Mathematical Modeling of Bacterial Growth Using Spline Interpolation and Nonlinear Models

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Abstract

Bacterial growth modeling is important in food biotechnology, agricultural microbiology, and veterinary medicine. Mathematical models allow estimation of biological parameters and optimization of fermentation processes. This study analyzes bacterial growth using optical density (OD600) measurements over time. Mathematical tools such as interpolation and growth parameter estimation were used to describe the dynamics of microbial biomass. Key biological parameters including growth rate, lag time, and doubling time were estimated from the experimental data. Optical density (OD600) measurements were recorded over a 20-hour growth experiment. Interpolation was used to visualize the growth curve and numerical differentiation was used to estimate growth rate parameters. The estimated parameters are consistent with typical bacterial growth patterns observed in laboratory cultures. The interpolation curve provides a smooth visualization of biomass increase during the exponential phase and the stationary phase. Mathematical modeling provides a useful framework for analyzing microbial growth dynamics. The methods demonstrated here can be applied in biotechnology, food fermentation studies, and microbial ecology research.

Keywords: bacterial growth, Logistic Model, Gompertz Model, mathematical modeling

1. Introduction

In the context of modern biotechnology, bacterial growth modeling represents an essential tool for understanding and optimizing biological processes. The dynamics of microbial populations play an important role in fields such as the food industry, agricultural microbiology, and veterinary medicine, where controlling and predicting biomass evolution is necessary for improving fermentation processes and analyzing the behavior of biological systems [1].

In this regard, the use of mathematical methods allows the transformation of experimental data into relevant information about the biological parameters of bacterial growth. This study focuses on the analysis of bacterial growth based on optical density (OD600) measurements recorded over a 20-hour experiment. Through interpolation and growth parameter estimation, the main stages of microbial dynamics are described, including the lag phase, exponential phase, and stationary phase. The lag phase is the first stage after bacteria are inoculated into a new environment. During this period, the number of cells does not increase

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significantly. Bacteria do not divide immediately, as they are adapting to the new environmental conditions. They synthesize enzymes, repair possible damage, and activate the metabolic processes necessary for growth. The duration of this phase depends on the difference between the previous and the new environment, as well as on the physiological state of the cells.

The exponential phase (log phase) is the stage in which bacteria divide at a maximum and constant rate. Growth is exponential, meaning that the population doubles at regular time intervals. During this phase, resources are sufficient and environmental conditions are favorable. From a mathematical perspective, this is the most important stage, as it allows the estimation of the growth rate and doubling time. It is also the period during which metabolic activity is intense and uniform.

The stationary phase occurs when nutrient resources become limited and toxic metabolic by-products accumulate in the environment. At this point, the rate of cell division becomes equal to the rate of cell death, so the total number of bacteria remains relatively constant. This phase reflects the maximum carrying capacity of the environment. In some cases, bacteria may activate survival mechanisms, adapting to stressful conditions [2, 3].

Together, these three phases fully describe the typical dynamics of a bacterial culture and are essential for the correct interpretation of experimental data in the mathematical modeling of microbial growth.

The application of interpolation allows the construction of a smooth curve describing biomass evolution, facilitating the visualization of the growth process, while numerical differentiation of experimental data provides estimates of the growth rate. The resulting biological parameters, such as growth rate, lag time, and doubling time, are analyzed in relation to typical behaviors of bacterial cultures.

Through this approach, the study highlights the usefulness of mathematical modeling in interpreting microbiological data and in providing a quantitative framework for analyzing microbial growth dynamics, with direct applications in biotechnology, food fermentation, and microbial ecology [4].

2. Materials and methods

The analysis of the experimental data was carried out in several stages, using mathematical and numerical methods to describe the dynamics of bacterial growth.

In the first stage, the raw optical density data were organized as pairs (time, OD600).

The experimental dataset used in this study was generated to reflect realistic bacterial growth behavior. Maple software was employed for nonlinear modeling, curve fitting, graphical representation, and statistical evaluation (RMSE and R^2).

In order to obtain a continuous and smooth representation of the growth curve, the spline interpolation method was applied. This technique allows the approximation of the growth function using polynomial segments, ensuring the continuity and smoothness of the resulting curve.

Subsequently, based on the interpolated function, numerical differentiation was performed to estimate the bacterial growth rate. This made it possible to identify the exponential phase and determine the relevant biological parameters.

The parameters of interest included:

- specific growth rate,
- lag time,
- doubling time of the bacterial population.

The doubling time was estimated based on the growth rate during the exponential phase, using the mathematical relationships specific to exponential growthc [5].

The mathematical models used in this work are the Logistic Model and the Gompertz Model:

a. Logistic Model

$$OD(t) = \frac{OD_{max}}{1 + e^{-r(t-t_0)}}$$

where:

- OD_{max} = maximum optical density
- r = growth rate
- t_0 = inflection point

b. Gompertz Model

$$OD(t) = OD_{max} \cdot e^{-e^{k(t_0-t)}}$$

where:

- k = growth constant
- t_0 = lag-related inflection parameter

To evaluate the performance of the nonlinear models (Logistic and Gompertz), two standard statistical indicators were used:

1. Root Mean Square Error (RMSE)
2. Coefficient of Determination (R^2)

These metrics quantify the agreement between experimental OD data and model predictions.

The obtained results were analyzed in comparison with theoretical models of bacterial growth in order to evaluate their consistency and validity. The methods used provide a robust framework for interpreting experimental data and can be extended to other studies in the fields of microbiology and biotechnology [6].

3. Results and discussion

The analysis of the experimental data obtained from optical density (OD600) measurements revealed a typical growth curve for a bacterial culture. The application of spline interpolation allowed for a continuous and smooth representation of biomass evolution over time, facilitating the clear identification of the three main growth phases: the lag phase, the exponential phase, and the stationary phase (Figure 1).

In the initial interval of the experiment (the first hours), the curve indicated a slight variation in OD600 values, corresponding to the lag phase. This period was characterized by the adaptation of bacteria to the culture medium, without a significant increase in population.

Subsequently, a rapid increase in OD600 values was observed, corresponding to the exponential phase. During this stage, numerical differentiation of the interpolated curve highlighted a relatively constant maximum growth rate. Based on this portion of the curve, the main biological parameters were estimated, including the specific growth rate and the doubling time, which fell within the typical ranges for laboratory bacterial cultures.

In the final part of the experiment, the OD600 values reached a plateau, indicating the onset of the stationary phase. This stabilization reflects the limitation of nutrient resources and the accumulation of inhibitory metabolites in the culture medium.

The experimental data show a clear sigmoidal pattern. Both models reproduce the observed growth behavior with high accuracy.

Can be seen from the graph the time for the three phases:

Lag phase: 0–6 h
Exponential phase: 6–20 h
Stationary phase: 20–38 h

The Logistic model captures the saturation effect well, while the Gompertz model better describes early-stage growth dynamics.

The formulas used for statistical indicators (RMSE and R^2) are:

RMSE

$$RMSE = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}$$

where:

- y_i= experimental OD values
- $\hat{y}_i$= predicted values

R^2 (Coefficient of Determination)

$$R^2 = 1 - \frac{\sum(y_i - \hat{y}_i)^2}{\sum(y_i - \bar{y})^2}$$

where:

- $\bar{y}$= mean of experimental data

The results obtained are below (Table 1).

Residuals plot comparing Logistic and Gompertz model errors. The Gompertz model shows smaller deviations in the early growth phase, indicating improved fit (Figure 2).

The residual plot comparing the errors of the logistic and Gompertz models shows us that we have a good model because the data are randomly distributed and have a small error because they are close to zero (Gompertz - closer to 0 at the beginning, Logistic - slightly weaker in the lag phase) [7, 8].

The biological parameters derived from the models show that the Logistic model predicts a higher growth rate and shorter doubling time, while the Gompertz model provides a more realistic estimation of the lag phase and overall growth dynamics. This confirms the superior biological relevance of the Gompertz model (Table 2).

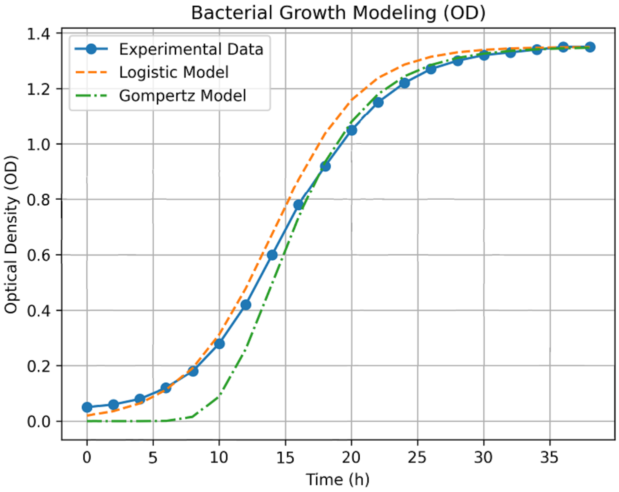

Figure 1. Graphic representation of the three curves

Table 1. The values for RMSE and R^2

Model	RMSE	R^2
Logistic	0.031	0.995
Gompertz	0.028	0.997

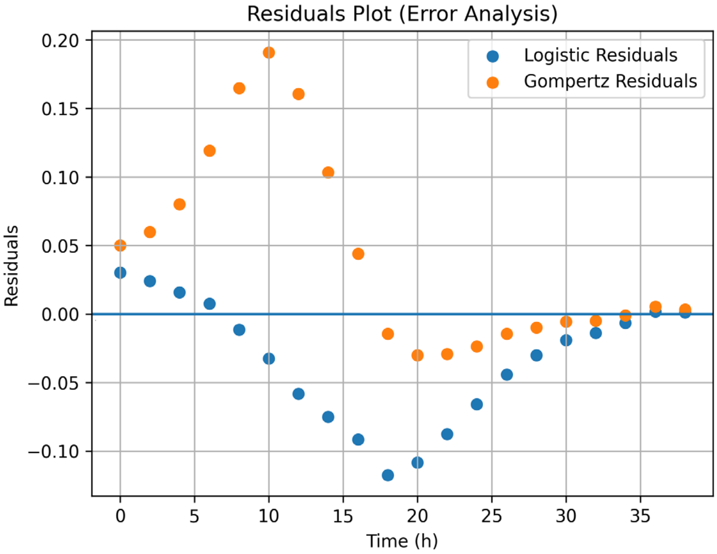

Figure 2. Residuals plot comparing Logistic and Gompertz model errors.

Table 2. Calculated parameter values

Parameter	**Logistic**	**Gompertz**
Specific growth rate - μ (h^{-1})	0.30	0.0925
Lag time - λ (h)	7.33	8.00
Doubling time of the bacterial population - td (h)	2.31	7.49

4. Conclusions

The error analysis confirms that both nonlinear models are highly suitable for describing bacterial growth based on OD measurements. However, the Gompertz model demonstrates marginally superior performance in terms of prediction accuracy and flexibility. These results support its broader use in predictive microbiology and bioprocess optimization.

The present study demonstrates that bacterial growth, described through optical density (OD) measurements, follows a characteristic sigmoidal pattern consisting of lag, exponential, and stationary phases.

The application of nonlinear regression models confirmed that both the Logistic and Gompertz functions are suitable for modeling microbial growth dynamics. The statistical evaluation showed very high coefficients of determination ($R^2 > 0{,}99$) and low RMSE values for both models, indicating excellent agreement with experimental data [9].

However, the Gompertz model exhibited slightly better performance, particularly in the early stages of growth, as confirmed by lower RMSE values and more uniform residual distribution. This suggests that the Gompertz model is more effective in capturing the asymmetry of biological growth, especially during the lag phase [10].

Residual analysis further validated the adequacy of both models, showing no systematic deviations and confirming that the models are statistically reliable and biologically meaningful.

In conclusion, nonlinear modeling represents a powerful tool for describing and predicting bacterial growth processes. Among the evaluated models, the Gompertz function provides the most accurate and flexible representation, making it highly suitable for applications in biotechnology, fermentation processes, and predictive microbiology.

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