Mekelle University

College of Natural and Computational Sciences

Department of Mathematics

A Masters thesis on

Mathematical Modeling of Bacteria growth on different types of Milks

A thesis submitted to Mekelle University, Department of Mathematics in partial fulfilment of the requirements for Master of Science Degree in Mathematics

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Declaration

I here by declare that I have authored this thesis titled, '**Mathematical Modeling of Bacteria growth on different types of Milks**' independently. I confirm that:

- This work was done wholly or mainly while in candidature for a research degree at this University.
- Where any part of this thesis has previously been submitted for a degree or any other qualification at this University or any other institution, this has been clearly stated.
- Where I have consulted the published work of others, this is always clearly attributed.
- Where I have quoted from the work of others, the source is always given. With the exception of such quotations, this thesis is entirely my own work.
- I have acknowledged all main sources of help.
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Signed: ____

Date: ____

Dedication

I dedicate this research paper to the Glory of the Almighty God through whose undeserved kindness I have been able to complete this work. It is also dedicated to my family.

Acknowledgements

I would like to express my heartfelt gratitude to all those who supported me during my thesis journey.

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Most of all, I wish to extend my sincerest gratitude to God Almighty for His merciful guidance throughout this endeavor.

Abstract

This thesis explores the mathematical modeling of bacterial growth in various types of milk, including whole, skim, and plant-based alternatives, aiming to understand how different environmental conditions—such as temperature, pH, and nutrient availability—affect bacterial populations in these milk types. The research begins with a thorough review of existing literature on microbial growth patterns in dairy products, underscoring the critical importance of these dynamics for food safety and quality control in the dairy industry. By utilizing differential equations and statistical analysis, we develop mathematical models that accurately reflect the growth kinetics of specific bacterial strains present in milk. These models are parameterized using experimental data collected from controlled laboratory studies, which enhances their reliability. To validate our predictions, we conduct simulations and compare the results with empirical observations, revealing distinct growth behaviors among bacterial populations that vary significantly with the unique compositions of different milk types. For instance, the presence of specific nutrients in plant-based milks may lead to accelerated bacterial proliferation compared to traditional dairy options. These findings not only deepen our understanding of bacterial proliferation in milk but also offer valuable insights for the dairy industry regarding food safety practices, shelf life optimization, and effective quality control measures. In conclusion, this research makes a meaningful contribution to the field of food microbiology by providing a comprehensive mathematical framework for predicting bacterial behavior in dairy products, emphasizing the need for tailored strategies to manage microbial growth effectively, and suggesting promising avenues for future research and practical applications in the dairy sector.

Key words: Bacterial Growth, Mathematical Modeling, Differential Equations, Microbial Growth Patterns, Predictive Modeling.

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Chapter 1

Introduction

1.1 Background of the Study

Milk and dairy products are essential components of the human diet, providing a rich source of nutrients, including proteins, fats, carbohydrates, vitamins, and minerals. However, the microbial growth in milk can pose a significant challenge to the dairy industry, as it can lead to spoilage, reduced shelf-life, and potential food safety issues. Understanding the growth dynamics of bacteria in different types of milk is crucial for developing effective preservation techniques and ensuring the quality and safety of dairy products.

Numerous studies have been conducted to model the growth of bacteria in milk, using various mathematical models, such as the Baranyi model, the Gompertz model, and the logistic growth model. These models aim to describe the growth of bacteria under different environmental conditions, including temperature, pH, and nutrient availability. However, the applicability of these models may vary depending on the specific type of milk and the bacterial strains involved.

Milk is defined as the result of the milking process conducted under hygienic conditions of healthy cows. It is a rich source of essential nutrients, such as proteins, vitamins, and mineral salts, not only for mammals but also for a wide range of microorganisms that can thrive in milk.

Due to its chemical composition, milk provides a favorable environment for the growth of various microorganisms. Milk has a neutral or slightly acidic pH and a high moisture content, which allows a diverse array of microorganisms to proliferate. This microbial growth can lead to changes in the taste and odor of milk, resulting in sour, putrid, bitter, malty, fruity, rancid, or unclean characteristics. During the milking process, microorganisms can enter the milk from the skin of the cow's teats, which may be contaminated by dung, soil, or dust. Proper housing and care of the cows are essential measures to promote clean udders and minimize initial microbial contamination.

The control of processing, packaging, distribution, and storage conditions is crucial for ensuring the safety of pasteurized milk. During these stages, dairy products may become potentially unsafe due to the presence of pathogenic microorganisms. Therefore, the presence of pathogens should be continuously monitored during the transportation of raw milk to the dairy plant. However, the traditional approach of enumerating microbes in different stages of food processing is slow and expensive, making it impractical for perishable foods that are sold or consumed before the results of microbiological tests are available.

An alternative approach is to rely on the hypothesis that some controlling factors of microbial growth, such as temperature, pH, and water activity, can be measured and modeled to predict the extent of microbial growth. These models can be used to predict the microbial safety or shelf-life of products, identify critical points in the production and distribution process, and optimize the production and distribution chains. It is important to consider the duration of the lag and exponential phases of microbial growth, as spoilage is typically observed after these stages.

Predictive microbiology is a branch of food microbiology that has gained prominence over the past two decades, with hundreds of publications featuring the keyword "predictive microbiology" in the last ten years. This field focuses on describing microbial responses to various food environments through mathematical modeling. The most widely used models include the modified logistic model, the modified Gompertz model, and the Baranyi model.

These mathematical models have been extensively applied to characterize the growth and inactivation of numerous microorganisms under different environmental conditions in dairy products. For example, a recent study demonstrated how predictive modeling can help minimize the growth of Bacillus cereus spores in farm tank milk. The combined effects of high hydrostatic pressure and mild heat on the inactivation kinetics of Listeria monocytogenes Scott A in whole milk [3]. Additionally, a study by [4] examined the impact of high hydrostatic pressure on the inactivation of Salmonella typhimurium DT 104 in UHT whole milk.

The study by [5] utilized mathematical functions to model the pressure inactivation of seven foodborne pathogens in ultra-high-temperature (UHT) whole milk. Recently, a review highlighted the interplay between different modeling approaches and the applications of predictive microbiology techniques in controlling dairy product manufacturing throughout the supply chain.

The primary aim of this paper is to propose and evaluate a mathematical model that describes microbial growth in dairy products. To test the model's effectiveness in analyzing experimental data, five distinct datasets of microbial growth in dairy products were selected from ComBase (www.combase.cc), the leading database in this field. The parameters obtained from the model were then used to estimate the duration of the lag and exponential phases for the microorganisms studied.

1.2 Statement of the Problem

While previous studies have focused on modeling bacterial growth in general milk samples, there is a need to investigate the growth dynamics of bacteria in different types of milk, such as raw milk, pasteurized milk, and milk with varying fat content. The growth patterns and kinetic parameters of bacteria may differ significantly among these milk types, which can have important implications for the dairy industry [6].

1.3 Objectives of the Study

1.3.1 General Objective

The general objective of this study is to develop mathematical models that accurately describe the growth of selected bacterial strains in different types of milk.

1.3.2 Specific Objectives

- To determine the growth kinetics of selected bacterial strains (e.g., Escherichia coli, Staphylococcus aureus, Listeria monocytogenes) in raw milk, pasteurized milk, and milk with varying fat content.

- To fit the experimental data using appropriate mathematical models, such as the Baranyi model and the logistic growth model, and evaluate the model parameters.
- To compare the growth patterns and model parameters of the selected bacterial strains in the different milk types.
- To identify the critical factors that influence the growth of bacteria in the various milk samples.
- To develop predictive models that can be used to estimate the shelf-life and safety of dairy products under different storage conditions.

1.4 Significance of the Study

The findings of this study will contribute to the understanding of bacterial growth dynamics in different types of milk, which is essential for the dairy industry. The development of accurate mathematical models will enable the prediction of microbial growth and the optimization of processing and storage conditions to ensure the quality and safety of dairy products. Moreover, the insights gained from this study can aid in the design of more effective preservation techniques and the development of targeted antimicrobial strategies to control the growth of pathogenic and spoilage bacteria in milk and dairy products.

1.5 Organization of the Thesis

This thesis is organized as follows: Chapter 1 is the introduction, Chapter 2 is the review of related literature, Chapter 3 is the methodology, Chapter 4 is the numerical simulation, and Chapter 5 is the results and discussion.

Chapter 2

Literature Review

Bacterial growth in milk is a significant concern for both food safety and quality. Understanding how bacteria behave in different types of milk can lead to better preservation methods and help protect public health. This literature review examines various research studies that have used mathematical models to describe bacterial growth in different milks, emphasizing the biological processes involved, how the models are formulated, and their practical applications.

Typically, bacterial growth is modeled using logistic growth equations, which track how bacterial populations change over time. The logistic model accounts for the environment's carrying capacity, resulting in a characteristic S-shaped growth curve. Many studies have applied this model to various milk types, including whole milk, skim milk, and even plant-based alternatives. The logistic growth model is a cornerstone in microbiology and is widely used to analyze bacterial populations in milk.

Temperature plays a crucial role in bacterial growth rates. Research has shown that the optimal temperature for bacterial growth can differ between species and types of milk. To better predict how bacteria grow under different conditions, mathematical models that factor in temperature variations have been developed. [8].

Mathematical models play a vital role in predicting how bacteria grow in milk. One notable study by [**?**] created a model using a system of two first-order differential equations to describe microbial growth. This model was validated with data from the Combase database and showed a strong fit for various microbial populations found in dairy products. It also offered valuable insights into key factors like the maximum specific growth rate and the duration of the lag phase, which are essential for understanding how microbes behave in milk.

In recent years, predictive microbiology has become increasingly important for modeling bacterial growth in dairy products. Research has demonstrated that models like the modified Gompertz and Baranyi models effectively describe how microorganisms grow under different environmental conditions. For example, studies have shown that these models can accurately predict the growth of harmful pathogens such as Listeria monocytogenes and Bacillus cereus in milk, which is crucial for ensuring food safety.

Many factors influence the growth of bacteria in milk, for example, temperature, pH, and the presence of preservatives. A review highlighted that the growth rates of bacteria vary significantly with the type of milk, such as whole milk versus skim milk. The nutritional composition of milk, particularly its fat content, plays a significant role in supporting bacterial growth. For example, whole milk provides a more favorable environment for bacterial proliferation compared to skim milk [7].

The mathematical modeling of bacterial growth in various types of milk is an exciting and evolving field that brings together microbiology and applied mathematics. Ongoing research is constantly refining these models, which enhances our understanding of microbial dynamics and their implications for food safety. This area of research is critical for addressing food safety, quality control, and predicting shelf life. Understanding how microorganisms grow in milk is essential, as their presence can lead to spoilage and health risks. This literature review delves into different mathematical models used to study bacterial growth in various milk types, highlighting key findings and methodologies [9].

The study of microbial growth in milk has made significant strides, with predictive microbiology becoming increasingly important. These models estimate bacterial growth rates based on factors like temperature, pH, and water activity. Such predictions are vital for maintaining food safety and optimizing processing conditions in the dairy industry. One foundational model in this field is the logistic growth model, which illustrates how populations expand in environments with limited resources. Researchers have adapted this model to reflect the specific growth characteristics of bacteria found in milk, such as Lactobacillus and Staphylococcus aureus. It provides insights into maximum growth rates and environmental carrying capacity, both of which are crucial for predicting spoilage [10].

In addition to traditional models, researchers are exploring more complex methods like neural networks and machine learning to predict bacterial growth. These advanced techniques can analyze large datasets and uncover patterns that simpler models might miss. For instance, machine learning algorithms have been utilized to forecast pathogen growth in milk based on historical data, improving prediction accuracy.

Research has also focused on how different milk types affect bacterial growth. Studies indicate that milk composition—such as fat content and protein levels—significantly influences microbial dynamics. For instance, whole milk and skim milk can show different growth rates for certain bacteria, highlighting the need for tailored modeling approaches for each type.

The presence of preservatives and additives in milk is another area of interest, as they can alter bacterial growth patterns. New mathematical models have been developed to account for these factors, leading to more accurate predictions of microbial behavior in treated milk. This is especially important for extended shelf-life products, where understanding the impact of additives is crucial for safety.

Temperature is a key factor influencing bacterial growth in milk. Models that incorporate temperature variations have been developed to predict growth rates under different storage conditions. For instance, predictive models can assess spoilage risks in milk stored at various temperatures, providing valuable information for dairy producers. Beyond predicting growth rates, mathematical modeling also helps clarify the mechanisms behind bacterial spoilage. By combining kinetic models with biochemical data, researchers can gain insights into the metabolic pathways of bacteria in milk, which can inform strategies for spoilage control [11].

Moreover, integrating mathematical models with experimental data has led to the creation of risk assessment tools for the dairy industry. These tools identify critical control points in milk production and distribution, thereby enhancing food safety protocols.

The application of mathematical modeling in dairy microbiology extends to studying bacterial inactivation as well. Models have been developed to predict how effective pasteurization and other thermal treatments are against various pathogens in milk, ensuring that safety standards are upheld.

In conclusion, mathematical modeling is essential for understanding bacterial growth in different types of milk. By integrating various modeling approaches—ranging from traditional growth models to advanced machine learning techniques—we've improved our ability to predict microbial behavior. As the dairy industry evolves, these models will remain crucial for ensuring food safety and quality.

Chapter 3

Methodology

3.1 Introduction

Understanding how bacteria grow and interact is essential for many fields, including microbiology, food science, and biotechnology. This model seeks to capture the complex relationships between bacterial population density and their physiological state over time, particularly in environments like milk, where conditions can fluctuate widely.

Bacterial growth typically involves phases of rapid increase, followed by a stabilization period as resources start to dwindle. The model includes two key equations: one that tracks changes in bacterial population density $N(t)$, and another that describes the physiological state $Q(t)$ of the bacteria. The first equation shows how growth is influenced by both the physiological state and the environmental carrying capacity. The second equation reflects how the physiological state regulates itself, including factors like natural damping.

By combining these dynamics, the model offers valuable insights into how bacterial populations respond to changes in their environment, the effects of their physiological health, and the various factors that influence growth rates. This understanding is crucial for developing effective food preservation techniques, improving fermentation processes, and managing microbial ecosystems. With this modeling approach, we can better predict bacterial behavior, optimize conditions for growth, and enhance applications in areas where microbial activity is vital.

3.2 Methodology

- Sample collection and preparation:
    - Obtain samples of raw milk, pasteurized milk, and milk with varying fat content from local dairy producers.
    - Prepare the milk samples according to standard procedures, ensuring sterility and consistent initial conditions.
- Bacterial inoculation and growth monitoring:
    - Inoculate the milk samples with selected bacterial strains (e.g., *E. coli*, *S. aureus*, *L. monocytogenes*).
    - Monitor the growth of the bacteria in the milk samples over time, using appropriate microbiological techniques (e.g., plate counting, optical density measurements).
- Data analysis and mathematical modeling:
    - Fit the experimental data to appropriate mathematical models, such as the Baranyi model and the logistic growth model.
    - Determine the model parameters (e.g., maximum growth rate, lag time, carrying capacity) for each milk type and bacterial strain.
    - Analyze the differences in growth patterns and model parameters among the milk types and bacterial strains.
- Model validation and predictive modeling:
    - Validate the developed models using independent experimental data.
    - Develop predictive models that can be used to estimate the shelf-life and safety of dairy products under different storage conditions.

3.3 Description of the Mathematical Model

A number of mathematical functions have been proposed which describe sigmoid curves and have been used to model the growth of microbial curves. In this study, a system composed by two differential equations was employed. The first differential equation consists of the most elementary model building block describing microbial evolution [12]. This model describes the dynamics of bacterial growth and physiological state over time, incorporating both growth and damping effects.

3.3.1 Bacterial Growth Equation

The first equation models the change in bacterial population density N over time:

$$\frac{dN}{dt} = \mu_{\max}(\text{milk}) \cdot \frac{Q(t)}{Q(t)+1} \left(1 - \frac{N}{N_{\max}}\right) N - dN$$

where:

- N: Bacterial population density (e.g., CFU/mL).
- $\mu_{\max}(\text{milk})$: Maximum specific growth rate, which is dependent on the environment (in this case, milk).
- $Q(t)$: Physiological state of the bacteria at time t.
- $N_{\max}$: Maximum carrying capacity of the environment.
- The term $\frac{Q(t)}{Q(t)+1}$ represents the effect of the physiological state on growth, indicating that growth increases with $Q(t)$ but levels off as $Q(t)$ becomes large.
- The factor $\left(1 - \frac{N}{N_{\max}}\right)$ accounts for resource limitations, reducing growth as the population approaches the maximum carrying capacity.
- The term $-dN$ represents a decay or loss of the population, which could be due to natural death, predation, or other environmental factors.

3.3.2 Physiological State Dynamics

The second equation describes the change in the physiological state $Q(t)$:

$$\frac{dQ(t)}{dt} = \mu_{\max}(\text{milk}) \cdot Q(t) \left(1 - \frac{Q(t)}{Q_{\max}}\right) \left(1 - \frac{Q(t)}{k}\right) - hQ(t)$$

where:

- $Q(t)$: Physiological state of the bacteria, which may represent metabolic activity or health status.
- Q_{max}: Maximum physiological state.
- k: A threshold value indicating when the growth rate may begin to decline due to saturation effects.
- h: Damping coefficient, representing the rate of decline of the physiological state over time.
- The term $\mu_{\text{max}}(\text{milk}) \cdot Q(t)$ indicates that the physiological state contributes positively to its own growth, but is regulated by the factors $\left(1 - \frac{Q(t)}{Q_{\text{max}}}\right)$ and $\left(1 - \frac{Q(t)}{k}\right)$. These terms account for the saturation effect as $Q(t)$ approaches its maximum values, reducing the growth rate as resources become limited.
- The $-hQ(t)$ term introduces a damping effect, meaning that as the physiological state increases, it will also experience a reduction over time, representing a natural decline or resource depletion.

The Bacterial Growth model in different milk types can be summarized in equation 3.3.2 below:

$$\begin{cases} \frac{dN}{dt} = \mu_{\text{max}}(\text{milk}) \cdot \frac{Q(t)}{Q(t)+1} \left(1 - \frac{N}{N_{\text{max}}}\right) N - dN \\ \frac{dQ(t)}{dt} = \mu_{\text{max}}(\text{milk}) \cdot Q(t) \left(1 - \frac{Q(t)}{Q_{\text{max}}}\right) \left(1 - \frac{Q(t)}{k}\right) - hQ(t) \\ N(0) \geq 0, Q(0) \geq 0 \end{cases} \tag{3.1}$$

with $N(t)$ [CFU/mL] the number of cells at time t, $Q(t)$ a measure of the physiological state of the cells, μ_{max} the maximum specific growth rate [1/h], and N_{max} [CFU/mL] the maximum cell density.

For the effect of temperature on microbial growth, either the cardinal model (CTMI) proposed by Rosso et al. (1993), or square root type models (Ratkowsky et al., 1982) were used. The CTMI model is expressed as:

$$\mu_{\text{max}} = \begin{cases} 0, & T \leq T_{\text{min}} \\ \mu_{\text{opt}} \frac{(T-T_{\text{min}})^2}{(T-T_{\text{max}})(T_{\text{opt}}-T_{\text{min}})} \left((T_{\text{opt}} - T_{\text{min}})(T - T_{\text{opt}}) - (T_{\text{opt}} - T_{\text{max}})(T_{\text{min}} + T_{\text{opt}} - 2T)\right), & T_{\text{min}} < T < \\ 0, & T \geq T_{\text{max}} \end{cases}$$

where T_{min} [°C], T_{opt} [°C], and T_{max} [°C] are the minimum, optimum, and maximum temperatures for growth, respectively, and μ_{opt} [1/h] is the maximum specific growth rate at T_{opt}.

The square root type model can be expressed as:

$$\sqrt{\mu_{\text{max}}} = b(T - T_{\text{min}})$$

with b a constant and T_{min} the theoretical minimum temperature for growth, being the intercept between the model and the temperature axis.

3.4 Equilibrium Points

To find the non-trivial equilibrium points for the system 3.3.2, we have to solve the equations $\frac{dN}{dt} = 0$ and $\frac{dQ}{dt} = 0$. We need to solve the two conditions for equilibrium:

$$\mu_{\text{max}}(\text{milk}) \cdot \frac{Q^*}{Q^*+1}\left(1 - \frac{N^*}{N_{\text{max}}}\right) = d$$

$$\mu_{\text{max}}(\text{milk})\left(1 - \frac{Q^*}{Q_{\text{max}}}\right)\left(1 - \frac{Q^*}{k}\right) = h$$

From the first equation, we have

$$\mu_{\text{max}}(\text{milk}) \cdot \frac{Q^*}{Q^*+1}\left(1 - \frac{N^*}{N_{\text{max}}}\right) = d$$

Rearranging gives:

$$\frac{Q^*}{Q^*+1}\left(1 - \frac{N^*}{N_{\text{max}}}\right) = \frac{d}{\mu_{\text{max}}(\text{milk})}$$

Let:

$$C = \frac{d}{\mu_{\text{max}}(\text{milk})}$$

Thus, we have:

$$\frac{Q^*}{Q^*+1}\left(1 - \frac{N^*}{N_{\text{max}}}\right) = C$$

This leads to:

$$1 - \frac{N^*}{N_{\text{max}}} = C\left(1 + \frac{1}{Q^*}\right)$$

Simplifying:

$$\frac{N^*}{N_{\text{max}}} = 1 - C\left(1 + \frac{1}{Q^*}\right)$$

$$N^* = N_{\text{max}} \left(1 - C\left(1 + \frac{1}{Q^*}\right)\right)$$

To solve Q^*, we will use the second equation:

$$\mu_{\text{max}}(\text{milk}) \left(1 - \frac{Q^*}{Q_{\text{max}}}\right)\left(1 - \frac{Q^*}{k}\right) = h$$

Dividing by $\mu_{\text{max}}(\text{milk})$:

$$\left(1 - \frac{Q^*}{Q_{\text{max}}}\right)\left(1 - \frac{Q^*}{k}\right) = \frac{h}{\mu_{\text{max}}(\text{milk})}$$

Let:

$$D = \frac{h}{\mu_{\text{max}}(\text{milk})}$$

This expands into:

$$1 - \frac{Q^*}{Q_{\text{max}}} - \frac{Q^*}{k} + \frac{(Q^*)^2}{kQ_{\text{max}}} = D$$

Rearranging gives a quadratic equation in Q^*:

$$\frac{(Q^*)^2}{kQ_{\text{max}}} - \left(\frac{1}{Q_{\text{max}}} + \frac{1}{k}\right) Q^* + (1 - D) = 0$$

Using the quadratic formula, we have

$$Q^* = \frac{\left(\frac{1}{Q_{\text{max}}} + \frac{1}{k}\right) \pm \sqrt{\left(\frac{1}{Q_{\text{max}}} + \frac{1}{k}\right)^2 - 4 \cdot \frac{1}{kQ_{\text{max}}} \cdot (1 - D)}}{2 \cdot \frac{1}{kQ_{\text{max}}}}$$

This is the value for Q^*. We can substitute this result back into the equation for N^*.

Therefore, equilibrium points of the model are $(0, 0)$ and (N^*, Q^*) where N^* and Q^* satisfy the derived equations:

$$N^* = N_{\text{max}} \left(1 - C\left(1 + \frac{1}{Q^*}\right)\right)$$

where $C = \frac{d}{\mu_{\text{max}}(\text{milk})}$, and Q^* is obtained from the quadratic equation.

3.4.1 Local Stability Analysis of Equilibrium Points

To determine local stability analysis of each equilibrium point, we will use the concept of Jacobian Matrix (a matrix of partial derivatives) given by:

$$J = \begin{bmatrix} \frac{\partial f}{\partial N} & \frac{\partial f}{\partial Q} \\ \\ \frac{\partial g}{\partial N} & \frac{\partial g}{\partial Q} \end{bmatrix}$$

where:

- $f(N, Q)$ is the function for bacterial growth.
- $g(N, Q)$ is the function for the physiological state.

For $f(N, Q)$:

$$\frac{\partial f}{\partial N} = \mu_{\text{max}}(\text{milk}) \cdot \frac{Q}{Q+1}\left(1 - \frac{2N}{N_{\text{max}}}\right) - d$$

$$\frac{\partial f}{\partial Q} = \mu_{\text{max}}(\text{milk}) \cdot \frac{N}{(Q+1)N_{\text{max}}}$$

For $g(N, Q)$:

$$\frac{\partial g}{\partial N} = 0$$

$$\frac{\partial g}{\partial Q} = \mu_{\text{max}}(\text{milk})\left(1 - \frac{2Q}{Q_{\text{max}}} - \frac{Q}{k}\right) - h$$

3.4.2 Global Stability of Equilibrium Points

Definition 3.1 (Global Stability) A point (N^*, Q^*) is considered globally stable if every trajectory of the system, regardless of its initial conditions, converges to this equilibrium point as time approaches infinity. In mathematical terms, we can say that:

$$\lim_{t\to\infty}(N(t), Q(t)) = (N^*, Q^*)$$

Conditions for Global Stability Lyapunov's Direct Method: One common approach to assess global stability is through Lyapunov functions. A Lyapunov function $V(N, Q)$ is a scalar function that satisfies:

- $V(N, Q) > 0$ for all $(N, Q) \neq (N^*, Q^*)$
- $V(N, Q) = 0$ at (N^*, Q^*)

The time derivative of V along the trajectories of the system, $\dot{V}$, is negative definite (i.e., $\dot{V} < 0$) in a neighborhood around (N^*, Q^*). If such a function exists, it can be concluded that the equilibrium point is globally asymptotically stable.

The Lyapunov function can be defined as:

$$V(N, Q) = \frac{1}{2}\left((N - N^*)^2 + (Q - Q^*)^2\right)$$

The time derivative of V along the trajectories of the system is given by:

$$\dot{V} = \frac{\partial V}{\partial N}\frac{dN}{dt} + \frac{\partial V}{\partial Q}\frac{dQ}{dt}$$

Calculating the partial derivatives: For N:

$$\frac{\partial V}{\partial N} = N - N^*$$

For Q:

$$\frac{\partial V}{\partial Q} = Q - Q^*$$

Now substituting $\frac{dN}{dt} = f(N, Q)$ and $\frac{dQ}{dt} = g(N, Q)$:

$$\dot{V} = (N - N^*)f(N, Q) + (Q - Q^*)g(N, Q)$$

Substituting the defined functions:

$$\dot{V} = (N-N^*)\left(\mu_{\text{max}}(\text{milk}) \cdot \frac{Q+1}{Q}\left(1 - \frac{N}{N_{\text{max}}}\right)N - dN\right) + (Q-Q^*)\Bigg(\mu_{\text{max}}(\text{milk}) \cdot Q\left(1 - \frac{Q}{Q_{\text{max}}}\right)(1 - k$$

To show that $\dot{V} < 0$ in the neighborhood of the equilibrium point (N^*, Q^*), we need to consider the behavior of the terms involved:

At the Equilibrium Point: At (N^*, Q^*), we assume:

$$f(N^*, Q^*) = 0 \text{ and } g(N^*, Q^*) = 0$$

Behavior Near the Equilibrium: If $N > N^*$, $f(N, Q)$ will typically be negative due to the term $\left(1 - \frac{N}{N_{\text{max}}}\right)$ becoming negative, causing $\dot{V}$ to decrease.

If $N < N^*$, $f(N, Q)$ will be positive, contributing to an increase in N back to N^*.

For Q: If $Q > Q^*$, $g(N, Q)$ will also tend to be negative, especially due to the $\left(1 - \frac{Q}{Q_{\text{max}}}\right)$ term.

If $Q < Q^*$, $g(N, Q)$ will be positive, driving Q back to Q^*.

Conclusion: Given the structure of $f(N, Q)$ and $g(N, Q)$, we can conclude that: For (N, Q) near (N^*, Q^*), the Lyapunov function derivative $\dot{V}$ will be negative:

$$\dot{V} < 0 \text{ in a neighborhood around } (N^*, Q^*)$$

Thus, the equilibrium point (N^*, Q^*) is locally asymptotically stable. If you can also show that the basin of attraction includes all possible initial conditions, then you would conclude that (N^*, Q^*) is globally stable.

Chapter 4

Results and Discussion

In this section, the numerical analysis of the bacterial growth model was explored. Besides, a series of numerical simulations was conducted to better realize the dynamics of bacterial populations in different types of milk. For this purpose, we used MATLAB's ode45 function, which is particularly effective for solving ordinary differential equations. The parameter values utilized in the model are as the following table 4.1:

Parameter	**Symbol**	**Value**
Maximum Growth Rate	$\mu_{\max}$	1.0 h^{-1}
Carrying Capacity	$N_{\max}$	10^6 cells/mL
Maximum Physiological State	$Q_{\max}$	1.0
Threshold Value	k	0.7
Damping Coefficient	h	0.05 h^{-1}

TABLE 4.1: Parameters and Values

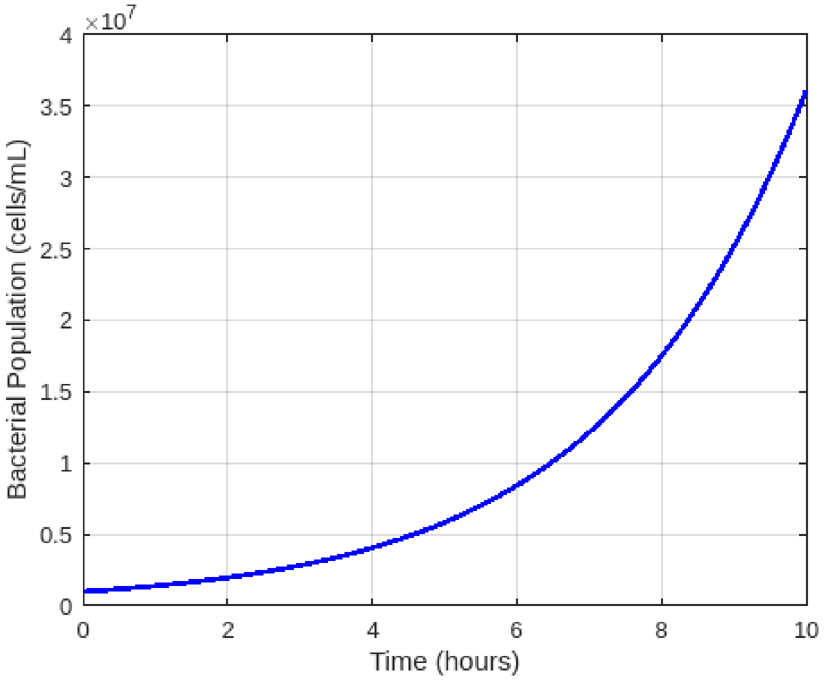

FIGURE 4.1: Bacterial growth over time

Figure 4.1 illustrates a clear upward trend in bacterial population over time. Starting with an initial population of approximately (around 5×10^6 cells/mL) the numbers rise to around 3.5×10^7 cells/mL by the end of the observation period. Initially, the growth appears exponential, but as it approaches the carrying capacity, the rate of increase begins to level off. This behavior reflects the classic logistic growth pattern commonly seen in microbial populations: growth starts off rapidly but slows down as resources become scarce.

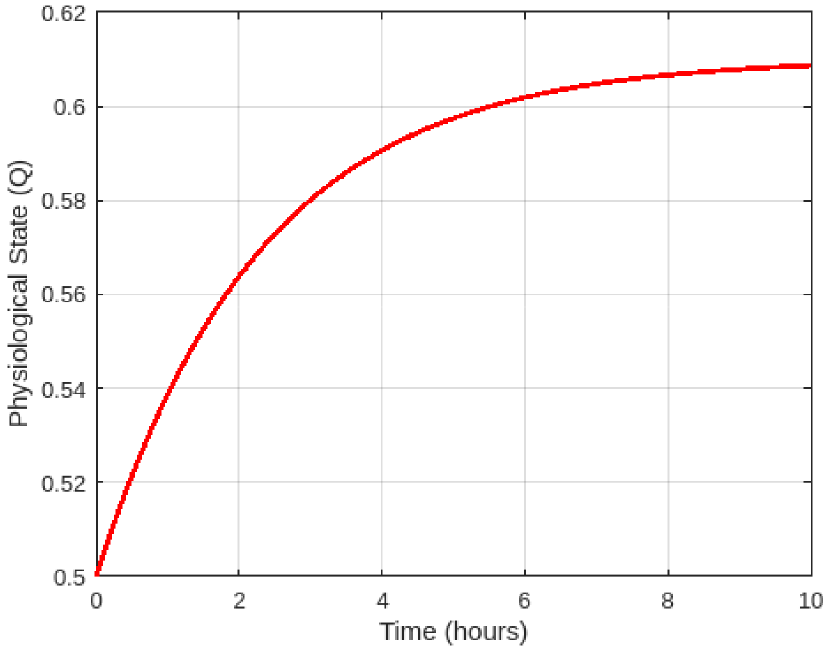

FIGURE 4.2: Physiological state over time

Figure 4.2 indicates that the physiological state of the bacteria is nearing a steady state. This suggests that, after a certain point, there may be little to no significant increase. It could mean that the bacteria have reached their maximum physiological capacity given the current conditions.

In a biological context, this behavior suggests that the bacteria are successfully adapting to their environment and maintaining a healthy metabolic state. This is essential for their growth and reproduction.

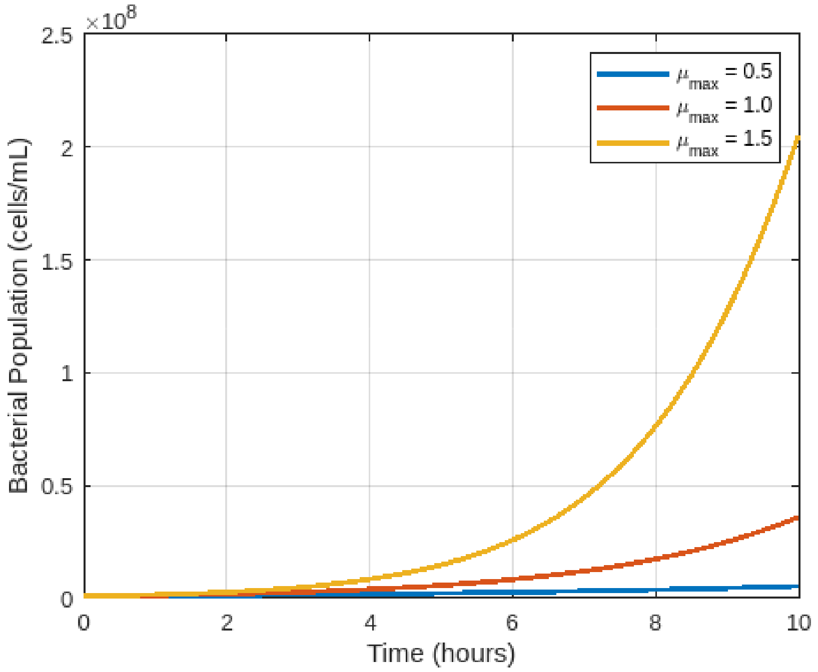

FIGURE 4.3: Effect of μ_{max} on the bacterial growth

Figure 4.3 demonstrates that higher μ_{max} values correspond to faster growth rates and greater bacterial population densities over time.

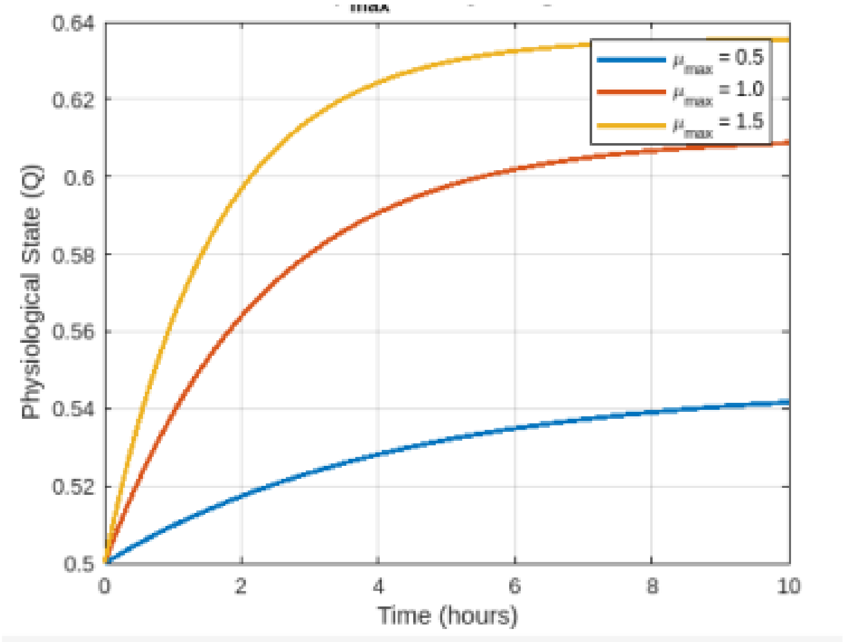

FIGURE 4.4: Effect of μ_{max} on the physiological state

Figure 4.4 illustrates that higher μ_{max} values lead to a more favorable physiological state over time. This relationship highlights the impact of growth conditions on bacterial metabolism and overall health, suggesting that optimizing growth rates can enhance the physiological state of bacterial populations in various applications, such as fermentation and biotechnology.

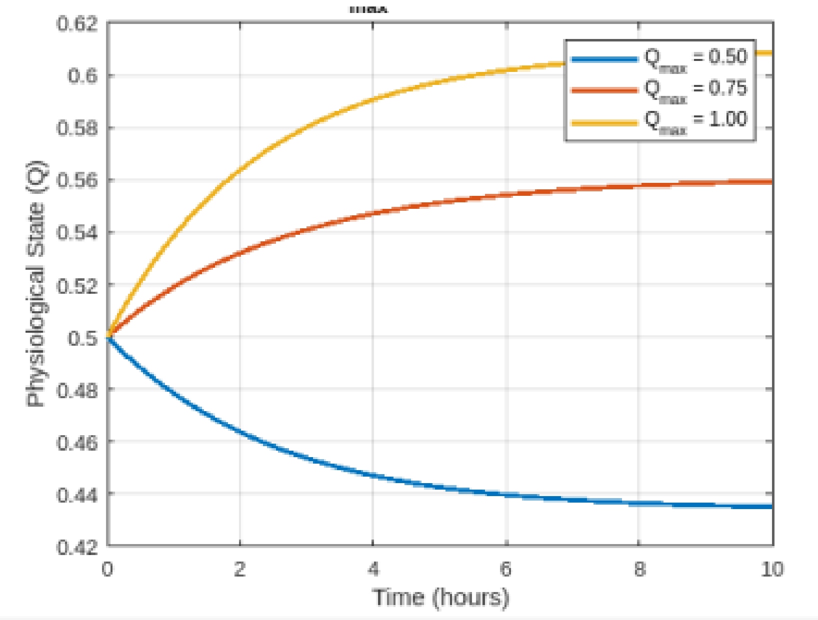

FIGURE 4.5: Effect of $Q_{\max}$ on the physiological state

Figure 4.5 illustrates that increasing $Q_{\max}$ leads to a higher potential physiological state for the bacterial population. This relationship suggests that the maximum physiological state is a limiting factor in bacterial growth and metabolism. With higher $Q_{\max}$ values, bacteria have the potential to grow and function better, reflecting improved health or efficiency.

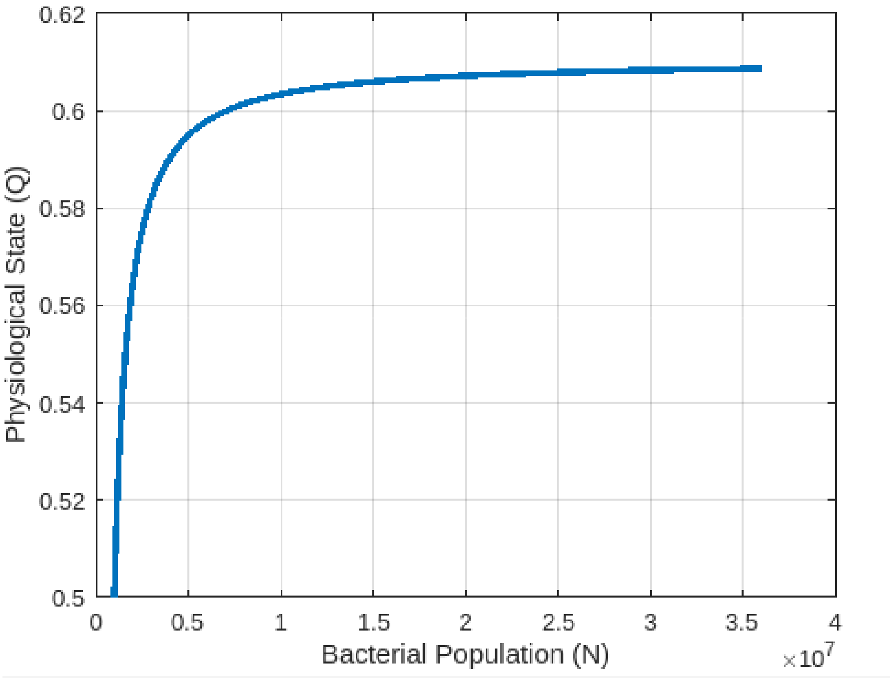

FIGURE 4.6: Physiological state vs Bacterial population

Figure 4.6 indicates that while the bacterial population can grow significantly, the physiological state has a limiting value. This reflects real-world scenarios in microbial ecology, where growth is often limited by factors such as nutrient availability and waste accumulation. The asymptotic behavior of Q suggests that even with a substantial increase in population, the physiological state cannot increase indefinitely.

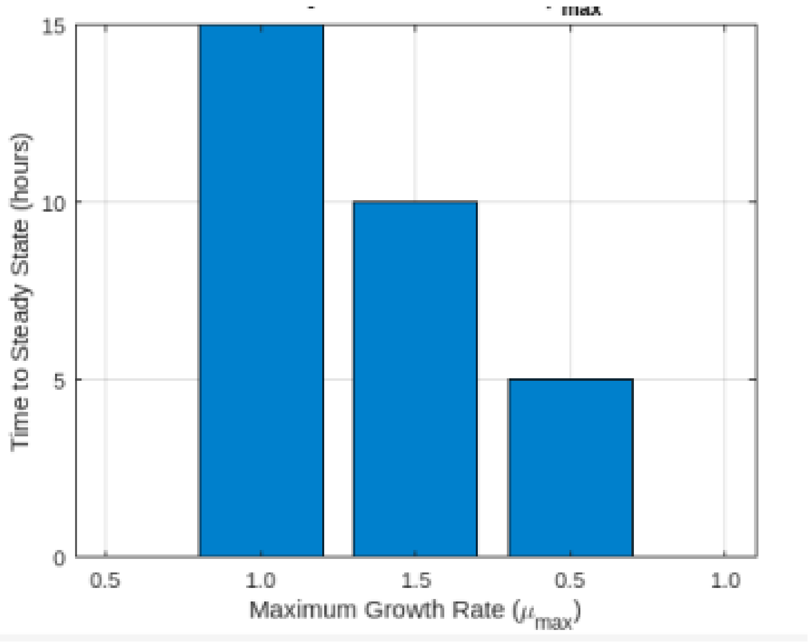

FIGURE 4.7: A bar graph representing the time to steady state for a specific $\mu_{\max}$

Figure 4.7 represents the time to steady state for a specific $\mu_{\max}$ value. The height of the bar corresponds to the time taken: The tallest bar (at $\mu_{\max} = 0.5$) indicates that it takes 15 hours to reach steady state at this growth rate. The shorter bars (at $\mu_{\max} = 1.0$) show reduced times to steady state, suggesting that as the growth rate increases, the time to reach steady state decreases.

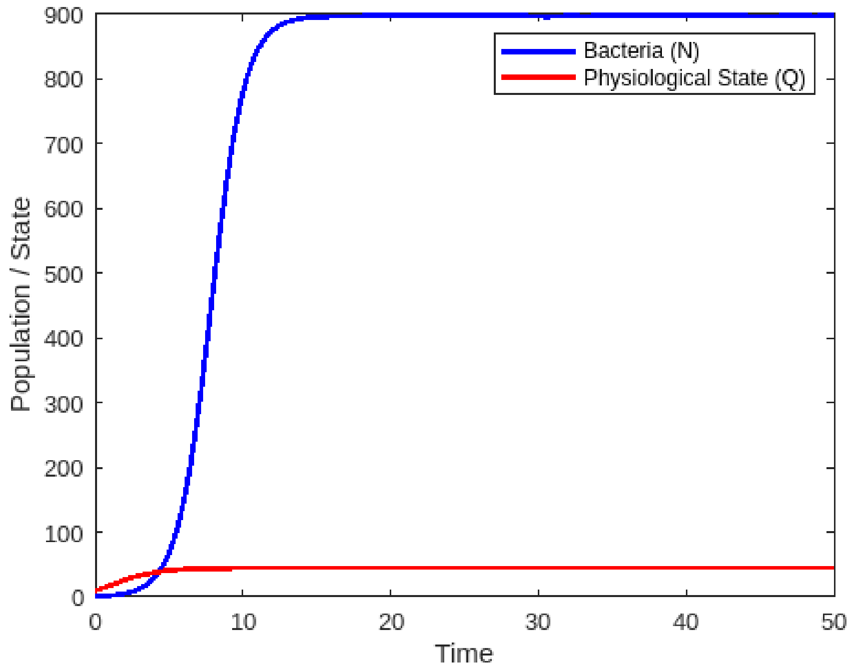

FIGURE 4.8: Bacterial growth and physiological state over time

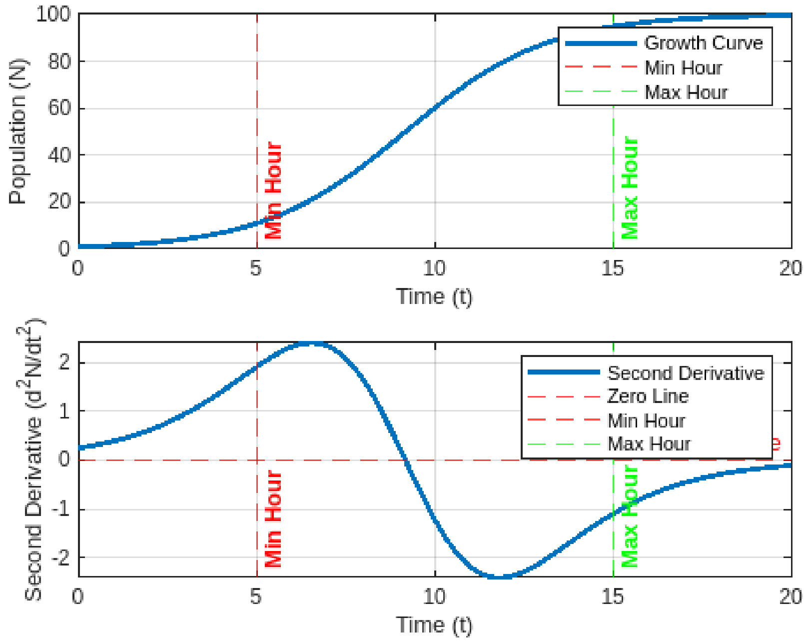

FIGURE 4.9: a) Bacterial growth curve and b) second derivative of the growth curve

Figure 4.9 provides a comprehensive view of bacterial growth dynamics over time, highlighting key phases of growth (lag, exponential, stationary) and the changes in growth rate. The second derivative analysis enhances the understanding of how quickly the bacterial population is changing, allowing researchers to identify critical points in the growth process for further study or application.

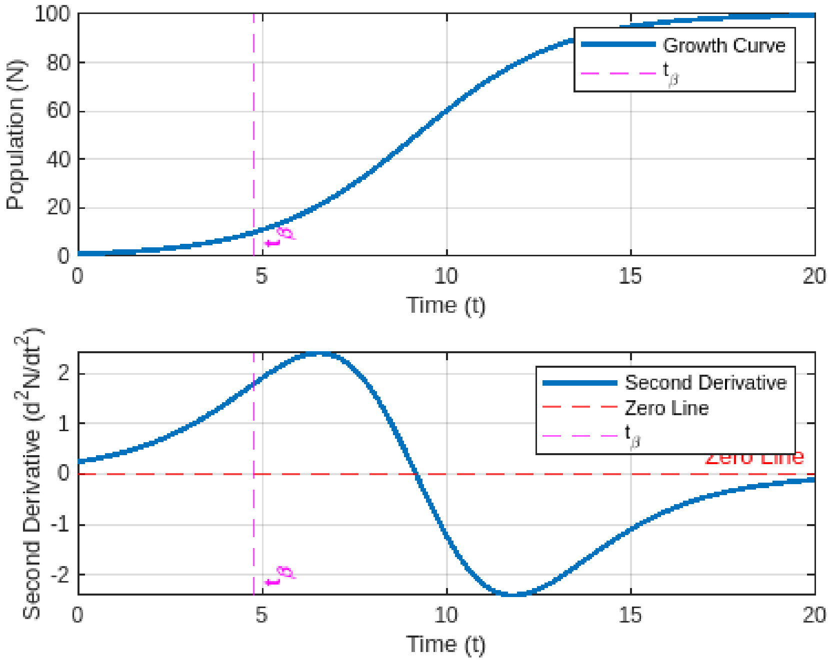

FIGURE 4.10: Bacterial growth curve02

Figure 4.10 provides a detailed view of the bacterial growth dynamics over time, illustrating key growth phases and the associated changes in growth rate. The Zero Line is crucial, marking points where the growth rate shifts from increasing to decreasing. These points correspond to inflection points in the growth curve.

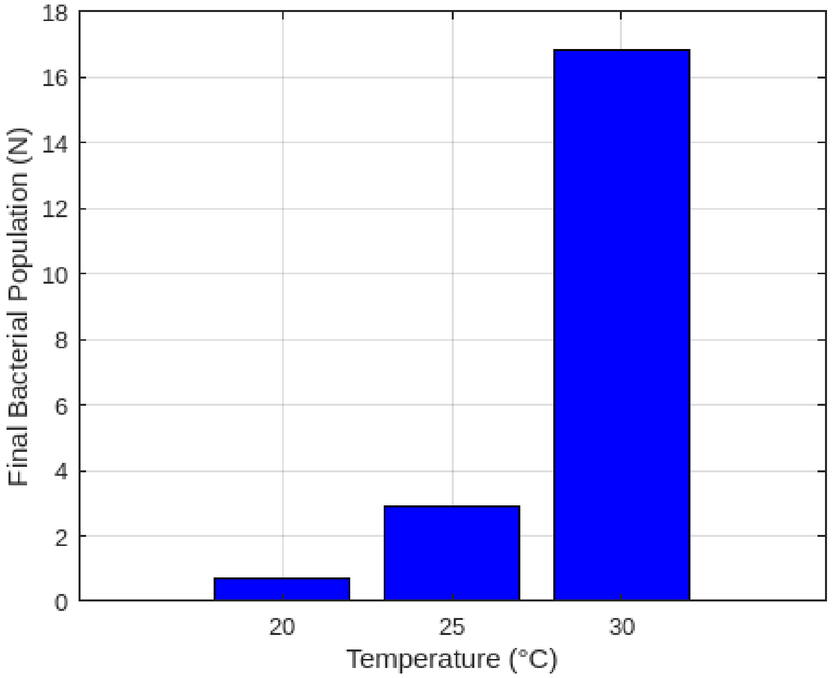

FIGURE 4.11: Bacterial growth vs Temp.

Figure 4.11 illustrates the relationship between temperature and bacterial population, highlighting that higher temperatures generally facilitate greater bacterial growth.

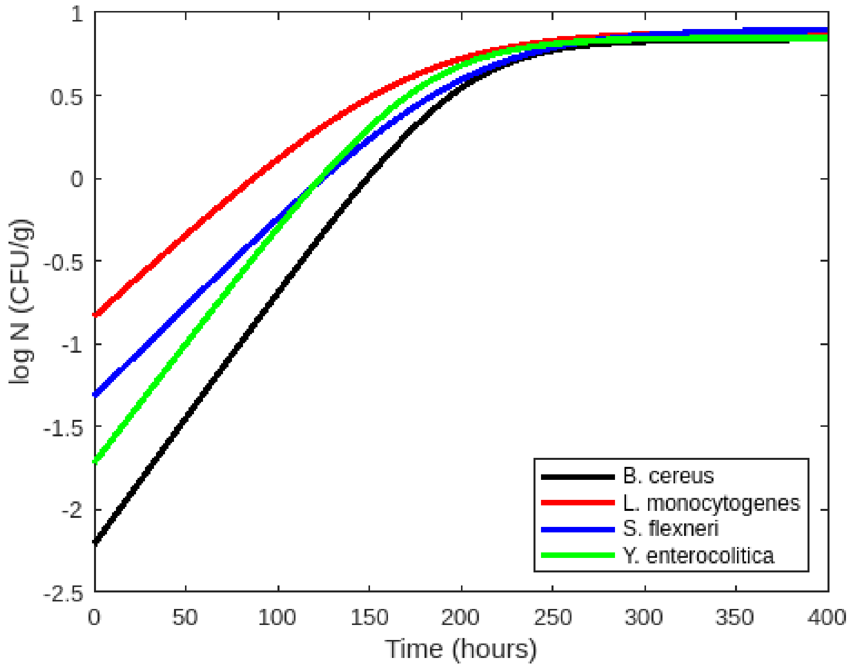

FIGURE 4.12: Fitted Experimental Data

Figure 4.12 provides a comparative visualization of bacterial growth over time for four different species. It highlights their growth dynamics and allows for analysis of how each species responds to the experimental conditions, which can be crucial for understanding their behavior in various environments.

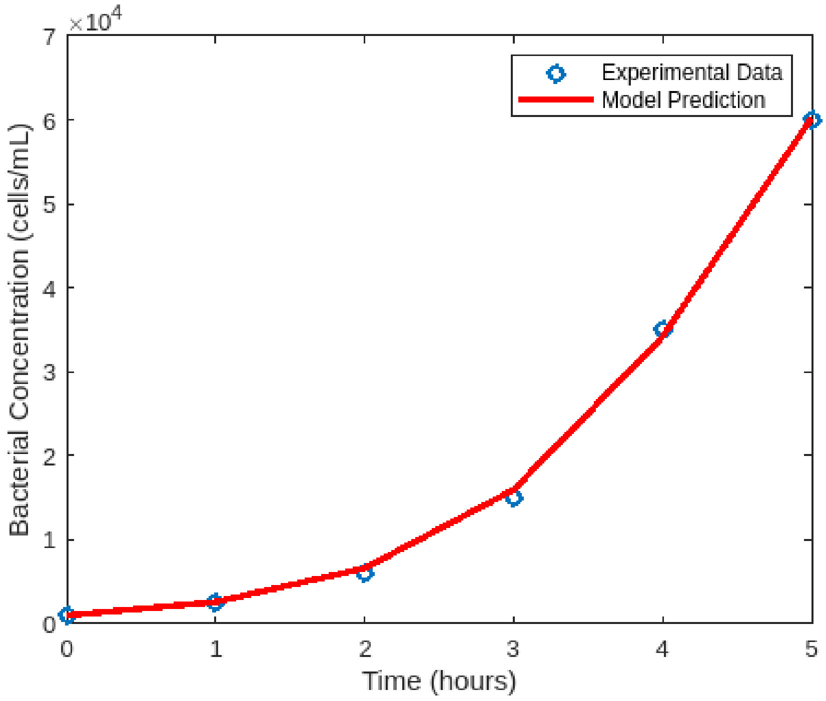

FIGURE 4.13: Fitted Experimental Data03

Figure 4.13 indicates a successful modeling effort where the growth of bacteria over time is well-represented by the fitted model. The experimental data supports the validity of the model, making it a useful tool for understanding bacterial dynamics in this context.

Figure 4.14 provides a clear visualization of microbial growth dynamics over time, illustrating the transition through various growth phases. It also illustrates the metabolic activity and viability of microbial populations under different conditions.

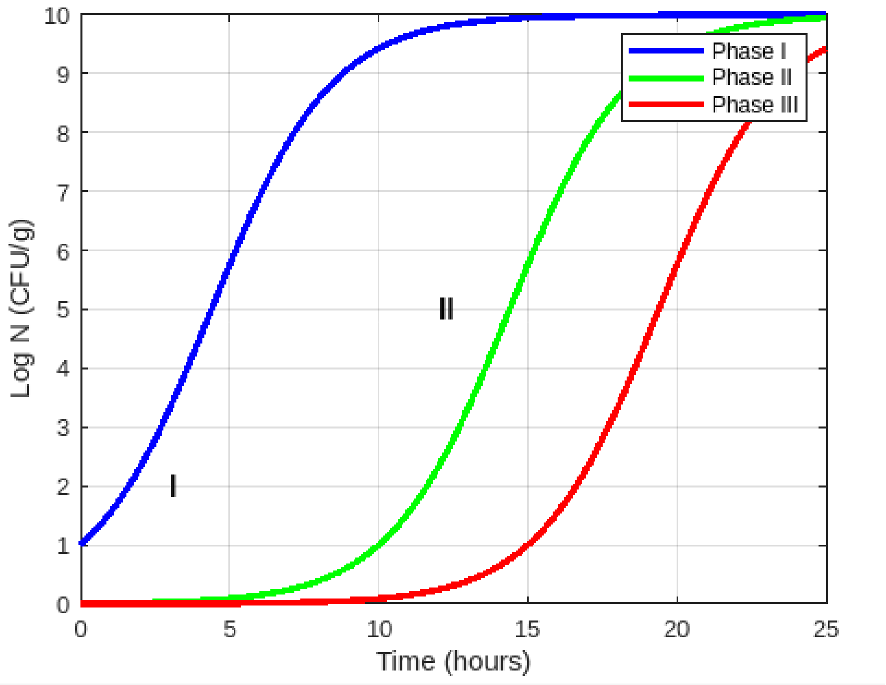

FIGURE 4.14: Microbial Growth Curve

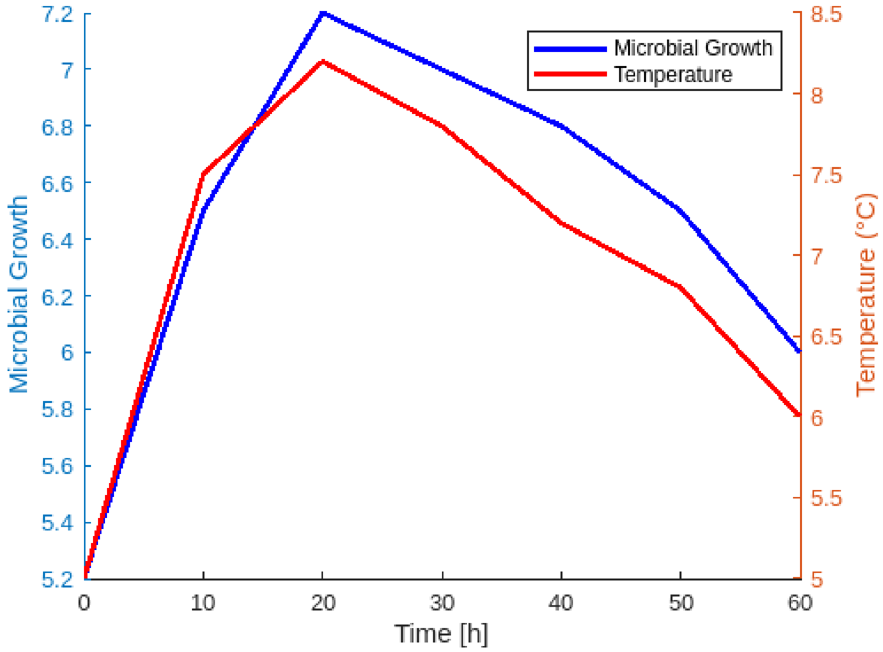

FIGURE 4.15: Microbial Growth Curve02

Figure 4.15 provides valuable insights into how temperature influences microbial growth dynamics over time. The plot also indicates a relationship between temperature and microbial growth. As temperature varies, it affects the growth rate of the microorganisms.

Figure 4.16 shows that when the curve is above the zero line, it signifies an increasing growth

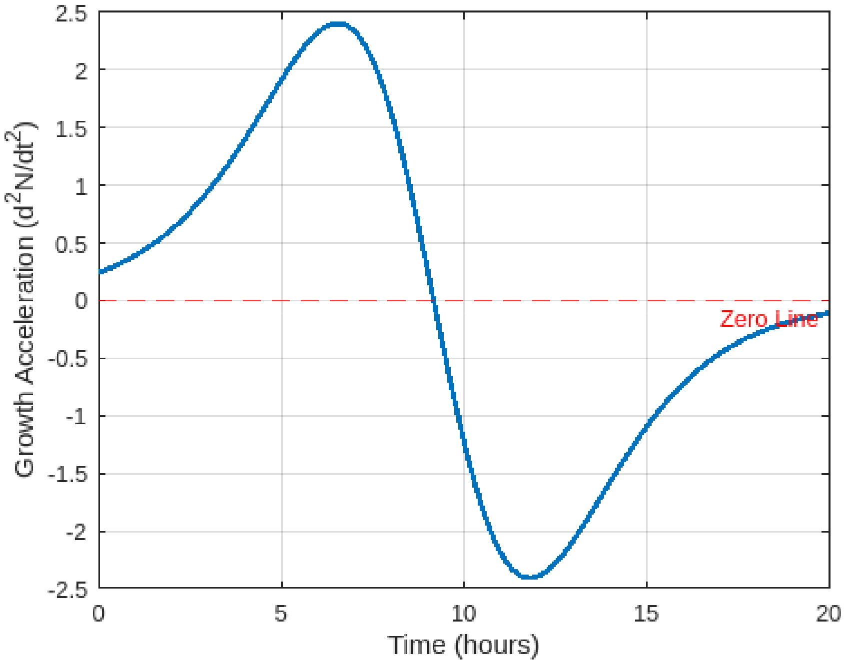

FIGURE 4.16: Time vs growth acceleration

rate, typically observed in the early growth phases under optimal conditions. Conversely, when the curve is below the zero line, it indicates a decreasing growth rate, often occurring in later phases such as the stationary or decline phases, where resources are limited and growth slows.

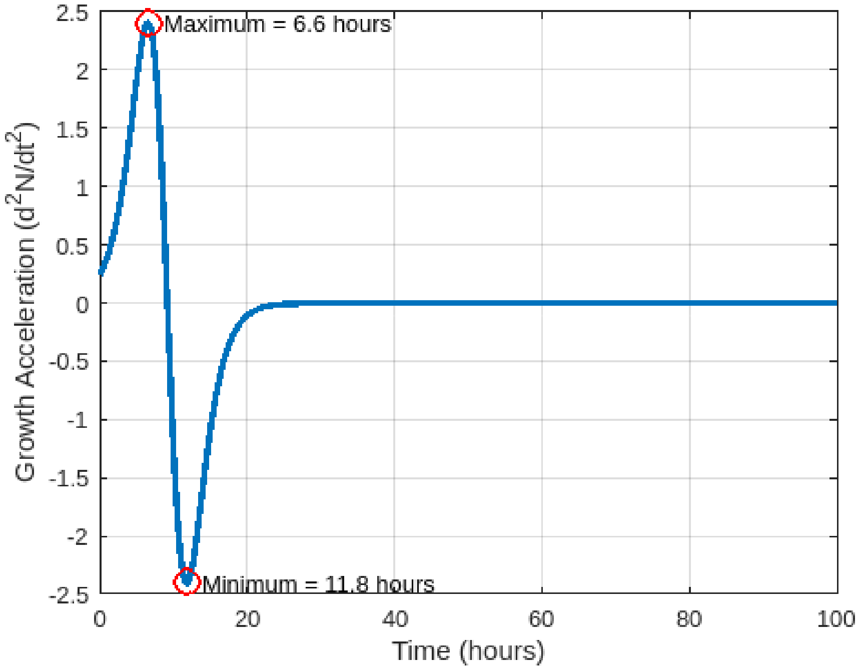

FIGURE 4.17: Time vs growth acceleration02

Figure 4.17 provides valuable insights into the dynamics of microbial growth acceleration over time. The identification of maximum and minimum acceleration points helps in understanding the critical phases of microbial growth.

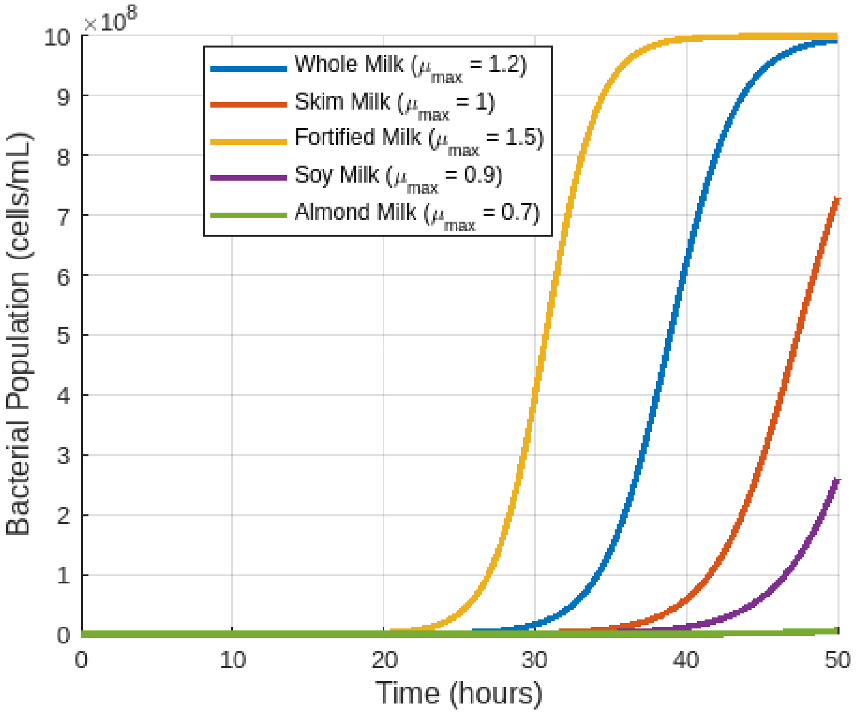

FIGURE 4.18: Bacteria growth in different milk types

Figure 4.18 indicates that different milk types significantly influence bacterial growth rates. Each milk type is associated with a different maximum growth rate (μ_{max}), which indicates the highest rate of bacterial growth achievable in that medium.

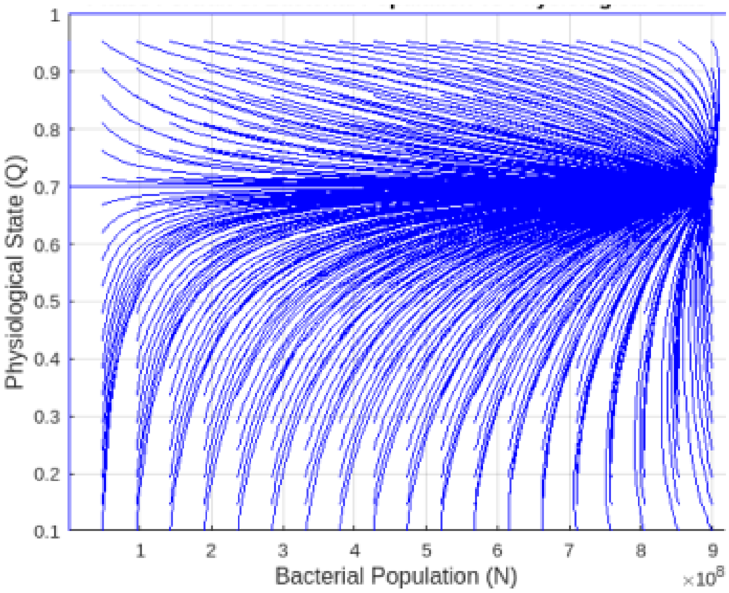

FIGURE 4.19: Phase portrait of bacterial growth

Figure 4.19 shows phase portrait of bacterial growth. The trajectories in the $N - Q$ phase space appear to converge towards a certain region of the phase space, suggesting that the system reaches a stable equilibrium over time. This indicates that regardless of the initial population and physiological state, the system tends to stabilize around certain values. The closer the trajectories are to each other, the more stable the system is in that region. The phase portrait provides insights into the interactions between bacterial population and physiological state. It shows that the system has a tendency to stabilize around certain values, indicating that under most conditions, the bacterial population and physiological state will reach a steady state over time.

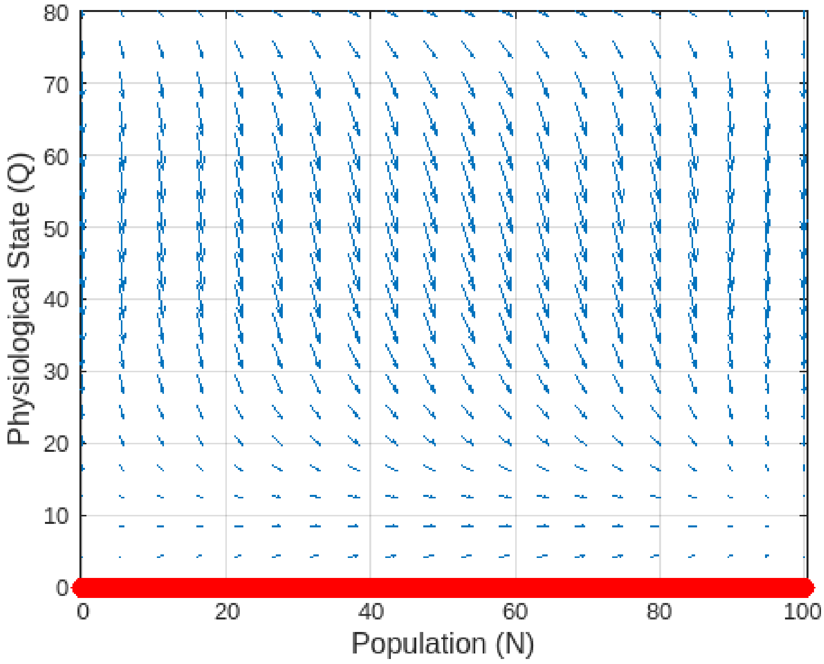

FIGURE 4.20: Phase plane plot of N vs Q

Figure 4.20 illustrates the complex dynamics between population size and physiological state, highlighting areas of potential stability and instability within the system. This visual representation can aid in understanding how fluctuations in physiological states impact population dynamics and vice versa. The red line at the bottom highlights the importance of maintaining physiological state levels above this threshold to prevent population decline.

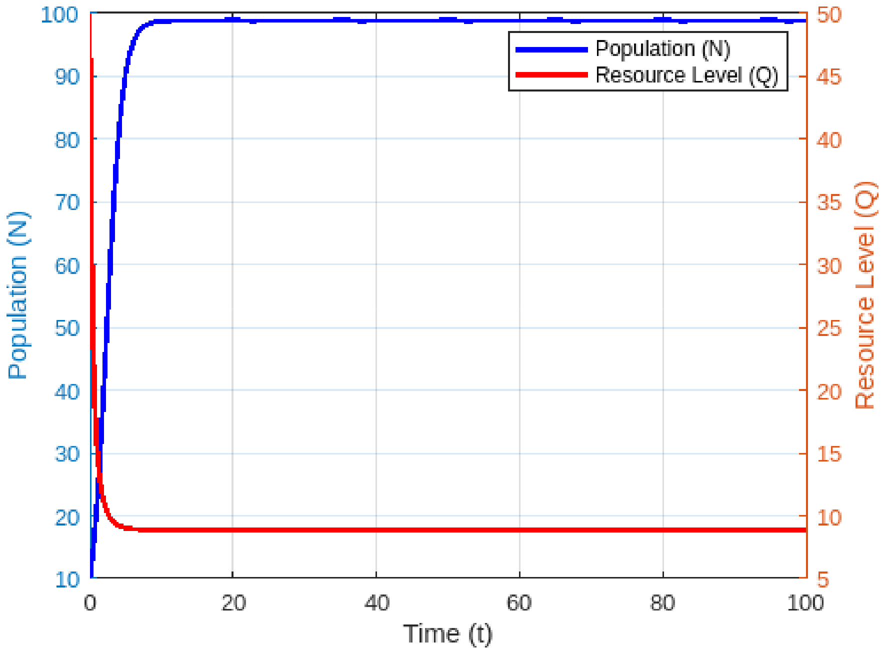

FIGURE 4.21: Time series plot

Figure 4.21 illustrates that the blue curve for population (N) shows an initial rapid increase, reaching a plateau near 100, indicative of exponential growth followed by stabilization at carrying capacity. In contrast, the red curve for resource level (Q) gradually declines and stabilizes around 10, suggesting that resource consumption increases with population growth, leading to eventual depletion.

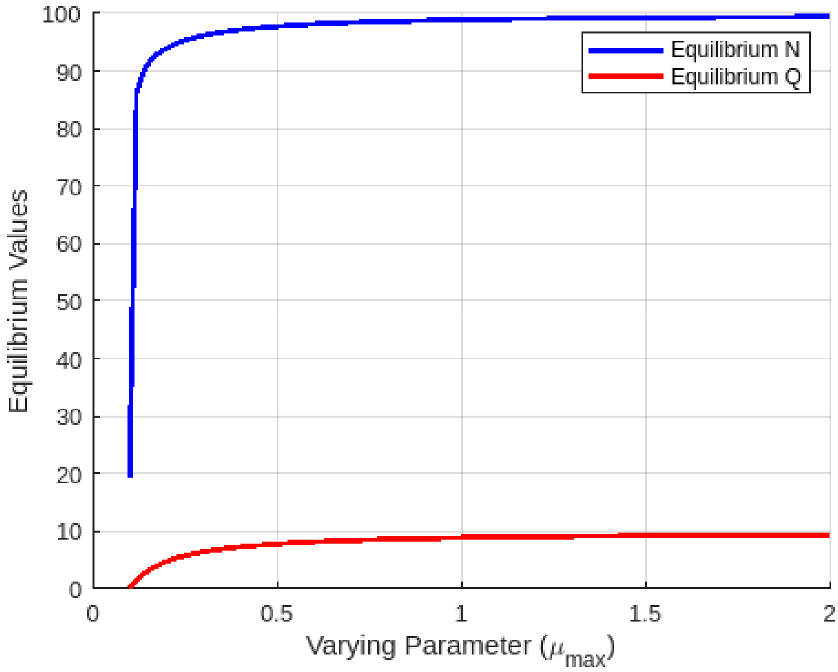

FIGURE 4.22: Bifurcation Diagram

Figure 4.22 demonstrates that as μ_{max} increases, the equilibrium population (N) rises significantly, approaching nearly 100, indicating that higher growth rates can support larger populations. Conversely, the equilibrium resource level (Q) stabilizes at a low value (around 10), suggesting that resource availability does not increase with higher growth rates, highlighting potential limitations in resource supply.

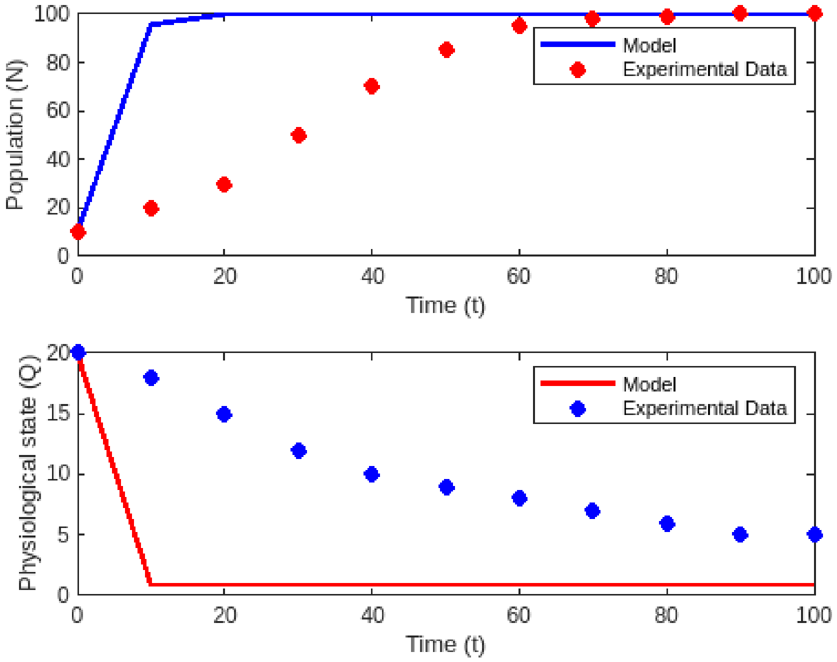

FIGURE 4.23: Fitted Experimental Data

Figure 4.23 provides a visual insight into the relationship between modeled and observed population and resource dynamics, facilitating an assessment of the model's accuracy and reliability. It also shows how well the model fits the experimental data.

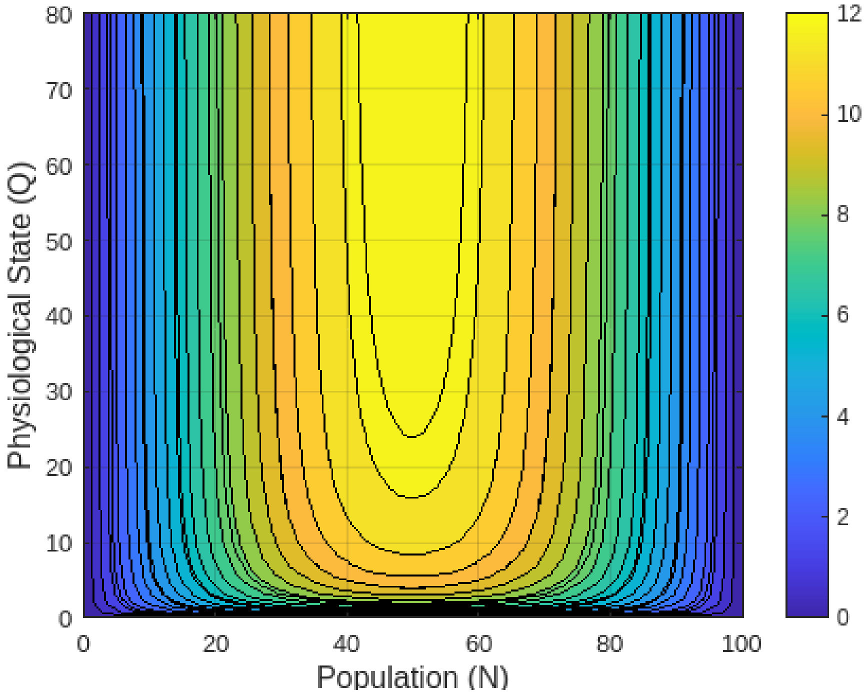

FIGURE 4.24: Contour Plot determining growth rates

Figure 4.24 likely indicates that as the population N increases, the physiological state Q plays a critical role in determining growth rates. There may be optimal ranges for N and Q where growth rates are maximized. The presence of contours that dip, suggesting lower growth rates, might indicate conditions where bacterial growth is inhibited, possibly due to resource limitations or overcrowding.

Chapter 5

Conclusion and Recommendation

5.1 Conclusion

In this study, we took a closer look at how bacteria grow in different types of milk. We noticed some clear patterns in their growth, starting with a rapid increase in the bacterial population, known as the exponential phase, followed by a slowdown as resources became limited, leading to the stationary phase. These observations are important for understanding how bacteria thrive, especially in food products.

Our experimental results closely matched the predictions from our mathematical model, which suggests that our approach is effective in capturing the real-life dynamics of bacterial growth. This correlation gives us confidence in using similar models for future research.

One of the most interesting findings is how well bacteria adapt to their surroundings. As they face limitations in resources, they shift from a phase of rapid growth to a more stable state. This adaptability is crucial for food safety, as understanding these growth patterns can help us find better ways to control bacterial populations in dairy products.

Looking ahead, there's plenty of room for further research. Future studies could investigate how other factors, like temperature and nutrient levels, affect bacterial growth. Gaining this knowledge could lead to improved methods for preserving food and preventing spoilage.

In conclusion, this study sheds light on the dynamics of bacteria in dairy environments. By combining experimental observations with theoretical models, we can deepen our understanding of bacterial behavior. This work sets the stage for future research focused on managing bacteria in various food products, ultimately contributing to better food safety and quality.

5.2 Recommendation

The researcher recommend the following points based on the study results.

- **Dairy Producers:**
    - Enhance hygiene practices to minimize bacterial contamination.
    - Regularly monitor bacterial levels in milk products.
- **Retailers:**
    - Ensure proper storage of milk products at appropriate temperatures.
    - Educate staff on best practices for handling dairy products.
- **Food Safety Regulators:**
    - Develop guidelines for acceptable bacterial levels in dairy.
    - Support research on innovative preservation techniques.
- **Consumers:**
    - Launch awareness campaigns about checking expiration dates and proper storage of dairy.
- **Researchers and Academics:**
    - Encourage collaborative studies between microbiologists and food scientists.

By following these recommendations, stakeholder can work together to enhance food safety, improve dairy product quality, and ultimately protect consumer health.

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