

# A Stochastic Model of Earthworm Population Evolution

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## Abstract

Earthworms play a critical role in soil ecosystems, contributing to nutrient cycling, soil structure, and carbon sequestration. Understanding their population dynamics under environmental and evolutionary pressures is crucial for ecological modeling and conservation. This paper implements a stochastic birth-death model, incorporating mutation and preferential attachment mechanisms, to study earthworm population evolution. Our findings reveal the interplay between mutation-driven variability and fitness-based reproduction, shedding light on population resilience and adaptation.

## Introduction

Earthworms, often referred to as “ecosystem engineers,” are essential for maintaining soil health and fertility. They influence critical processes such as nutrient cycling, organic matter decomposition, soil aeration, and carbon sequestration, making their population dynamics pivotal for both natural and agricultural ecosystems (Edwards & Bohlen, 1996; Lavelle & Spain, 2001). Despite their ecological importance, earthworm populations are under constant threat from environmental changes, pollution, and habitat loss. These stressors necessitate the development of robust, predictive models that can capture the complexity of earthworm population dynamics.

## Importance of Modeling Earthworm Populations

The ecological roles of earthworms are intricately tied to their population dynamics. Variability in population traits, such as reproduction rate and stress resistance, determines the resilience of earthworm communities to environmental perturbations. By modeling these dynamics, we can: - Assess the impact of environmental changes on soil health. - Predict population trends under various ecological scenarios. - Inform conservation strategies and sustainable agricultural practices.

Mathematically, earthworm populations can be represented as systems of interacting agents with fitness values  $F_i$  that evolve over time. Fitness encapsulates traits such as reproduction efficiency, survival under stress, and resource utilization. The evolution of fitness is driven by stochastic processes of birth, mutation, and death.

## Mathematical Framework

The population dynamics of earthworms are modeled using a stochastic birth-death process with preferential attachment:

1. **Mutation Dynamics:** Mutations introduce genetic variability, represented as:

$$F_i = F_0 + \Delta F,$$

where  $F_0$  is the baseline fitness, and  $\Delta F$  is the fitness increment drawn from a probability distribution  $P(\Delta F)$ . This accounts for random variations in genetic and phenotypic traits.

2. **Birth Events:** New individuals are introduced into the population with probability  $p$ . If a mutation occurs (with probability  $r$ ), the new individual has a fitness value  $F_{\text{mut}}$  sampled from a uniform distribution  $[0, 1]$ :

$$F_{\text{mut}} \sim U(0, 1).$$

Otherwise, the fitness is assigned via preferential attachment, where the probability of selecting a fitness level  $F_j$  is proportional to its population size  $N_j$ :

$$P(F_j) = \frac{N_j}{\sum_k N_k}.$$

3. **Death Events:** Individuals die with probability  $1 - p$ , with removal targeting the least fit group to simulate natural selection:

$$\text{Remove individual from } \arg \min_j (F_j).$$

## Evolutionary Implications

The interplay of mutation and preferential attachment shapes the fitness landscape of the population. High mutation rates promote diversity, enabling populations to explore a broader range of traits, while preferential attachment stabilizes the population by favoring individuals with higher fitness. The balance between these processes determines the adaptability and resilience of earthworm populations.

## Related Work

This model draws inspiration from established evolutionary frameworks: - **Bak and Sneppen (1993):** Explored self-organized criticality in evolutionary dynamics, providing a basis for stochastic modeling. - **Ben-Ari and Schinazi (2016):** Developed stochastic models for populations with high mutation rates, highlighting phase transitions between survival and extinction. - **Guiol, Machado, and Schinazi (2010):** Investigated spatial ecological models with mutation and selection, emphasizing the role of stochastic processes.

## Objectives of the Study

This work aims to: - Develop a comprehensive stochastic model tailored to earthworm populations. - Quantify the effects of mutation and selection on population dynamics. - Provide insights into population resilience under environmental stressors. - Inform conservation strategies by linking theoretical models with ecological data.

## Key Equations

The core dynamics of the model are encapsulated by the following equations: 1. Mutation-driven fitness updates:

$$F_{i,t+1} = F_{i,t} + \Delta F_t,$$

where  $\Delta F_t$  is a stochastic term capturing genetic changes.

2. Population update through birth and death processes:

$$N_{j,t+1} = \begin{cases} N_{j,t} + 1 & \text{(birth at fitness level } F_j), \\ N_{j,t} - 1 & \text{(death at fitness level } F_j). \end{cases}$$

3. Preferential attachment probability:

$$P(F_j) = \frac{N_j}{\sum_k N_k}.$$

By integrating these components, the model provides a robust framework for simulating earthworm population dynamics under various ecological scenarios.

# The Model

## Parameters

Define initial population and key parameters.

```
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

library(tidyr)

set.seed(123)
p <- 0.7 # Birth probability
r <- 0.3 # Mutation probability
n_steps <- 200 # Number of simulation steps
initial_population <- data.frame(fitness = c(0.2, 0.5, 0.8), size = c(10, 15, 8))
```

## Simulation Framework

### Rules of the Model

#### 1. Birth Events:

- With probability  $p$ , an individual is born.
- If a mutation occurs (with probability  $r$ ), the new individual has a fitness value  $F_{\text{mut}}$  drawn from a uniform distribution:

$$F_{\text{mut}} \sim U(0, 1).$$

- If no mutation occurs ( $1 - r$ ), the fitness value is assigned via preferential attachment:

$$P(F_j) = \frac{N_j}{\sum_k N_k},$$

where  $N_j$  represents the population size at fitness level  $F_j$ , and the denominator ensures normalization.

#### 2. Death Events:

- With probability  $1 - p$ , a death event occurs.
- The individual removed is chosen from the least fit group, simulating natural selection:

$$\text{Remove individual from } \arg \min_j (F_j).$$

#### 3. Time Evolution:

- At each time step, the model evaluates whether a birth or death event occurs and updates the population accordingly.

## Implementation

```

simulate_population <- function(initial_population, n_steps, p, r) {
  population <- initial_population
  results <- list()

  for (t in 1:n_steps) {
    if (runif(1) < p) {
      # Birth event
      if (runif(1) < r) {
        # Mutation: New fitness value
        new_fitness <- runif(1)
        population <- population %>% add_row(fitness = new_fitness, size = 1)
      } else {
        # Preferential attachment
        total_size <- sum(population$size)
        probabilities <- population$size / total_size
        chosen <- sample(seq_len(nrow(population)), size = 1, prob = probabilities)
        population$size[chosen] <- population$size[chosen] + 1
      }
    } else {
      # Death event
      least_fit <- which.min(population$fitness)
      if (population$size[least_fit] > 1) {
        population$size[least_fit] <- population$size[least_fit] - 1
      } else {
        population <- population[-least_fit, ]
      }
    }
    results[[t]] <- population
  }
  results
}

```