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A model based on the assumption that the specific growth rate is normally distributed as a function of time to describe microbial growth under isothermal and non-isothermal temperature profiles

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Abstract

A primary mathematical model was applied to describe microbial growth both in isothermal and dynamic temperature profiles for different datasets found in the literature. The model consists in the assumption that specific growth rate follows a Gaussian distribution as a function of the time. The parameters included in the model are the duration of the lag phase, the maximum specific growth rate and the logarithmic inflection point. The values generated by the model were, mostly, compatible with those predicted by the Baranyi-Roberts growth model. Further studies are necessary in order to study the mathematical properties and implications of the equation.

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1. Main Text

1.1. Introduction

Mathematical models have been used to explain natural phenomena long ago, and many problems have been, and many problems of different fields have been formulated mathematically. Some functions of these models include the need to explain phenomena and to make predictions. In addition, they are used to help decision making. In this

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respect, predictive microbiology can be considered an emerging scientific discipline that can provide useful answers to important questions regarding microbial growth in food products and food safety.

Although the early models can be traced back to 1920s[1], it can be said that the field of predictive microbiology achieved a great development in the 1980s because computers and specific software facilitated the development of complex and more precise models[2]. The early models were mainly empirical and essentially consisted in any mathematical function that could fit a sigmoidal curve[3,4]. The next generation models searched a more mechanistic approach in order to provide insight into the underlying principles governing microbial growth[5,6,7]. Between these models, Baranyi and Roberts model has come to be the most used model mainly due to its ability of correctly predicting the lag phase of the microbial growth curve[8]. Nowadays, there are many models devoted to different specific applications such as growth/no growth models to define the limits for growth in specified food environments[2,9], bacterial transfer models[10] and stochastic models[11].

The main objective of this study is to provide an alternative model that can describe microbial growth both in isothermal and non-isothermal temperature regimes. This mathematical model is based on assumption that the specific growth rate is normally distributed as a function of time. This hypothesis relies on the central limit theorem that establishes that an effect caused by many variables with influences of similar magnitudes is normally distributed.

Nomenclature

λ	duration of the lag phase
σ	standard deviation
$\mu(t)$	specific growth rate as a function of time
μ_m	maximum specific growth rate
erf	error function
exp	exponential function
$N(t)$	microbial population as a function of time
t	time
t_a	mean value of the time
t_{LIP}	logarithmic inflection point of the abscissa in the growth curve
y_0	natural logarithm of the initial microbial population
$y(t)$	natural logarithm of the microbial population as a function of the time
$\mathbf{Z_i}(t)$	variable that affects the specific growth rate

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1.2. Derivation of the model

Generically speaking the central limit theorem establishes that the sum of a large number of independent random variables each of which contributing to a small amount of the total is normally distributed[12]. If the temporal dependence of the specific growth rate is considered as being a vector that depends on many different variables as functions of the time, it will be given by Equation 1[13].

$$\mu(t) = \begin{bmatrix} Z_1(t) \\ Z_2(t) \\ \dots \\ Z_n(t) \end{bmatrix} \tag{1}$$

Therefore, if each element of the vector $\mathbf{Z_i}(t)$ contributes similarly to the global value of the specific growth rate, then the following expression holds.