Exponential Population Growth
Chapter 1: Gotelli's Primer of Ecology

Ecological Modeling Tutorial

2025-07-15

Concepts in Ecology

My Story

I come from Veterinary Medicine background with bare minimum knowledge of Ecology. When I got into PhD program in Ecology my first impression was ohh! Ecology its gonna be so easy for me, because I had taken hardcore courses in my prior degress (DVM and Masters in Microbiology and Immunology) - guess, what that was my biggest assumption which was busted when I came across Phase Plans explained by Dr. Craig (Program Cordinator and Association Professor in Ecology @ UGA). He is one of the best Professor in Ecology, who was inspiration to think critically in Ecological Concepts. That was moment when I thought well Abdul its not gonna be easy for you boy. That was just begining, the MATH was just waiting for me to put hammer on my head. It was here and there, tried my best to understand basic concepts with thought in my mind, I gotta get back to basic concepts If I want to be an Ecologist.

Few months back I started preparing for Comprehensive Exam and I thought to myself why not try to make a booklet for students like me to summarize those concepts that I had hard time comprehending.

Well here we go!

*This booklet explains concepts from Gotelli (2008) A Primer of Ecology - https://www.academia.edu/35171352/Gotelli_2008_A_Primer_of_Ecology

```r
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
library(knitr)
```

Introduction to Exponential Population Growth

Exponential population growth is the foundation of population ecology and represents the simplest model of population dynamics. This chapter explores the mathematical foundations and ecological implications of exponential growth as presented in Gotelli's Primer of Ecology.

Key Concepts

- **Population Growth Rate**: The change in population size over time
- **Intrinsic Rate of Increase**: The maximum theoretical growth rate (r)
- **Carrying Capacity**: The maximum population size an environment can sustain
- **Density-Independent Growth**: Growth that is not affected by population density

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Mathematical Foundation

The Exponential Growth Model

The exponential growth model is expressed as a differential equation:

$$\frac{dN}{dt} = rN$$

Where: - N = Population size at time t - r = Intrinsic rate of increase (per capita growth rate) - t = Time - $\frac{dN}{dt}$ = Rate of change of population size

trust me you will see it in your bad dreams too

Key Parameters

Intrinsic Rate of Increase (r): - $r > 0$: Population grows exponentially - $r = 0$: Population remains constant - $r < 0$: Population declines exponentially

Analytical Solution

The differential equation can be solved analytically:

$$N(t) = N_0 e^{rt}$$

Where: - N_0 = Initial population size - e = Base of natural logarithm (2.718)

Derivation

Starting with the differential equation:

$$\frac{dN}{dt} = rN$$

Separating variables:

$$\frac{dN}{N} = r\,dt$$

Integrating both sides:

$$\int \frac{dN}{N} = \int r\,dt$$

$$\ln(N) = rt + C$$

Where C is the constant of integration. At $t = 0$, $N = N_0$:

$$\ln(N_0) = C$$

Therefore:

$$\ln(N) = rt + \ln(N_0)$$

$$\ln(N) - \ln(N_0) = rt$$

$$\ln\left(\frac{N}{N_0}\right) = rt$$

Taking the exponential of both sides:

$$N = N_0 e^{rt}$$

Ecological Interpretation

Population Doubling Time

The time required for a population to double in size is:

$$t_{double} = \frac{\ln(2)}{r}$$

```r
# Calculate doubling time for different growth rates
r_values <- c(0.01, 0.05, 0.1, 0.2, 0.3, 0.5)
doubling_times <- log(2) / r_values

doubling_df <- data.frame(
  Growth_Rate = r_values,
  Doubling_Time = doubling_times
)
```

```
kable(doubling_df,
      col.names = c("Growth Rate (r)", "Doubling Time"),
      caption = "Population Doubling Times for Different Growth Rates",
      digits = 2)
```

Table 1: Population Doubling Times for Different Growth Rates

Growth Rate (r)	Doubling Time
0.01	69.31
0.05	13.86
0.10	6.93
0.20	3.47
0.30	2.31
0.50	1.39

Discrete vs. Continuous Growth

Discrete Growth Model

For populations with non-overlapping generations:

$$N_{t+1} = N_t \lambda$$

Where λ is the finite rate of increase.

The relationship between r and λ is:

$$\lambda = e^r$$

$$r = \ln(\lambda)$$

```
# Demonstrate relationship between r and lambda
r_vals <- seq(0, 0.5, by = 0.05)
lambda_vals <- exp(r_vals)

relationship_df <- data.frame(
  r = r_vals,
  lambda = lambda_vals
)

ggplot(relationship_df, aes(x = r, y = lambda)) +
  geom_line(color = "blue", size = 1.2) +
  geom_point(color = "red", size = 2) +
  labs(title = "Relationship between r and  ",
       x = "Intrinsic Rate of Increase (r)",
       y = "Finite Rate of Increase ( )") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5))
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

Relationship between r and .
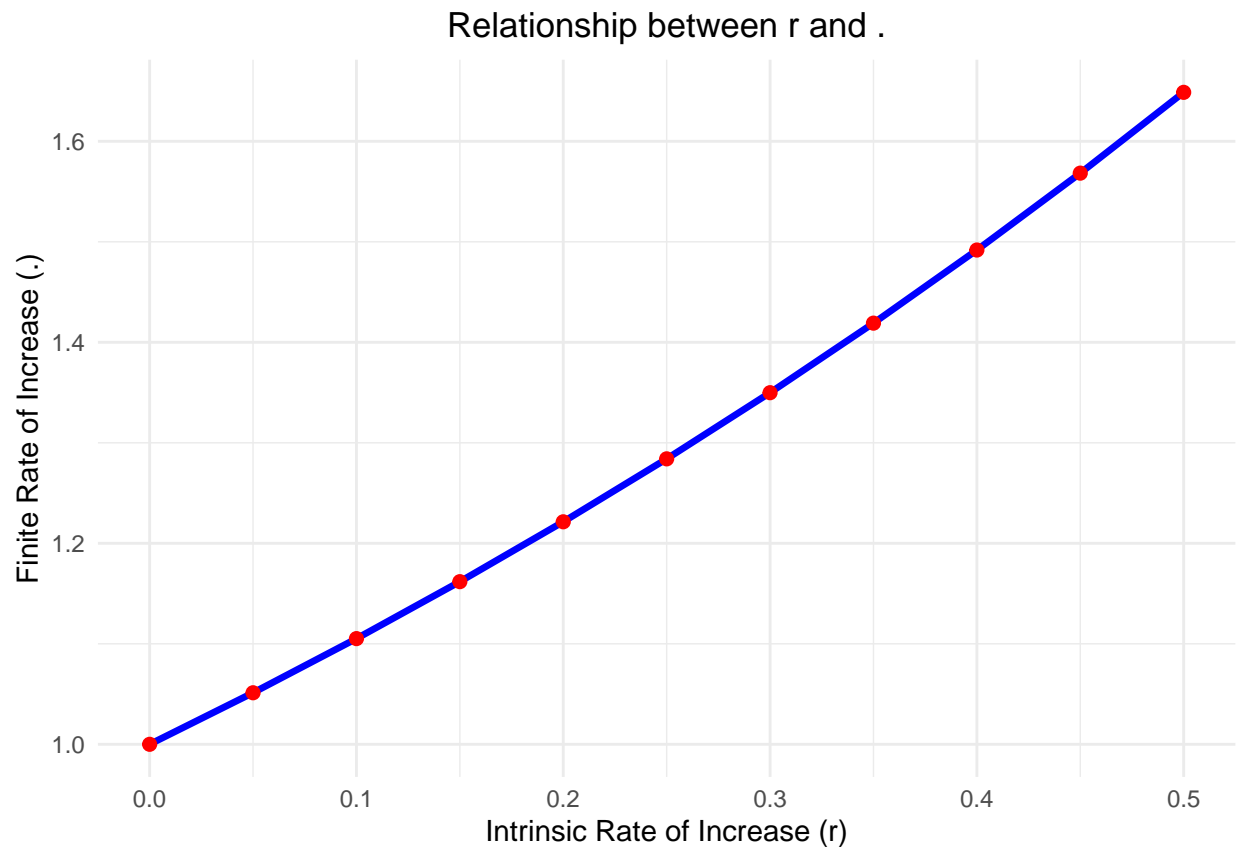
R Simulations

Basic Exponential Growth Simulation

```r
# Parameters
N0 <- 10          # Initial population size
r <- 0.1          # Intrinsic rate of increase
t_max <- 50       # Maximum time
dt <- 0.1         # Time step

# Create time sequence
time <- seq(0, t_max, by = dt)

# Calculate population using analytical solution
N_analytical <- N0 * exp(r * time)

# Create data frame
growth_data <- data.frame(
  Time = time,
  Population = N_analytical,
  Type = "Analytical"
```
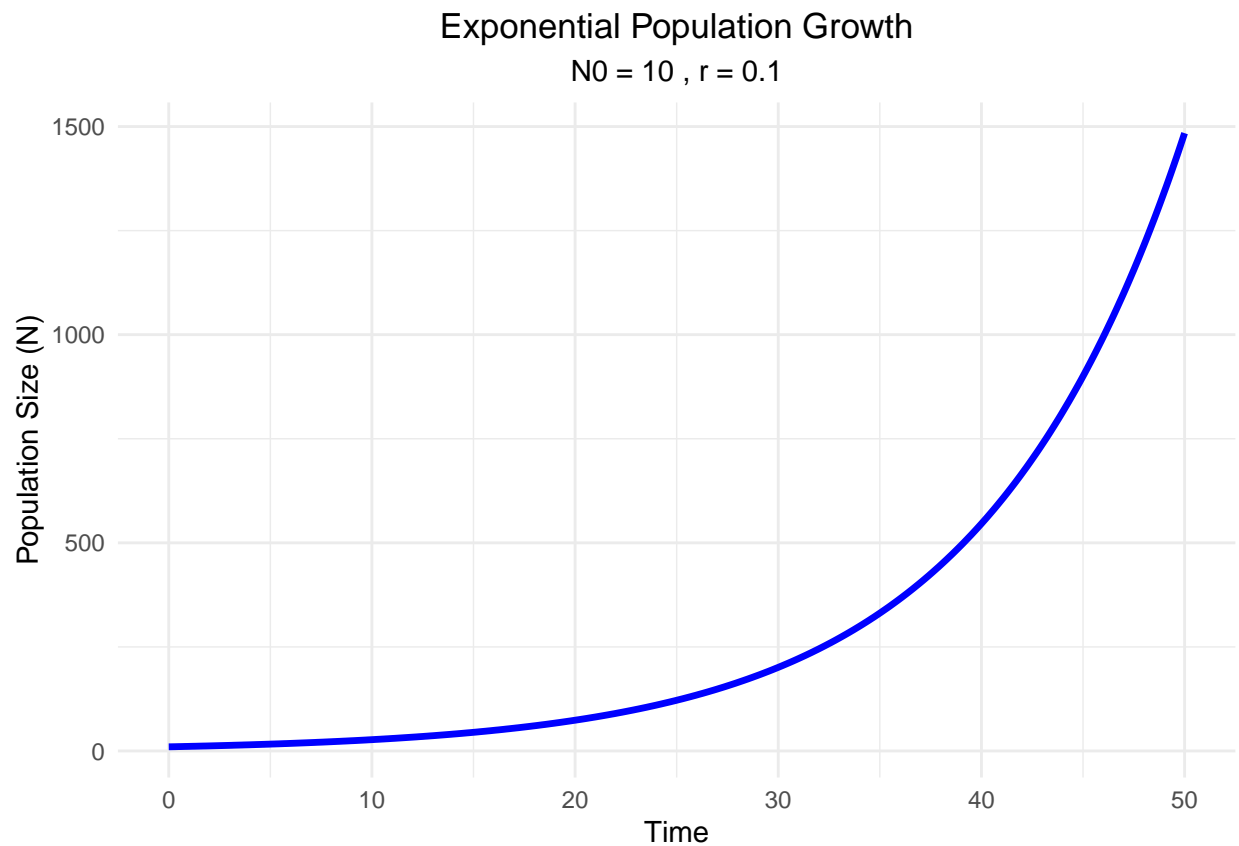
```
)

# Plot exponential growth
ggplot(growth_data, aes(x = Time, y = Population)) +
  geom_line(color = "blue", size = 1.2) +
  labs(title = "Exponential Population Growth",
       subtitle = paste("N =", N0, ", r =", r),
       x = "Time",
       y = "Population Size (N)") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```

Exponential Population Growth
N0 = 10 , r = 0.1

Numerical Integration (Euler's Method)

```
# Numerical integration using Euler's method
euler_integration <- function(N0, r, t_max, dt) {
  time <- seq(0, t_max, by = dt)
  N <- numeric(length(time))
  N[1] <- N0

  for (i in 2:length(time)) {
    dN_dt <- r * N[i-1]
```

```
    N[i] <- N[i-1] + dN_dt * dt
  }

  return(data.frame(Time = time, Population = N))
}

# Run numerical simulation
numerical_data <- euler_integration(N0 = 10, r = 0.1, t_max = 50, dt = 0.1)
numerical_data$Type <- "Numerical"

# Combine analytical and numerical results
combined_data <- rbind(growth_data, numerical_data)

# Plot comparison
ggplot(combined_data, aes(x = Time, y = Population, color = Type)) +
  geom_line(size = 1.2) +
  labs(title = "Analytical vs. Numerical Solutions",
       subtitle = "Exponential Growth Model",
       x = "Time",
       y = "Population Size (N)") +
  scale_color_manual(values = c("Analytical" = "blue", "Numerical" = "red")) +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```
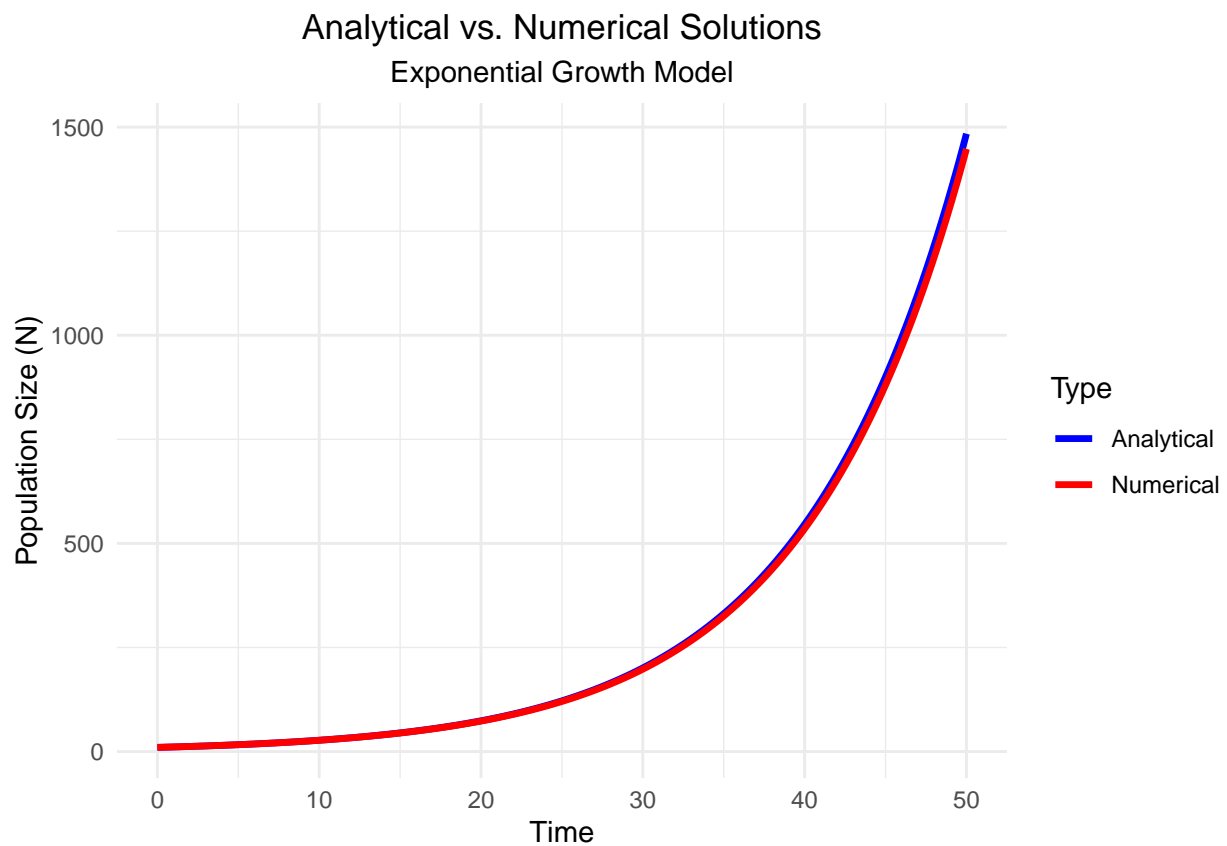

Analytical vs. Numerical Solutions
Exponential Growth Model

Effect of Different Growth Rates

```r
# Simulate multiple growth rates
r_values <- c(0.05, 0.1, 0.15, 0.2, 0.25)
N0 <- 10
t_max <- 30
time <- seq(0, t_max, by = 0.1)

# Create data frame for all growth rates
multi_growth_data <- data.frame()

for (r in r_values) {
  N_vals <- N0 * exp(r * time)
  temp_data <- data.frame(
    Time = time,
    Population = N_vals,
    Growth_Rate = as.factor(r)
  )
  multi_growth_data <- rbind(multi_growth_data, temp_data)
}

# Plot multiple growth rates
ggplot(multi_growth_data, aes(x = Time, y = Population, color = Growth_Rate)) +
  geom_line(size = 1.2) +
  labs(title = "Exponential Growth with Different Growth Rates",
       subtitle = "Effect of r on Population Dynamics",
       x = "Time",
       y = "Population Size (N)",
       color = "Growth Rate (r)") +
  scale_y_log10() +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```
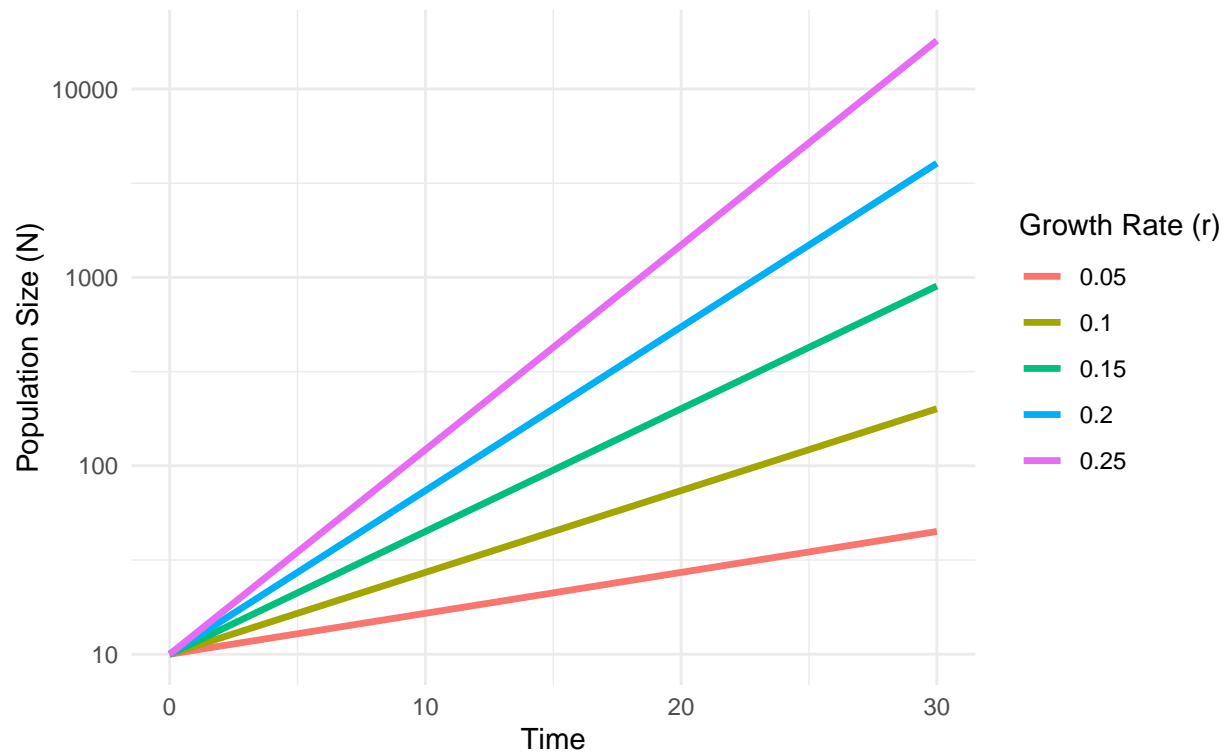
Exponential Growth with Different Growth Rates
Effect of r on Population Dynamics

Semi-log Plot

```r
# Create semi-log plot to show linear relationship
ggplot(growth_data, aes(x = Time, y = Population)) +
  geom_line(color = "blue", size = 1.2) +
  scale_y_log10() +
  labs(title = "Semi-log Plot of Exponential Growth",
       subtitle = "Linear relationship in log scale",
       x = "Time",
       y = "Population Size (N) - Log Scale") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```

Semi−log Plot of Exponential Growth
Linear relationship in log scale

_____
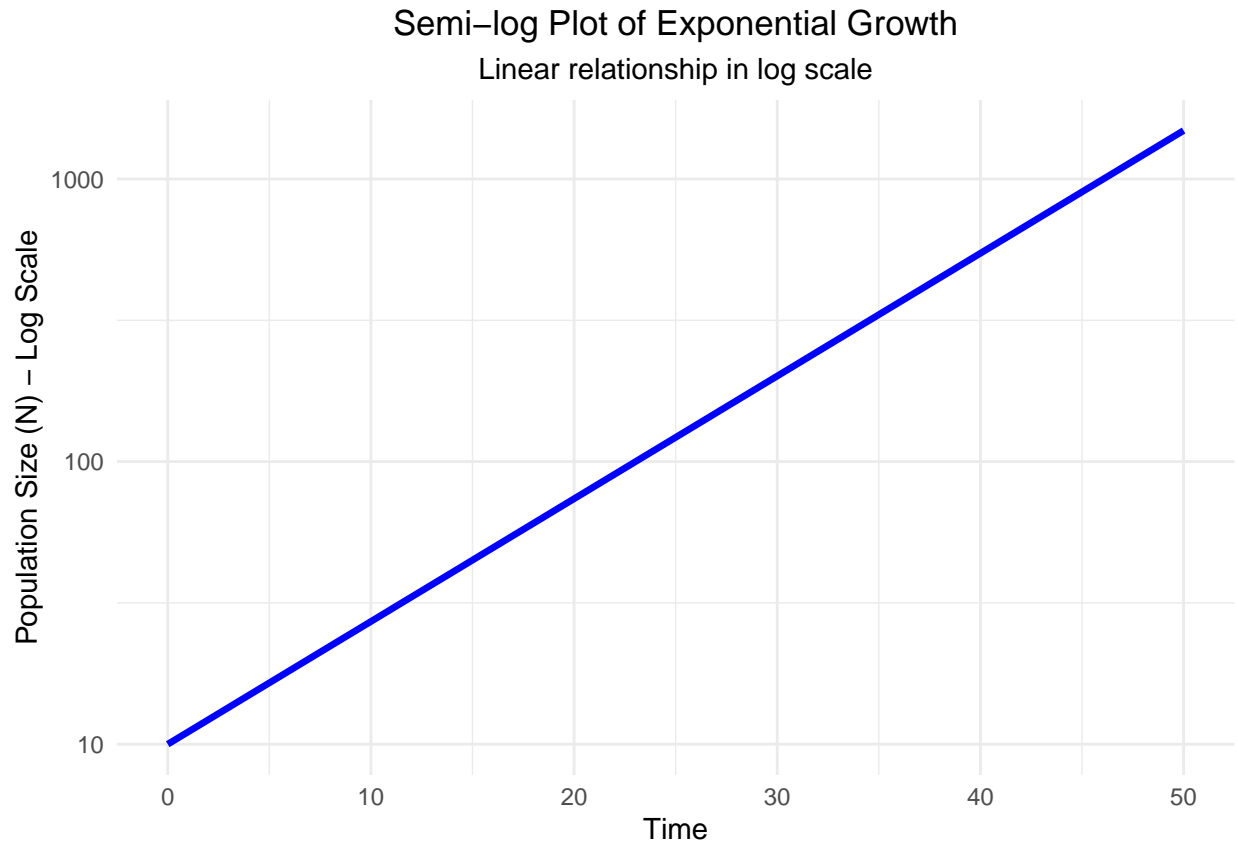
Population Growth with Stochasticity

Environmental Stochasticity

Real populations experience random environmental fluctuations. We can model this by adding random variation to the growth rate:

$$\frac{dN}{dt} = (r + \epsilon_t)N$$

Where ϵ_t is a random variable with mean 0.

```r
# Stochastic growth simulation
stochastic_growth <- function(N0, r, sigma, t_max, dt) {
  time <- seq(0, t_max, by = dt)
  N <- numeric(length(time))
  N[1] <- N0

  for (i in 2:length(time)) {
    epsilon <- rnorm(1, mean = 0, sd = sigma)
    r_effective <- r + epsilon
    dN_dt <- r_effective * N[i-1]
```

```r
    N[i] <- N[i-1] + dN_dt * dt
  }

  return(data.frame(Time = time, Population = N))
}

# Run multiple stochastic simulations
set.seed(123)
n_simulations <- 10
sigma <- 0.05   # Environmental stochasticity

stochastic_data <- data.frame()

for (i in 1:n_simulations) {
  sim_data <- stochastic_growth(N0 = 10, r = 0.1, sigma = sigma, t_max = 30, dt = 0.1)
  sim_data$Simulation <- i
  stochastic_data <- rbind(stochastic_data, sim_data)
}

# Plot stochastic simulations
ggplot(stochastic_data, aes(x = Time, y = Population, group = Simulation)) +
  geom_line(alpha = 0.6, color = "blue") +
  geom_line(data = growth_data[growth_data$Time <= 30, ],
            aes(x = Time, y = Population),
            color = "red", size = 1.5, inherit.aes = FALSE) +
  labs(title = "Stochastic vs. Deterministic Growth",
       subtitle = "Red line: Deterministic, Blue lines: Stochastic",
       x = "Time",
       y = "Population Size (N)") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```
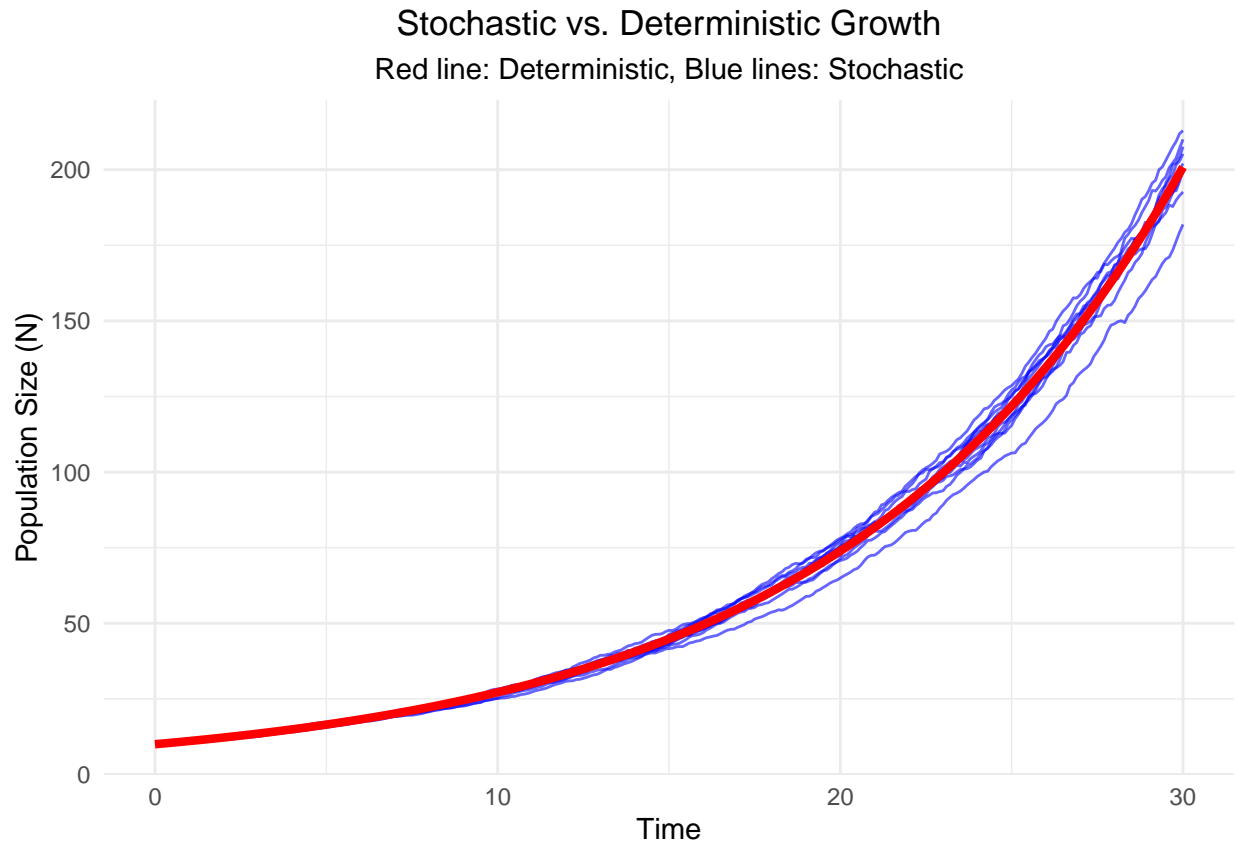
Stochastic vs. Deterministic Growth
Red line: Deterministic, Blue lines: Stochastic

Demographic Stochasticity

For small populations, random births and deaths can significantly affect population dynamics.

```r
# Demographic stochasticity simulation
demographic_growth <- function(N0, r, t_max, dt) {
  time <- seq(0, t_max, by = dt)
  N <- numeric(length(time))
  N[1] <- N0

  for (i in 2:length(time)) {
    lambda <- r * N[i-1] * dt  # Expected number of births/deaths
    if (lambda > 0) {
      change <- rpois(1, lambda)
    } else {
      change <- -rpois(1, abs(lambda))
    }
    N[i] <- max(0, N[i-1] + change)  # Prevent negative populations
  }

  return(data.frame(Time = time, Population = N))
}
```

```
# Run demographic simulations for small populations
set.seed(456)
n_demo_sims <- 5
demo_data <- data.frame()

for (i in 1:n_demo_sims) {
  sim_data <- demographic_growth(N0 = 5, r = 0.1, t_max = 30, dt = 0.1)
  sim_data$Simulation <- i
  demo_data <- rbind(demo_data, sim_data)
}

# Plot demographic stochasticity
ggplot(demo_data, aes(x = Time, y = Population, group = Simulation)) +
  geom_line(alpha = 0.8, size = 1) +
  labs(title = "Demographic Stochasticity in Small Populations",
       subtitle = "N = 5, r = 0.1",
       x = "Time",
       y = "Population Size (N)") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```


Demographic Stochasticity in Small Populations

N0 = 5, r = 0.1
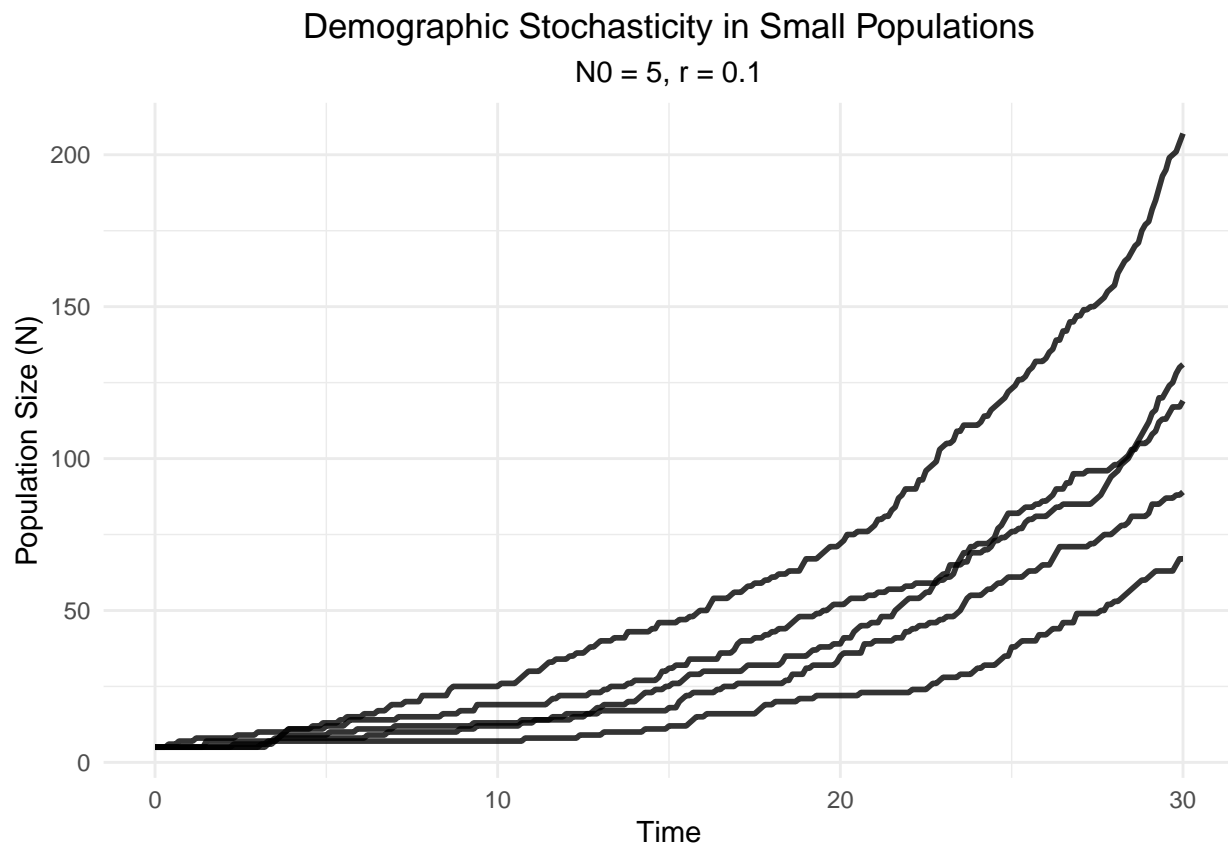
Key Ecological Insights

1. Exponential Growth Characteristics

- **J-shaped curve**: Population size increases at an accelerating rate
- **Constant doubling time**: Time to double remains constant regardless of population size
- **Unrealistic for real populations**: No population can grow exponentially indefinitely

2. Parameter Sensitivity

```r
# Analyze sensitivity to initial conditions
N0_values <- c(5, 10, 20, 50)
r <- 0.1
t_max <- 20
time <- seq(0, t_max, by = 0.1)

sensitivity_data <- data.frame()

for (N0 in N0_values) {
  N_vals <- N0 * exp(r * time)
  temp_data <- data.frame(
    Time = time,
    Population = N_vals,
    Initial_N = as.factor(N0)
  )
  sensitivity_data <- rbind(sensitivity_data, temp_data)
}

# Plot sensitivity analysis
ggplot(sensitivity_data, aes(x = Time, y = Population, color = Initial_N)) +
  geom_line(size = 1.2) +
  labs(title = "Sensitivity to Initial Population Size",
       subtitle = "Same growth rate (r = 0.1), different N ",
       x = "Time",
       y = "Population Size (N)",
       color = "Initial N ") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```

Sensitivity to Initial Population Size
Same growth rate (r = 0.1), different N0
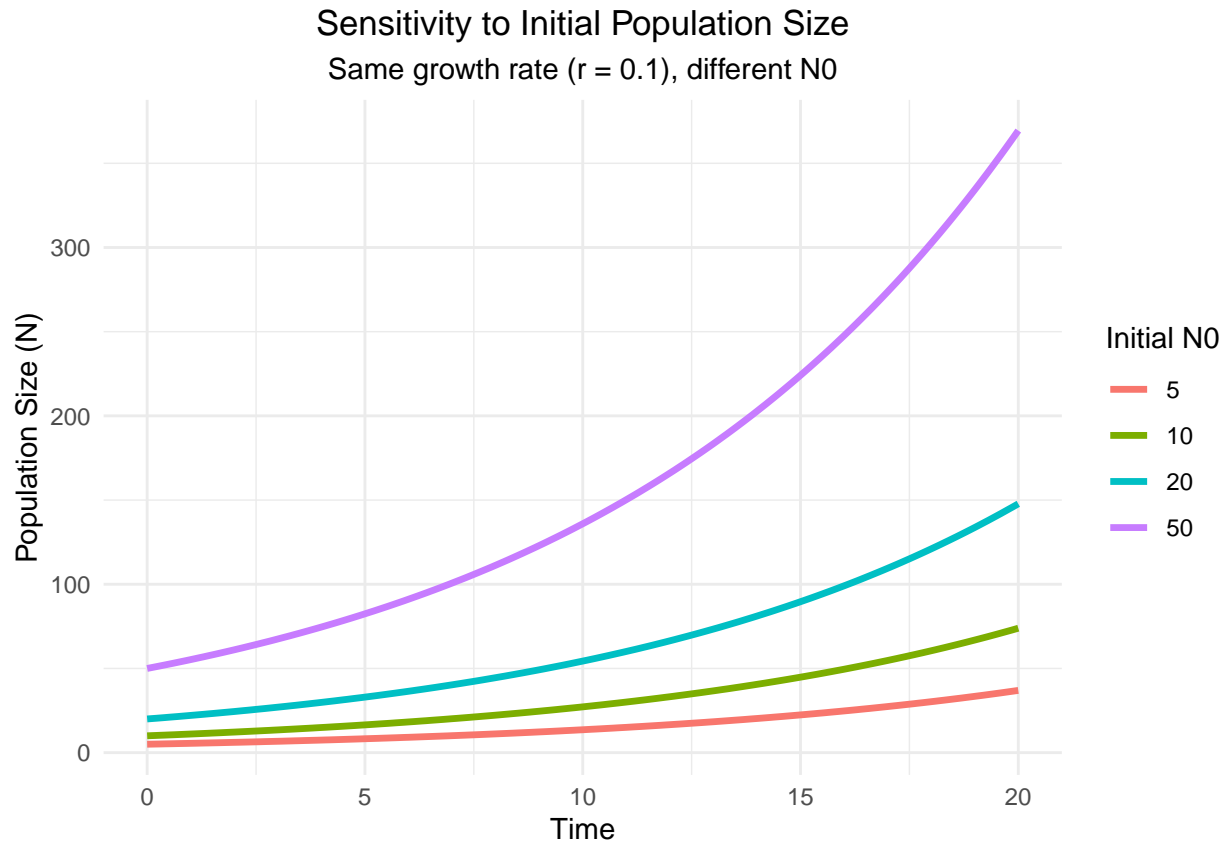
3. Real-World Applications

Exponential growth models are applicable to:

- **Early colonization**: When populations are small and resources are abundant
- **Bacterial growth**: In ideal laboratory conditions
- **Invasive species**: During initial establishment phases
- **Human populations**: Historical growth patterns in some regions

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Mathematical Extensions

Population Projection Matrix

For age-structured populations, we can extend the exponential model:

$$\mathbf{n}_{t+1} = \mathbf{A}\mathbf{n}_t$$

Where $\mathbf{n}_t$ is the population vector and $\mathbf{A}$ is the projection matrix.

```r
# Simple 2-age class example
# A = [0.5  2.0]  # [survival to age 1, fecundity of age 1]
#     [0.8  0.0]  # [survival to age 2, fecundity of age 2]

A <- matrix(c(0.5, 0.8, 2.0, 0.0), nrow = 2, byrow = TRUE)
print("Projection Matrix A:")
```

```
## [1] "Projection Matrix A:"
```

```r
print(A)
```

```
##      [,1] [,2]
## [1,]  0.5  0.8
## [2,]  2.0  0.0
```

```r
# Initial population vector [juveniles, adults]
n0 <- c(10, 5)

# Project population for 20 time steps
time_steps <- 20
population_trajectory <- matrix(0, nrow = 2, ncol = time_steps + 1)
population_trajectory[, 1] <- n0

for (t in 1:time_steps) {
  population_trajectory[, t + 1] <- A %*% population_trajectory[, t]
}

# Convert to data frame for plotting
trajectory_df <- data.frame(
  Time = 0:time_steps,
  Juveniles = population_trajectory[1, ],
  Adults = population_trajectory[2, ],
  Total = population_trajectory[1, ] + population_trajectory[2, ]
)

# Plot age-structured population growth
library(reshape2)
trajectory_long <- melt(trajectory_df, id.vars = "Time", variable.name = "Age_Class")

ggplot(trajectory_long, aes(x = Time, y = value, color = Age_Class)) +
  geom_line(size = 1.2) +
  labs(title = "Age-Structured Population Growth",
       subtitle = "Two-age class model",
       x = "Time",
       y = "Population Size",
       color = "Age Class") +
  theme_minimal() +
  theme(plot.title = element_text(hjust = 0.5),
        plot.subtitle = element_text(hjust = 0.5))
```
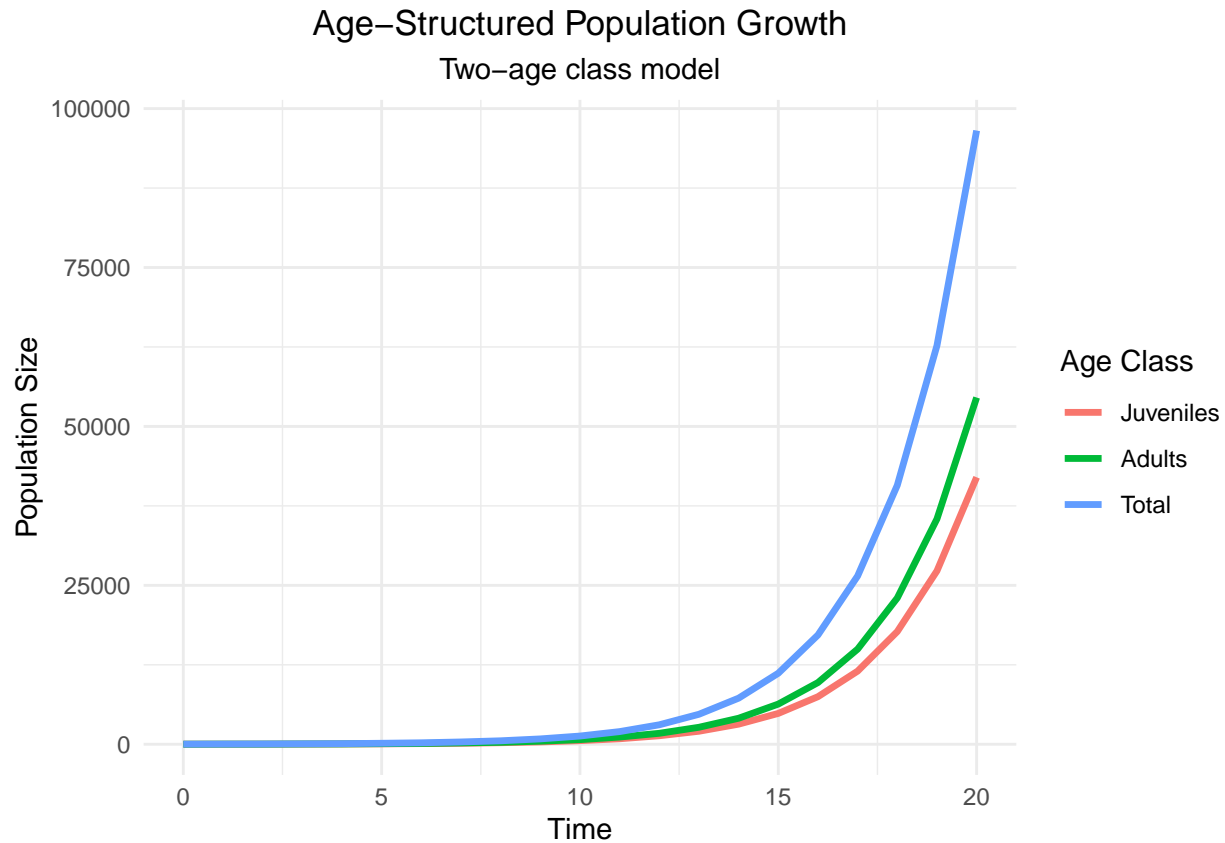
Age−Structured Population Growth
Two−age class model

Summary and Conclusions

The exponential growth model provides the foundation for understanding population dynamics in ecology. Key takeaways include:

1. **Mathematical simplicity**: The model is analytically solvable
2. **Biological realism**: Applicable under specific conditions (low density, abundant resources)
3. **Theoretical importance**: Serves as a null model for more complex population models
4. **Practical limitations**: Real populations cannot grow exponentially indefinitely

Next Steps

This exponential growth model sets the stage for more realistic models including:

- **Logistic growth**: Incorporating carrying capacity
- **Metapopulation dynamics**: Spatial structure
- **Predator-prey interactions**: Species interactions
- **Stochastic models**: Environmental variation

Understanding exponential growth is crucial for comprehending these more complex ecological phenomena.

This tutorial is based on Chapter 1 of Gotelli's "A Primer of Ecology" and provides both theoretical foundations and practical R implementations for understanding exponential population growth.