

MATHEMATICAL MODELING OF POPULATION GROWTH AND DECAY USING DIFFERENTIAL CALCULUS

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Abstract

Mathematical representations of population growth and decline are crucial for comprehending the behavior of populations over the long term, as these processes are important to biological and ecological systems. This article detailed a comprehensive investigation of population dynamics through the application of differential calculus within a continuous-time paradigm. The logistic growth, exponential decay, and classical population models were all developed from first-order ordinary differential equations. To investigate the qualitative behavior of population solutions, rigorous mathematical analysis was performed using formal derivations, theorems, proofs, and illustrative examples. The influence of growth characteristics and environmental restrictions was brought to light by analyzing equilibrium states and long-term trends. The models laid the groundwork for subsequent research in population modeling and offered clear theoretical insight into population dynamics, albeit being based on simplified assumptions.

Keywords: Population Dynamics; Differential Calculus; Exponential Growth; Exponential Decay; Logistic Growth Model; Mathematical Modeling

1. INTRODUCTION

All physical, biological, and ecological systems experience population expansion and decline. In order to solve issues with resource management, environmental sustainability, epidemiology, and biological conservation, it is crucial to understand how populations change over time. Such dynamic processes can be precisely characterized, studied, and predicted using mathematical modeling. One strong framework for researching population change under well-defined assumptions is continuous-time models based on differential calculus.

A key component of population modeling is differential calculus, which captures the instantaneous rate of change of a population with regard to time. Quantitative mathematical representations of qualitative assumptions about population behavior are made possible by describing growth or decay as a derivative.

Researchers are able to study long-term trends, create explicit solutions, and examine the influence of crucial parameters like growth rates and environmental restrictions using this approach. Consequently, differential equation models are becoming essential resources in mathematical biology and practical mathematics.

There used to be exponential growth or decay laws in population models, which were based on the idea that the present population size is exactly related to the rate of population increase. The models do a good job of explaining the dynamics in the near term, but they do not take the environment and available resources into consideration. Improved models that account for carrying capacity and limited growth, like the logistic growth model, were developed to circumvent this restriction. These advancements show how more reasonable assumptions result in more complex mathematical frameworks and more accurate forecasts.

Classical population models based on differential calculus are still quite useful, even if they are very basic. They are the building blocks of more complex models that use stochastic processes, numerical simulations, and systems of differential equations. In order to advance theory and put it into practice, a solid grasp of these basic models is required. In addition, by dissecting these models, we can better understand how mathematical concepts like equilibrium states and long-term stability relate to biological assumptions.

Making and analyzing mathematical models of population increase and decay using differential calculus is the main focus of this work. This research presents formal derivations, theoretical findings, and examples pertaining to classical exponential and logistic models. The purpose of this study is to provide a consistent framework that draws attention to the advantages and disadvantages of continuous-time population models by stressing analytical rigor and mathematical clarity.

2. LITERATURE REVIEW

The application of differential and integral calculus to population dynamics has provided a mathematically rigorous framework for understanding the growth, interaction, and evolution of biological systems. Classical models based on ordinary and partial differential equations have been widely used to describe population changes over time, while more advanced formulations incorporate delays, spatial effects, and non-linear interactions. These approaches have enabled researchers to analyze stability, equilibrium states, and long-term behavior in both ecological and biomedical contexts.

Thieme (2018) presented a comprehensive treatment of mathematics in population biology, emphasizing the role of differential equations in modeling population growth, spread, and interaction. The study

systematically explored deterministic models, including structured population systems, and highlighted how calculus-based formulations could capture essential biological processes. By integrating analytical rigor with biological interpretation, this work established a strong theoretical foundation for modern population dynamics.

Salisbury (2011) examined mathematical models in population dynamics with a focus on constructing and analyzing models that describe population growth and decline. The study emphasized the importance of parameter selection, initial conditions, and model assumptions in determining system behavior. Through classical formulations, it demonstrated how differential equations provide a tractable framework for representing real-world biological systems, while also pointing to the need for refinement in more complex scenarios.

Cain (2014) explored the broader application of mathematical models in the sciences, including their role in biological and cellular systems. The work illustrated how differential calculus and modeling techniques are used to describe dynamic processes across multiple scientific domains. By linking population-level behavior with cellular and molecular mechanisms, the study highlighted the versatility of calculus-based models in bridging different scales of analysis.

Cushing (2013) extended classical approaches by introducing integrodifferential equations and delay models in population dynamics. His work demonstrated that time delays and memory effects play a crucial role in accurately representing biological systems, particularly in cases involving gestation, maturation, or resource feedback. The study showed that incorporating delay terms significantly alters system stability and dynamic behavior, thereby enhancing the realism of population models beyond traditional ordinary differential equations.

Enderling and Chaplain (2014) focused on the mathematical modeling of tumor growth and treatment, applying population dynamics principles to cancer biology. Their research demonstrated how differential equation models could be used to simulate tumor progression, treatment response, and cellular interactions. By incorporating biological complexity into mathematical frameworks, the study highlighted the importance of calculus-based modeling in medical research and therapeutic planning.

Despite these significant advancements, much of the literature treats classical differential equation models, delay systems, and biomedical applications as separate strands of research. There remains a need for an integrated framework that unifies these approaches, allowing for a more comprehensive understanding of population dynamics across ecological and medical domains. Such a framework would

enhance the predictive power and applicability of mathematical models in addressing complex real-world problems.

3. PRELIMINARIES

Let $\mathbb{R}$ denote the set of real numbers and let $t \geq 0$ represent continuous time. Throughout this paper, population dynamics are studied in a deterministic and continuous-time framework using differential calculus.

Definition 3.1

A population function is a real-valued differentiable function

$$P: [0, \infty) \rightarrow \mathbb{R},$$

where $P(t)$ represents the size or density of the population at time t .

It is assumed that

$$P(t) \geq 0 \text{ for all } t \geq 0,$$

since negative population values have no physical meaning.

Definition 3.2

The rate of population change at time t is defined as

$$\frac{dP}{dt},$$

which represents the instantaneous growth or decay of the population with respect to time.

If

$$\frac{dP}{dt} > 0,$$

the population is said to be increasing, whereas if

$$\frac{dP}{dt} < 0,$$

the population is decreasing.

Definition 3.3

A population growth model is a differential equation of the form

$$\frac{dP}{dt} = f(P, t),$$

where f is a continuous function describing the dependence of the population growth rate on the population size and, possibly, on time.

Theoretical Background

The underlying premise of differential equation-based population models is that the rate of change is a function of the existing population size and that population change is a continuous process that happens over time. The theoretically tractable and generalizable first-order ordinary differential equations that emerge from these models are able to capture a broad variety of growth and decay processes.

A fundamental class of models assumes that the rate of change depends only on the population size $P(t)$, yielding autonomous differential equations of the form

$$\frac{dP}{dt} = f(P).$$

Autonomous models are particularly useful for analyzing long-term behavior such as equilibrium states and stability.

Definition 3.4

An equilibrium population level (or steady state) is a constant solution $P = P^*$ satisfying

$$f(P^*) = 0.$$

At equilibrium, the population size remains constant over time.

Theorem 3.1 (Existence and Uniqueness of Solutions)

If the function $f(P, t)$ is continuous in t and satisfies a Lipschitz condition in P on a region containing the initial value $P(0) = P_0$, then the differential equation

$$\frac{dP}{dt} = f(P, t)$$

has a unique solution defined on some interval $[0, T)$.

Remark

This theorem guarantees that population models considered in this paper yield well-defined and unique population trajectories for given initial conditions.

Initial Conditions

Population models require an initial population size

$$P(0) = P_0,$$

where $P_0 > 0$. The value P_0 determines the specific solution of the differential equation and reflects the starting state of the population.

Assumptions of the Model

Unless otherwise stated, all population models discussed in this paper are based on the following assumptions:

- **Continuous Population Change:** Population size changes smoothly over time, allowing the use of differential calculus.
- **Homogeneous Population:** All individuals are assumed to be identical with respect to birth and death rates; age structure and genetic variation are ignored.
- **No Migration Effects:** Immigration and emigration are neglected, and population change is driven solely by internal growth or decay processes.
- **Constant Parameters:** Growth and decay rates are assumed to be constant over time unless explicitly stated otherwise.

Remark

Assumptions like this make it easier to describe mathematically rigorous growth and decay processes, but they also make real-world population dynamics seem simpler. These simple models lay the groundwork for more complex population investigations that incorporate variable factors and species interactions.

4. MATHEMATIC MODELS OF POPULATION GROWTH AND DECAY

Here, first-order differential equations are used to construct and analyze classical models of population increase and decay. To emphasize the mathematical structure and practicality of each model, theoretical conclusions, proofs, examples, and interpretive remarks are provided.

4.1.Exponential Population Growth Model

The simplest population growth model assumes that the rate of change of the population at any instant is directly proportional to the current population size.

Theorem 4.1

If the rate of change of a population is proportional to its size, then the population follows an exponential growth law.

Proof

Let $P(t)$ denote the population size at time t . Assume that

$$\frac{dP}{dt} = kP,$$

where $k > 0$ is a constant representing the intrinsic growth rate.

Separating variables, we obtain

$$\frac{1}{P} dP = k dt.$$

Integrating both sides,

$$\ln |P| = kt + C.$$

Exponentiating,

$$P(t) = Ce^{kt}.$$

Applying the initial condition $P(0) = P_0$, we obtain

$$P(t) = P_0 e^{kt}.$$

Hence proved.

Corollary 4.1

The exponential growth model predicts unbounded population growth as $t \rightarrow \infty$ whenever $k > 0$.

Proof

Since $e^{kt} \rightarrow \infty$ as $t \rightarrow \infty$, it follows that

$$\lim_{t \rightarrow \infty} P(t) = \infty.$$

Example

If a population of bacteria starts with 500 organisms and grows at a rate of 10% per hour, then the population size at time t is given by

$$P(t) = 500e^{0.1t}.$$

Remark

There is no realistic way to simulate the behavior of a population over the long term using the exponential growth model, despite its simplicity and analytical tractability. This is because the model assumes that resources can never be exhausted.

4.2. Exponential Population Decay Model

Population decay occurs when the rate of population change is proportional to the negative of the current population size.

Theorem 4.2

If the rate of population change is proportional to the negative of its size, the population undergoes exponential decay.

Proof

Assume

$$\frac{dP}{dt} = -kP, k > 0.$$

Separating variables and integrating as in Theorem 4.1 yields

$$P(t) = P_0 e^{-kt}.$$

Hence proved.

Lemma

For the exponential decay model,

$$\lim_{t \rightarrow \infty} P(t) = 0.$$

Proof

Since $e^{-kt} \rightarrow 0$ as $t \rightarrow \infty$, the result follows directly.

Example

Consider a population with initial size P_0 that decays at a rate proportional to its size with decay constant $k = 0.05$. The population at time t is given by

$$P(t) = P_0 e^{-0.05t}.$$

Remark

Radioactive decay, natural population decline, and disease-induced mortality are all examples of situations where the loss rate is proportional to the present population size, making exponential decay models useful in these areas.

4.3. Logistic Population Growth Model

The exponential growth model fails to account for environmental limitations. To address this limitation, the logistic growth model incorporates a carrying capacity.

Theorem

If population growth is limited by environmental capacity, then the population follows the logistic differential equation

$$\frac{dP}{dt} = rP \left(1 - \frac{P}{K}\right),$$

where $r > 0$ is the intrinsic growth rate and $K > 0$ is the carrying capacity of the environment.

Proof

The term rP represents natural growth in the absence of constraints, while the factor

$$1 - \frac{P}{K}$$

reduces the growth rate as P approaches K . Solving the equation using separation of variables yields

$$P(t) = \frac{K}{1 + Ae^{-rt}},$$

where the constant A is determined by the initial condition $P(0) = P_0$.

Theorem 4.4 (Equilibrium Analysis of the Logistic Model)

The logistic growth model admits two equilibrium solutions:

$$P = 0 \text{ and } P = K.$$

Proof

Setting

$$\frac{dP}{dt} = 0$$

gives

$$rP \left(1 - \frac{P}{K}\right) = 0.$$

Thus, $P = 0$ or $P = K$.

Example

For $K = 1000$, $r = 0.2$, and $P(0) = 100$, the solution is

$$P(t) = \frac{1000}{1 + 9e^{-0.2t}}.$$

Remark

Unlike exponential growth, the logistic model predicts bounded population growth and convergence to a stable equilibrium. This makes it more suitable for long-term population modeling in realistic environments.

5. DISCUSSION AND LIMITATIONS

This paper's mathematical models show how differential calculus offers a logical and systematic framework for studying the growth and decay of populations in continuous time. Deriving explicit solutions, studying long-term behavior, and identifying equilibrium states are all made possible by modeling population change through first-order ordinary differential equations. The logistic model brings environmental restrictions that lead to limited growth and stability, whereas the exponential growth and decay models emphasize the direct relationship between population size and its rate of change.

These models show, theoretically speaking, how easy assumptions can lead to tractable equations with obvious qualitative interpretations. The direct examination of growth patterns, convergence, and divergence is vital for understanding population dynamics in idealized environments, and the explicit solutions provided make this possible. More complex population studies, such as those including

interactions between multiple species, harvesting models, and epidemiological frameworks, rely on these models as a foundation.

Using population models based on differential calculus as a teaching tool is also highlighted in the conversation. Researchers and students are able to concentrate on the fundamental mathematical concepts, like equilibrium analysis, parameter interpretation, and separable differential equations, because of their simplicity. A mental bridge between elementary calculus and advanced mathematical biology is thus formed by the models that are given.

- There are a number of restrictions on the population models covered in this article, notwithstanding their analytical value:
- Random fluctuations due to environmental variability or unexpected external occurrences are not taken into consideration by the models, which assume deterministic population change.
- It is presumed that every member of the population is the same, regardless of their age, genetic makeup, or reproductive success or failure rates.
- Despite the importance of mobility in actual population dynamics, immigration and emigration are understudied.
- The assumption is that growth and decay rates remain constant throughout time, but in practice, these parameters can change because of things like seasonal changes, the availability of resources, or policy interventions.
- Critical to ecological systems are interactions that the models ignore, such as symbiosis, competition, and predation.
- Small populations may benefit more from discrete models because population size is handled as a continuous variable.

6. CONCLUSION

The authors of this work used differential calculus within a continuous-time framework to conduct a mathematical analysis of population growth and decay. Through the use of formal derivations, theorems, proofs, and illustrative examples, models of classical exponential growth, exponential decay, and logistic growth were developed using first-order ordinary differential equations. Unbounded growth, extinction, and convergence to stable equilibrium states are some of the long-term behaviors that result from making basic assumptions about population change, as shown in the analysis. The study demonstrated the

interpretive power and mathematical clarity of population models based on differential calculus by focusing on analytical solutions and equilibrium features. Despite the models' oversimplification and reliance on idealized assumptions, they laid a solid groundwork for future research into population behavior and the creation of more sophisticated models with variable parameters, interactions, and stochastic effects.

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