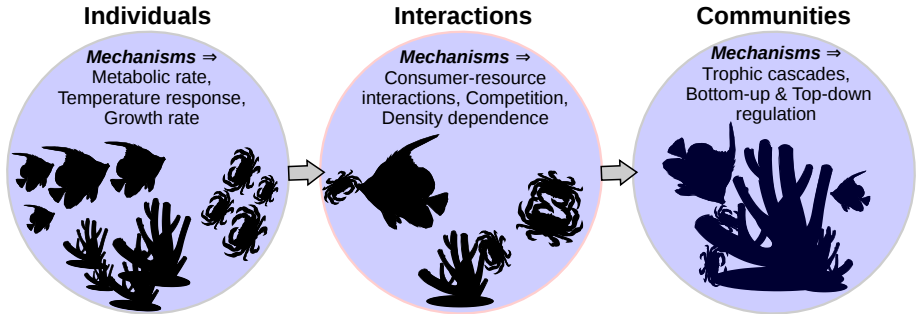
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- *Ultimately, successful, EMPIRICALLY-GROUNDED mechanistic models are the best path towards a THEORY in any scientific discipline (including ecology and evolution)*

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 - For example, disease outbreaks: Do we really need to care about the underlying mechanisms if we can predict a future event using phenomenological modelling (e.g., Machine-learning of time series patterns)?

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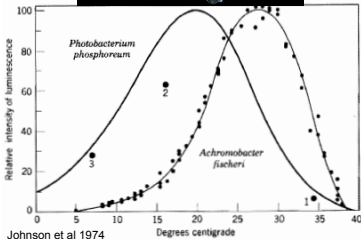
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- But is this REALLY mechanistic? What are r and k really?

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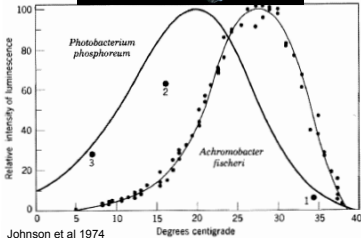
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Johnson et al 1974

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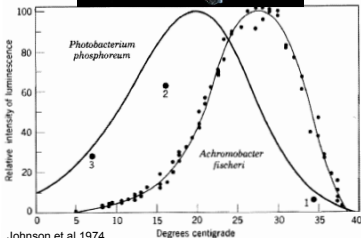
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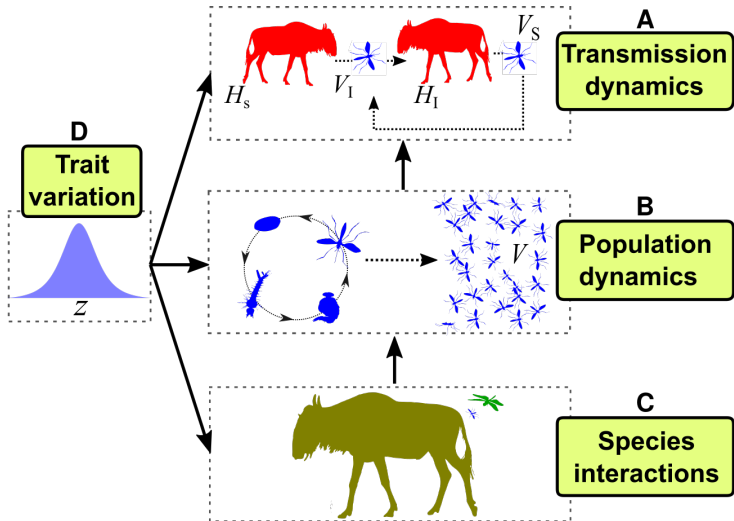
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- Surely there is more to thermal responses?
- What about alternative models?*

MECHANISMS IN VECTOR-BORNE DISEASE DYNAMICS?



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- Phenomenological/statistical models often perform better than mechanistic ones. *Why? — because they have less restrictive assumptions*

MODELS: HOW TO BUILD THEM?

- It's an art, takes practice
- Build models one mechanism at a time — in biology, it means start at the right level of organization!
- Always consider an alternative that is more parsimonious, even if it is phenomenological (the thermal performance curves example: Sharpe-Schoolfield, Briere, or Polynomial?)!
- For example, the Boltzmann-Arrhenius model is a good first try describe and uncover mechanisms underlying individual level rates (e.g., vector fecundity or development rate)
- The next step would be to include species interactions with temperature dependence of individuals (or go in an evolutionary direction)

FITTING MODELS TO DATA

Multiple ways to do it:

- Least Squares methods
 - Linear
 - Non-linear
- Likelihood-based methods
 - Maximum Likelihood Estimation (MLE)
 - Bayesian
- Artificial intelligence and Machine learning
 - Focus in on maximizing ability to discover pattern and predict at the cost of mechanistic insights

METHODS YOU CAN USE

- Least squares: along with Linear Model fitting, Non-linear Least Squares (NLLS) fitting is a particularly versatile and powerful approach because many mechanisms in biology and inherently non-linear
- MLE/Bayesian methods: more robust if you are able to calculate the likelihood function analytically or numerically.
- AI/machine Learning: most versatile for large amounts of noisy data

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- Necessary for developing the advancement of Biology from from an observational and axiomatic discipline to one with general theories.
- Necessary for understanding the mechanisms underlying biological patterns/phenomena

COMPARING AND SELECTING MODELS

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

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

- The easiest thing to do for you is to use information theory (including AIC and BIC) to compare models.
- Both AIC and BIC use the *estimated likelihoods of a model*:
AIC: $-2 \ln[\mathcal{L}(\theta|x)] + 2p$
Small sample AIC (AICc): $-2 \ln[\mathcal{L}(\theta|x)] + 2p$
BIC (Schwartz criterion): $-2 \ln[\mathcal{L}(\theta|x)] + p \ln(n)$
(where n = sample size, p number of free parameters)
- The lower the AIC or BIC, the better.

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(note n and p !)
- And BIC is $n + n * \log(2 * \pi) + n * \log(rss / n) + (\log(n)) * (p + 1)$
- That is, $\mathcal{L}(\theta|x) = -\frac{n}{2/\ln(RSS/n)}$
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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)

COMPARING AND SELECTING MODELS: MORE STUFF

- You can also calculate Akaike Weights, which is very useful/important when comparing > 2 models. These weights can then be used to perform *model averaging*.
- Model selection using the Likelihood-Ratio test (LRT) is another option when you are comparing 2 models.
- Adjusted R^2 can be used to get rigorous “idea” about how alternative models are performing.
- Very often, you will end up doing model simplification, especially in *for linear least squares model fitting* — starting with a complex model and then dropping terms till you have found a the most parsimonious version of the original model. There are functions in R to do this (of course!).

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.
- Bolker, B. M. et al. (2013) Strategies for fitting nonlinear ecological models in R, AD Model Builder, and BUGS. *Methods Ecol. Evol.* 4, 501–512 .
- Cator et al. More than a flying syringe: Using functional traits in vector-borne disease research (Under Review)
- Additional readings in the git repository