



University of Nevada, Reno

## Lecture 3: Deterministic Models

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NRES 779

Bayesian Hierarchical Modeling in Natural Resources

# Today

- Deterministic Models, and how we use them in hierarchical modeling

# Deterministic Models



Art is a lie that makes us  
realize the truth.

*Pablo Picasso*

All models are wrong, but  
some are useful.

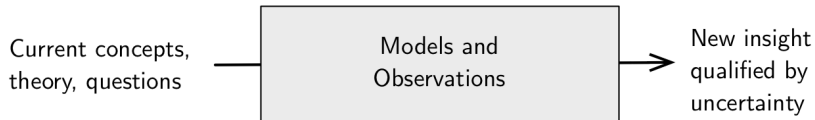
*G.E.P. Box*

It is better to invent reality  
than to copy it.

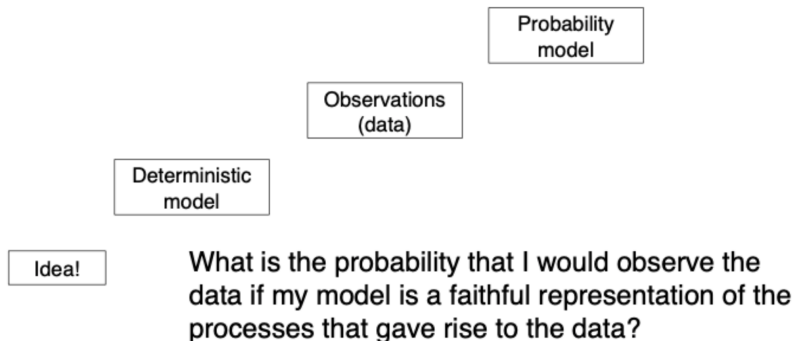
*G. Verdi*

$$\frac{dN}{dt} = rN \left(1 - \frac{N}{K}\right)$$

# Goal of Course



# Linking Models to Data



# Layout of next few lectures

- Today: Examples of deterministic models
- Friday: Basic laws of probability
- Wednesday: Probability distributions
- Friday: Likelihood and Bayes' Theorem

# Learning Objectives

- Distinguish between purely empirical models and models symbolizing processes.
- Introduce a set of functional forms useful for composing deterministic models.
- Cross cutting themes
  - A relatively small set of functions can be used to describe a broad array of (natural) processes.
  - The same process can be represented by different functional forms.
  - The same functional form can be used to represent different processes.

# Deterministic Models

## Recall from calculus

$$y_i = f(x_i)$$



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**But in our class, we use  $y$  for data, so let's use something else**

$$\mu_i = f(x_i)$$

# Deterministic Models

## Recall from calculus

$$y_i = f(x_i)$$

**But in our class, we use  $y$  for data, so let's use something else**

$$\mu_i = f(x_i)$$

**Also, we will be interested in estimating parameters, so let's include that too**

$$\mu_i = f(x_i, \theta)$$

# Deterministic Models

$$\underbrace{\mu_i}_{\text{expected response}} = f\left(\underbrace{x_i}_{\text{predictors}}, \underbrace{\theta}_{\text{parameters}}\right)$$

What makes this deterministic? Predictors are also known as predictor variables, independent variables, and covariates.

# Equation of a line

$$\mu_i = f(x_i, \boldsymbol{\theta}),$$

$$\mu_i = \beta_0 + \beta_1 x_i,$$

where  $\boldsymbol{\theta} = (\beta_0, \beta_1)'$

$$f(x_i, \theta)$$

## Any type of process

- Spread of white nose syndrome
- Decomposition in grassland soils
- Movement of elephants across landscapes
- Food web dynamics in streams
- Growth of waterfowl populations
- Influence of hydrologic regime on riparian plant communities
- Invasion of exotic species into native plant communities

$$f(x_i, \theta)$$

## Any type of mathematical function

- linear models
- non-linear models
- systems of differential equations
- systems of difference equations
- integral-projection models
- state-transition models
- matrix models

Any equation or system of equations making a prediction that can be compared with an observation.

# Nicholson-Bailey Model Equations

The Nicholson-Bailey Model describes the dynamics of host ( $H$ ) and parasitoid ( $P$ ) populations with the following coupled difference equations:

$$H_{t+1} = H_t e^{r(1-\frac{H_t}{K})} e^{-aP_t} \quad (1)$$

$$P_{t+1} = cH_t(1 - e^{-aP_t}) \quad (2)$$

where:

- $H_t$ : Population size of the host at time  $t$ .
- $P_t$ : Population size of the parasitoid at time  $t$ .
- $r$ : Reproductive rate of the host.
- $K$ : Carrying capacity of the host.
- $a$ : Attack rate of the parasitoid.
- $c$ : Average number of viable eggs the parasitoid lays in a host.

Prey Equation:  $H_{t+1} = H_t e^{r(1-\frac{H_t}{K})} e^{-aP_t}$

- $H_t$ : Population size of the host at time  $t$ .
- $r$ : Reproductive rate of the host.
- $K$ : Carrying capacity of the host.
- $a$ : Attack rate of the parasitoid.
- $P_t$ : Population size of the parasitoid at time  $t$ .

Assumptions:

- 1 The parasitoid finds hosts randomly.
- 2 Hosts and parasitoids are randomly distributed across a landscape.



## Predator Equation: $P_{t+1} = cH_t(1 - e^{-aP_t})$

- $P_t$ : Population size of the parasitoid at time  $t$ .
- $c$ : Average number of viable eggs the parasitoid lays in a host.
- $H_t$ : Population size of the host at time  $t$ .
- $a$ : Attack rate of the parasitoid.

Assumptions:

- 1 The parasitoid finds hosts randomly.
- 2 Hosts and parasitoids are randomly distributed across a landscape.

# Population Dynamics and Assumptions

The rate of host population growth,  $e^{r(1-\frac{H_t}{K})}$ , accounts for density-dependent effects. The term  $e^{-aP_t}$  represents the probability that the host will survive, and thus  $(1 - e^{-aP_t})$  is the probability that the parasitoid survives.

# Analysis

To analyze the model:

- Examine equilibrium points.
- Investigate stability.
- Explore bifurcations.

The system's dynamics can exhibit oscillations, stability, or chaos based on parameter values.

# Logistic Growth Equation (Biology and Ecology)

$$H_{t+1} = rH_t \left(1 - \frac{H_t}{K}\right)$$

The logistic growth equation describes how a population grows in an environment with limited resources, exhibiting a similar structure to the Nicholson-Bailey prey equation.

# Predator-Prey Model (Ecology)

$$\frac{dH}{dt} = rH \left( 1 - \frac{H}{K} \right) - aHP \quad (3)$$

$$\frac{dP}{dt} = cHP - dP \quad (4)$$

This system of differential equations represents a classic predator-prey model, sharing a similar structure with the Nicholson-Bailey model.

The discrete-time Lotka-Volterra model equations are given by:

$$x_{t+1} = x_t \cdot (1 + r_x - a_{xy} \cdot y_t)$$

$$y_{t+1} = y_t \cdot (1 - r_y + a_{yx} \cdot x_t)$$

# Exponential Decay (Physics and Chemistry)

$$N_{t+1} = N_t e^{-\lambda}$$

The exponential decay equation describes the decay of a substance over time, analogous to the decrease in the prey population in the Nicholson-Bailey model.

where:

- $x_t$ : Population of the prey species at time  $t$ .
- $y_t$ : Population of the predator species at time  $t$ .
- $r_x$ : Intrinsic growth rate of the prey in the absence of predators.
- $r_y$ : Death rate of the predators in the absence of prey.
- $a_{xy}$ : Rate at which predators capture and eat prey.
- $a_{yx}$ : Rate at which prey is produced by consuming predators.

These equations describe the discrete, non-overlapping generation dynamics of the prey and predator populations in an ecological system.



# Model of Political Repression and Democracy

The model is derived from Davenport and Armstrong II's (2004) study on the relationship between political repression and the level of democracy within a country.

$$R_t = D_t + D_t^2$$

Here:

- $R_t$ : Level of repression at time  $t$
- $D_t$ : Level of democracy at time  $t$

# Model Explanation

The equation  $R_t = D_t + D_t^2$  suggests a relationship where the level of political repression ( $R_t$ ) is influenced by the level of democracy ( $D_t$ ) at a given time  $t$ .

- As the level of democracy increases, so does the level of political repression in a linear fashion.
- There is a tipping point where the relationship becomes inverted, creating an inverse-U relationship.

# Interpretation

The model implies that initially, an increase in democracy leads to an increase in political repression, possibly due to certain instability or reactions. However, beyond a tipping point, increasing democracy results in a decrease in political repression, indicating a more stable and democratic society.

# Davenport and Armstrong II (2004)

- The model is based on the work of Davenport and Armstrong II in 2004.
- The goal was to understand how democracy influences a country's adherence to international norms of human rights.
- The model provides insights into the complex relationship between political repression and democracy.

# Ricker Growth Function

The classic Ricker model looks like this:

$$N_{t+1} = N_t e^{r(1-N_t/k)}$$

- $N$ : Number of individuals
- $t$ : Unit of time
- $r$ : Growth rate for the population
- $k$ : Carrying capacity or maximum number of individuals for the given environment (Ricker 1954)

## Ricker Growth Function (Contd.)

The Ricker model was created for stock and recruitment in fisheries by Dr. Bill Ricker. In this model, future population is dependent on previous but also influenced by the growth rate and limited by the carrying capacity. Unlike the logistic growth function,  $N_{t+1}$  cannot be negative.

# Modification in Freshwater Ecosystem Ecology

In freshwater ecosystem ecology, this function was modified to represent the density-dependent growth of photosynthetically active biomass for a discrete time step:

$$B_t = (B_{t-1} + r_{max} + \lambda e^{B_{t-1}})P_t$$

- $B_t$ : Log of latent photosynthetically active biomass at a daily time step  $t$
- $r_{max}$ : Maximum per capita biomass growth rate
- $\lambda = -r_{max}/K$ , where  $K$  is the estimated biomass carrying capacity of a river
- $P_t$ : Day-to-day persistence of biomass dependent on hydrologic disturbance and detachment (Błaszczak et al. 2023)

## Modification in Freshwater Ecosystem Ecology (Contd.)

This equation looks different from the original Ricker function above as it has taken the natural log of both sides of the equation, and the  $\lambda$  term has been introduced for simplification. The additional term,  $P_t$ , allows the growth function to account for external disturbances based on river discharge (e.g., a storm event that causes algal detachment would be associated with higher than normal flows).



# Ricker Growth Model

$$N_{t+1} = N_t e^{r(1-N_t/k)}$$

This is the original Ricker growth model.

# Natural Logarithm Transformation

Apply the natural logarithm ( $\log$ ) to both sides of the equation:

$$\log(N_{t+1}) = \log(N_t e^{r(1-N_t/k)})$$

# Product Rule of Logarithms

Use the product rule of logarithms ( $\log(xy) = \log(x) + \log(y)$ ):

$$\log(N_{t+1}) = \log(N_t) + \log(e^{r(1-N_t/k)})$$

# Exponential Property of Logarithms

Apply the exponential property of logarithms ( $\log(e^x) = x$ ):

$$\log(N_{t+1}) = \log(N_t) + r(1 - N_t/k)$$

# Introduction of Additional Terms

Introduce additional terms for the modified model representing freshwater ecosystems:

$$B_t = (B_{t-1} + r_{\max} + \lambda e^{B_{t-1}})P_t$$

Where:

- $B_t$  corresponds to  $\log(N_{t+1})$
- $B_{t-1}$  corresponds to  $\log(N_t)$
- $r_{\max}$  corresponds to  $r(1 - N_t/k)$
- $\lambda = -r_{\max}/K$
- $P_t$  represents day-to-day persistence of biomass

# Introduction: Limits in Natural Systems

- In biology and ecology, natural systems have inherent limits.
- Examples include the carrying capacity of a population and the finite size of organisms.
- Asymptotic equations help describe these limits.

# Asymptotic Equation Formulation

The asymptotic equation used is:

$$g(v_{\max}, \alpha, x) = \frac{v_{\max}x}{\alpha + x}$$

- $v_{\max}$ : Limit of the independent variable as  $x$  approaches infinity.
- $\alpha$ : Rate of change in the dependent variable.

# Application in Fisheries Management

- Growth curves are crucial in fisheries management.
- These curves help understand the age and maturity of a target species at a particular size.
- Maximum growth rate often precedes reproduction; after maturity, growth slows.
- Growth curves aid in defining minimum size limits for sustainable harvest.



# Conclusion

- Asymptotic equations are essential tools in understanding limits in natural systems.
- In fisheries management, they play a crucial role in defining harvest regulations for sustainable practices.

# Similarities with Other Equations

- **\*\*Ricker Model (Ecology):\*\***

$$y_t = y_{t-1} \cdot \exp(a(1 - y_{t-1}/b))$$

- **\*\*Logistic Growth Model (Ecology):\*\***

$$N_{t+1} = N_t \cdot \frac{r(1 - N_t/K)}{1 + r(1 - N_t/K)}$$

- **\*\*Verhulst Equation (Demography):\*\***

$$\frac{dN}{dt} = rN \left(1 - \frac{N}{K}\right)$$

- **\*\*Lotka-Volterra Equations (Ecology):\*\***

$$\frac{dx}{dt} = \alpha x - \beta xy$$

$$\frac{dy}{dt} = \delta xy - \gamma y$$

- **\*\*Gompertz Function (Biophysics, Tumor Growth):\*\***

# Introduction: Deterministic SWE Modeling

- In snow hydrology, modeling snow water equivalent (SWE) is essential.
- Direct measurements of SWE can be challenging, leading to the use of deterministic reconstruction models.
- The presented deterministic model includes two key equations for SWE and snow-covered area (SCA).

# Deterministic SWE Model (Equation 1)

$$SWE_n = SWE_0 - \sum_{j=1}^n M_j$$

- $SWE_n$ : SWE at time  $n$ .
- $SWE_0$ : Initial SWE.
- $M_j$ : Snowmelt for time step  $j$ .
- Equation 1 calculates the new SWE based on initial conditions and cumulative snowmelt.

## Snow-Covered Area Model (Equation 2)

$$SCA_j = SCA_i - \frac{(SCA_i - SCA_k)}{\sum_{i=1}^n Mp_i - \sum_{k=1}^n Mp_k} \times \left( \sum_{i=1}^n Mp_i - \sum_{j=1}^n Mp_j \right)$$

- $SCA_j$ : Snow-Covered Area at time step  $j$ .
- $SCA_i$ : Initial Snow-Covered Area.
- $SCA_k$ : Snow-Covered Area at time step  $k$ .
- $Mp_i$ : Snowmelt for time step  $i$ .
- Equation 2 models the evolution of snow-covered area considering initial conditions and cumulative snowmelt.

# Applications and Considerations

- Deterministic SWE modeling is crucial in snow hydrology for estimating SWE when direct measurements are challenging.
- These models provide insights into the changes in SWE and snow-covered area over time.
- Considerations include the accuracy of initial conditions and the cumulative impact of snowmelt on the system.

# Conclusion

- The presented deterministic SWE model offers a practical approach to estimating snow water equivalent.
- Equations 1 and 2 capture the dynamics of SWE and snow-covered area based on snowmelt and initial conditions.
- These models contribute to a better understanding of snowpack evolution in snow hydrology.

# Monomolecular Growth Model

The Monomolecular Growth Model is particularly relevant in agricultural research, explaining the relationship between crop yield and input variables like fertilizer or irrigation.

$$\frac{dN}{dt} = r(K - N)$$

Where:

- $N$ : Population size or biomass.
- $r$ : Intrinsic growth rate.
- $K$ : Carrying size of the system.



# Monomolecular Growth Model (Contd.)

Integrating the equation, we get:

$$N(t) = K - (K - N_0) \exp(-rt)$$

Where:

- $N(t)$ : Population size or biomass at time  $t$ .
- $N_0$ : Initial population size at  $t = 0$ .

The model captures the non-linear relationship between input variables and crop yield, showing saturation beyond a certain point.