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## MATHEMATICAL MODELING OF BACTERIAL GROWTH USING SPLINE INTERPOLATION AND NONLINEAR MODELS

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**• Abstract:** 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. The methods demonstrated here can be applied in biotechnology, food fermentation studies, and microbial ecology research.

### • Introduction

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

### • Material and method

Optical density (OD600) measurements were recorded over a 20-hour growth experiment. 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  $R^2$ ).

### • Results and discussions

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). 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 values obtained for statistical indicators (RMSE and  $R^2$ ) are for Logistic Model RMSE=0.031,  $R^2$ =0.995 and for Gompertz Model RMSE=0.028 and  $R^2$ =0.997.

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).

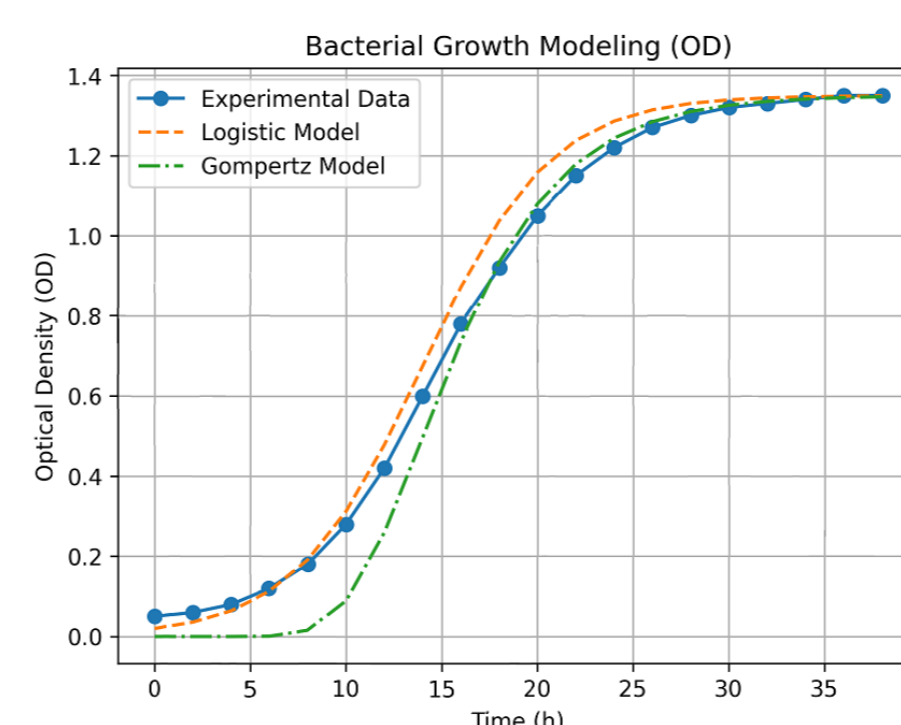


Figure 1. Graphic representation of the three curves

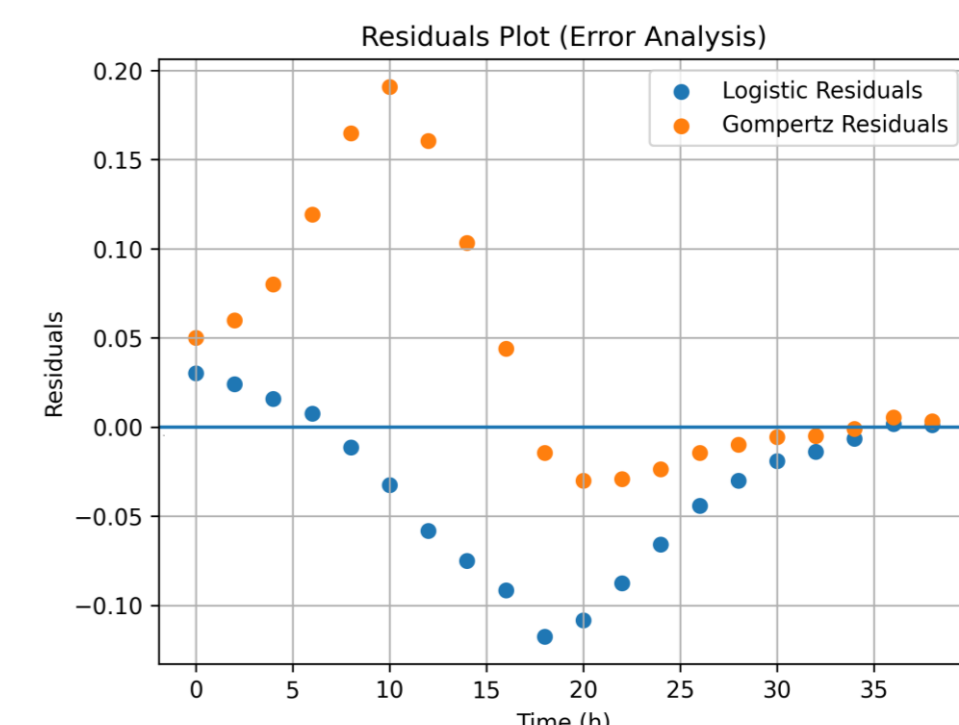


Figure 2. Residuals plot comparing Logistic and Gompertz model errors

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.

| Parametru  | Logistic | Gompertz |
|--|----------|----------|
| specific growth rate - $\mu$ ( $h^{-1}$ )            | 0,30     | 0,0925   |
| lag time - $\lambda$ (h)                             | 7,33     | 8,00     |
| doubling time of the bacterial population - $td$ (h) | 2,31     | 7,49     |

### • Conclusions

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 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.

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

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