

Lecture 1

Introduction to statistical inference in ecology

WILD6900 (Spring 2019)

Reading

Hobbs & Hooten 3-16

Ecology \(^1\)

the comprehensive sicence of the relationship of the organism to the environment (Haeckel 1866)

the study of the natural environment, particularly the interrelationships between organisms and their surroundings (Ricklefs 1973)

the scientific study of the distribution and abundance of organisms (Andrewartha 1961)

where organisms are found, how many occur there, and why (Krebs 1972)

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Occurence

the spatial distribution of organisms with a particular region at a particular point in time

Richness

the number of co-occuring species at a given location and a particular point in time

Parameters determine how the state variables change over space and time

Survival

- Survival
- Reproduction

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- Movement

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- Population growth rate

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- Colonization/extinction rate

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By necessity, models are simplifications of reality

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knowledge based on experience and understanding of the ecological system of interest

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2) Statistical expertise

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Useful models should be consistent with both domain and statistical expertise!

Notation

Parameter(s) \$\$\theta\$\$

\$\$y\$\$

\$\$y\$\$ Predictor(s)

\$\$x\$\$

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\$\$(y, \theta, x)\$\$

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\$\$[a|b,c]\$\$

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\$\$[a|b,c]\$\$ Deterministic function

\$\$g()\$\$

A line of inference in ecology

\$\$g(\theta_p, x)\$\$

• Mathematical description of our hypothesis about how the state variables we are interested in change over space and time

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- Represent the **true** value of our state variables at any given point in space or time

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- Abstraction

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- Unmodeled sources of variation = \(\sigma^2_p\)
- State variable \((z)\) modeled as a probability distribution

 $\[z|g(\theta_p, x), \sigma^2_p]$

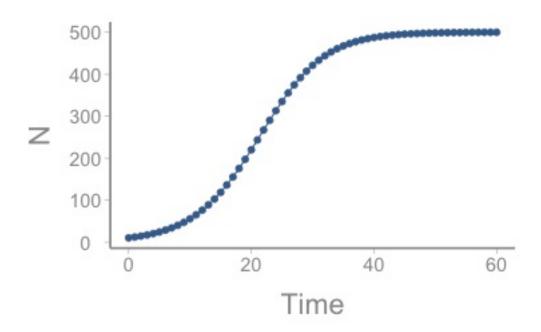
Example

We are interested in predicting the population growth on species (a) as a function of abundance in the previous year $(^4)$

We hypothesize that population growth rate will be highest at low densities and lowest (maybe even negative) at high density

This leads us to believe that the discrete logistic equation is a good descriptor of our system:

$$$N_{t+1} = g(\theta_p, x) = N_{te}^{r_0[1-(N_t/K)]}$$

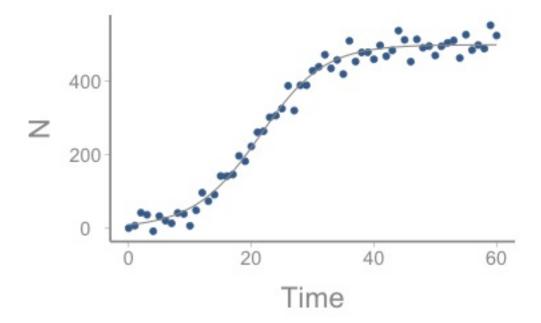


Example

In reality, \(N\) will not fall exactly on the line predicted by the Ricker model

There will obviously be processes other than density-dependence that are influencing population size in each year that are not accounted for by our model

• In other words, there is process uncertainty \((\sigma^2_p > 0)\):



Interpreting \(\sigma^2_p\)

- The process model represents the **true** value of \(N\), not our observation of it.
- \(\sigma^2_p\) is as a measure of how well our process model fits reality
- To minimize process uncertainty, we need a better model. No amount of additional data will lower \(\sigma^2_p\).

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In our example, maybe we have environmental covariates (rainfall, temperature, etc.) that we also think are important. To reduce process uncertainty, we would need to modify our process model to include these effects.

Sampling models

Sampling models

- Obtaining probability distributions about our state-variables and parameters requires data
- Data are samples of the true population
 - Our sample will not perfectly represent the true state of the system
- As for the process model, we can represent sampling uncertainty \(\sigma_s\) stochastically using a probability model \(^5\):

\$\$[u_i|z,\sigma^2_s]\$\$

Sampling models

Example

In our population size example, suppose we conduct (i = 1,2,3,...,K) transect or point counts to estimate abundance. The area of our counts (we'll call it (a)) is not the entire area of our population ((a < A)). If we want to estimate (N_t) , we need a model linking our counts (call them $(n_{t,i})$) to the true abundance. If we assume individuals are uniformly distributed across our study area, then perhaps we could use:

 $\$ \bigg[\sum_{i=1}^K n_{t,i}\bigg|\frac{N_t}{a}, \sigma^2_s\bigg]\$\$

In this case, our counts (n_t) will be different if we had chosen different transect routes or points. This is what (\sin^2_s) represents.

Separating (σ^2_s) from (σ^2_p) is important because we can lower (σ^2_s) by collecting larger sample sizes or increasing replication

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 - o Individuals may not be "available" during our sample
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- This observation uncertainty \((\sigma^2_o)\) can lead to biased estimates of model parameters, so generally requires its own model \(^6\)

 $\[y_i|d(\Theta_o,u_i), \simeq^2_o]$

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In our count model, we might define a parameter \(\psi\) that is the probability that individual that is present in our sample is counted by the observer (we could further use a generalized linear model to account for the effects of, e.g., weather or observer skill, on \(\psi\)):

\$\$[y_t|\psi n_t, \sigma^2_o]\$\$

where \(\sigma^2_o\) is uncertainty about the value of \(\psi\).

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• These distributions can provide a lot or a little information about the potential value of each parameter

With each of our models created, we are prepared to right out the full model:

```
$$\bigg[\underbrace{z, \theta_p, \theta_o, \sigma^2_p, \sigma^2_s, \sigma^2_o, u_i]_{unobserved}\big|\underbrace{y_i}_{observed} \bigg] \propto \underbrace{[y_i|d(\Theta_o,u_i), \sigma^2_o]}_{Observation \; model} \underbrace{[u_i|z, \sigma^2_s]}_{Sampling\; model} \underbrace{[z|g(\theta_p, x), \sigma^2_p]}_{Process\; model} \underbrace{[\theta_p][\theta_o][\sigma^2_p][\sigma^2_s][\sigma^2_o]}_{Parameter\; models}$$
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- treating all unobserved quantities as random variables and specifying probability distributions for each quantity is what makes this model Bayesian.