REVIEW OF MATHEMATICAL MODEL ON GROWTH OF MICROBIAL POPULATIONS IN THE LABORATORY

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Abstract:

Microorganisms are ubiquitous in nature, and they multiplied very rapidly in 2^n fashion under laboratory conditions. The Study of mathematical models provides excellent possibilities to analyze the growth of microorganisms in the laboratory. The application of mathematical models helps the undergraduate life sciences students to study various phases of microorganisms when it is placed in a suitable growth medium and imparting a proper perception on the processes of microbial growth. Microorganism undergoes various phases under a closed environment called a batch culture system namely "lag," "log or exponential," "stationary" and death phases. Mathematical models of differential equations and the model express symbolically as a finite combination of elementary functions provide us a detail study on microbial phases. Hence, we aimed at review on mathematical models in solving microbial growth study. This review paper amasses knowledge on applications of corresponding mathematical equations (simple differential equations) in the contribution to teach the under graduate life sciences students to study various phages of microbial growth curve and also giving emphasize on computational data analysis and interpretation.

Keywords: Mathematical model, differential equation, microbial growth, growth phases.

Need of Review:

This paper will become a resource for the importance of mathematical models even in microbial growth studies for under graduates, Post graduates as well as for the researchers doing research in microbiology specifically on growth studies as it is covering the information related to the applications of mathematical equations even in the other areas like microbiology, biochemistry, biotechnology, bio engineering and other

biology related branches. The review also emphasizes the need of intra disciplinary communication among various departments at undergraduate level. There are variety of mathematical models come up with biology have been published in many research articles; all these are confined to the research publications only, no one is including in the text books of biology at their graduate level. Though the growth equations has been explained by using Verhulst or logistic models there is no much appreciations has been given to the mathematical models. Hence, the applications of corresponding mathematical equations (simple differential equations) in the contribution to teach the under graduate life sciences students have to be reviewed up.

INTRODUCTION: The Logistic model was developed by Belgian mathematician Pierre Verhulst (1838), developed the logistic model they suggested that the rate of population increase may be limited & the dynamics of the population was explained by the differential equation:

$$\frac{dN(t)}{dt} = r\,N_t \left\{ 1 - \frac{N(t)}{K} \right\}, \quad (1)$$

Where N (t) is the population size at time t, r is the intrinsic growth rate, and K (>0) is the carrying capacity of the population.

With this Logistic model they combined two ecological processes: reproduction (growth) and competition (self-limiting). Both processes depend on population numbers (or density). The rate of both 2 processes match to the mass-action low with coefficients: r for reproduction and r/K for competition.

The Logistic model is explained by them provides a good mathematical description for many biological populations of microorganisms, plants, and animals. It is also applicable in other areas such as statistics, economics, medicine [1] [2], physics, chemistry, and other biology related branches.

The Logistic model contains some deficiencies. It does not account for at least some individual mortality that can occur at any time, including during the exponential growth stage. This difficulty can be partly overcome by considering N (t) in the equation as a number that represents the population's net growth [3]. If so, then any mortality that might occur during the 'lag', 'exponential' and 'stationary' stages is reflected in the observed magnitude of the model's parameters. In particular it has been suggested, (e.g., Corradini & Peleg, 2006) that the momentary growth rate might be proportional to $N(t)^a$ and to

$[1 - N(t)/K]^b$, in which case the logistic equation will become:

$$\frac{dN(t)}{dt} = r N(t)^a \left\{ 1 - \frac{N(t)}{K} \right\}^b , (2)$$

Where a is the growth regulator and b is the depletion factor

The logistic model assumed that the growth rate of a population at any time t depends on the relative number of individuals at that time. In practice, the process of reproduction is not instantaneous [4]. Therefore, one way of improving the Logistic growth model Eq (1) is the following more realistic equation:

$$\frac{dN(t)}{dt} = rN(t) \left\{ 1 - \frac{N(t------r)}{K} \right\} , (3)$$

Eq (3) proposed by Hutchinson (1948) [5]. Where r and K have the same meaning as in the Logistic equation Eq (1) , T>0 is the discrete delay term.

Eq (3) means that the controlling effect depends on the population at a fixed earlier time (t-r) rather than the present time t, effects of time delay t>0 on stability of equilibra has been well studied (Kaung 1999). In a more realistic model the delay effect should be an average over past populations. This results in an equation with a distributed delay. Thus another way of improving the logistic growth model Eq (1)was to include a delay term to examine a cumulative effect in the death rate of species , depending on the population at all times from the start of the experiment. The model is an integro- differential equation.

$$\frac{dN(t)}{dt} = rN(t) \left\{ 1 - \frac{1}{K} \int_{-\infty}^{t} N(s) G(t-s) ds \right\} , (4)$$

Eq.(4) was initially proposed by Volterra (1934) (6) (7), where r and K have the same meaning as in the logistic equation Eq.(1), G (t) is a weighting factor which indicates how much emphasis should be given to the size of population at earlier times to determine the present effect on resource availability . Eq (4) it includes a types of delay that is known as distributed delay which is the sum of infinitely numerous delays in the form of an integral.

Also , to further improve the Logisitic growth model Eq ( ) Mac donald (1978) (8) (9) discussed the following integro –differential equation.

$$\frac{dN(t)}{dt} = rN(t) \left\{ 1 - \frac{N(t)}{K} \int_0^t N(s) \, G(t-s) \, ds \right\}, \quad (5)$$

This includes both distributed delay integral term and the traditional Nt/K term. Here r and k are positive , and instantaneous self- crowding term G (t) is accompanied by a population term N (t).

In the present work we develop a more realistics model which takes advantage of the above mentioned modeling approaches and we employ the model to investigate the effect of decontamination on the bacterial population.
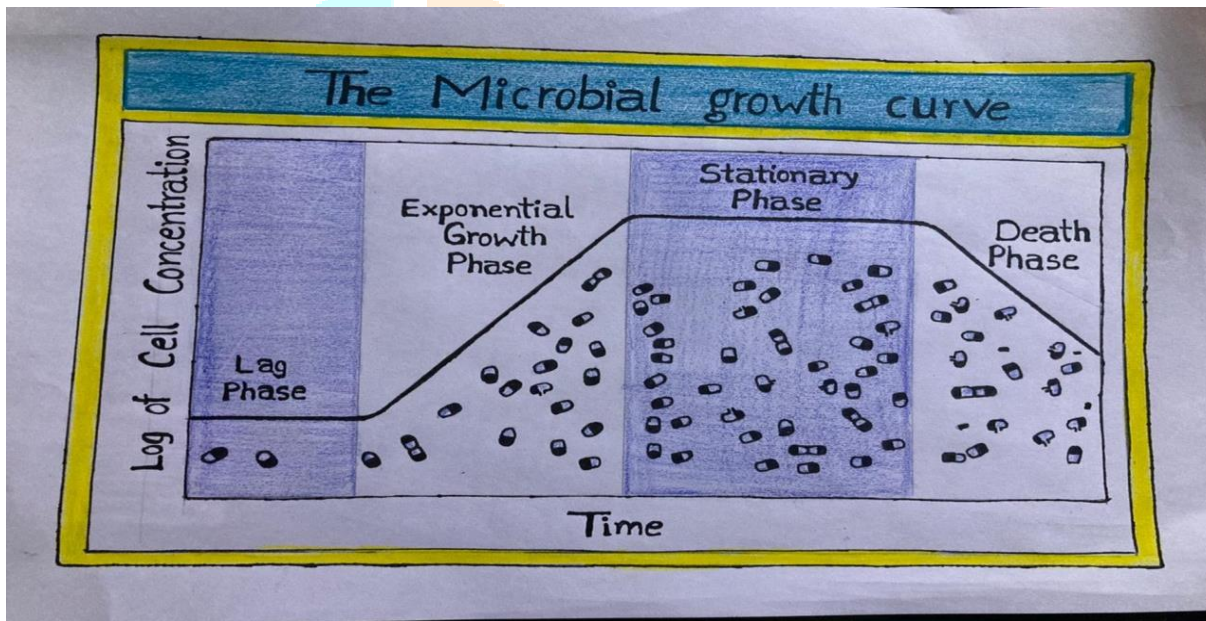

Fig-1 Bacterial Growth Curve of a Batch Culture

 Our goal is to use previous modeling approaches along with knowledge on how bacterial grow and develop a model describing the bacterial growth that is affected by decontamination.

4Bacterial population growth cells reproduce by dividing into two cells. Each individual (bacterium, virus,or microbe) takes about the same time to mature and divide. This principle is commonly used with the Peleg's model Eq. (2) and MacDonald's model Eq. (5).Peleg's model Eq. (2) is based on the replacement of r (the growth rate) in Eq. (1) by a term that presumably accounts for the initial population and links the 'lag time', and 'maximum specific growth rate'in a predetermined relationship. Moreover, it is based on assuming the momentary growth rate might be proportional to $N(t)a$and to$[1-N(t)K]b$, where a is the growth regulator and b is the depletion factor, in order to overcome the difficulty that the logistic model does not account for at least some cell mortality that can occur at any time, including during the exponential growth stage. Also, we will be using MacDonald's model Eq. (5) with a type of delay known as distributed delay which is the sum of infinitely numerous small delays in the form of an integral. The model below uses both

previous models and adds a term with a decontamination rate. To develop a mathematical model of bacterial population growth using extended logistic growth model with distributed delay.

$$\frac{dN(t)}{dt} = rN(t)^a \left\{ 1 - \frac{N(t)}{K} \int_0^t N(s)\, G(t-s)\, ds \right\}^b - d\, N(t), \quad (6)$$

Table – 1 Following is the table of variable and parameters.

Symbols	Descriptions
N(t)	The bacterial population size at time t
r	The growth rate of bacteria
K	The carrying capacity
a	Growth regulator
b	Depletion factor
G (t-s)	The weight functions
d	The decontamination rate of bacteria
S	Delay term

Analysis at the reduced model:

Our model Eq (6) cannot be integrated analytically, therefore we will focus on the qualitative behavior of the solution.

First, we will analyze at the reduced model

$$\frac{dN(t)}{dt} = r\, N(t)^a \left\{ 1 - \frac{N(t)}{K} \right\}^b - d\, N \quad (7$$

Which is the reduced form of Eq. (6) under the assumption that there is no delay effect (i.e., G (t) =0 for all T€R). WE consider two cases.

Analysis at the reduced model case 1 : a=b=1 :

This will reduce the model Eq. (7) to the original logistic growth model Eq (1) with an additional decontamination term. In this case to determine the equilibrium solution we know the rate of change of the population will be equal to zero, so there are two equilibrium N*=0 and N*=K (1-d/r). Moreover, if we let f(x)=rN(t) [1-Nt/K]-dN, then asymptotic stability is determined by the sign of the derivative of f(x) evaluated at the equilibrium point. For example
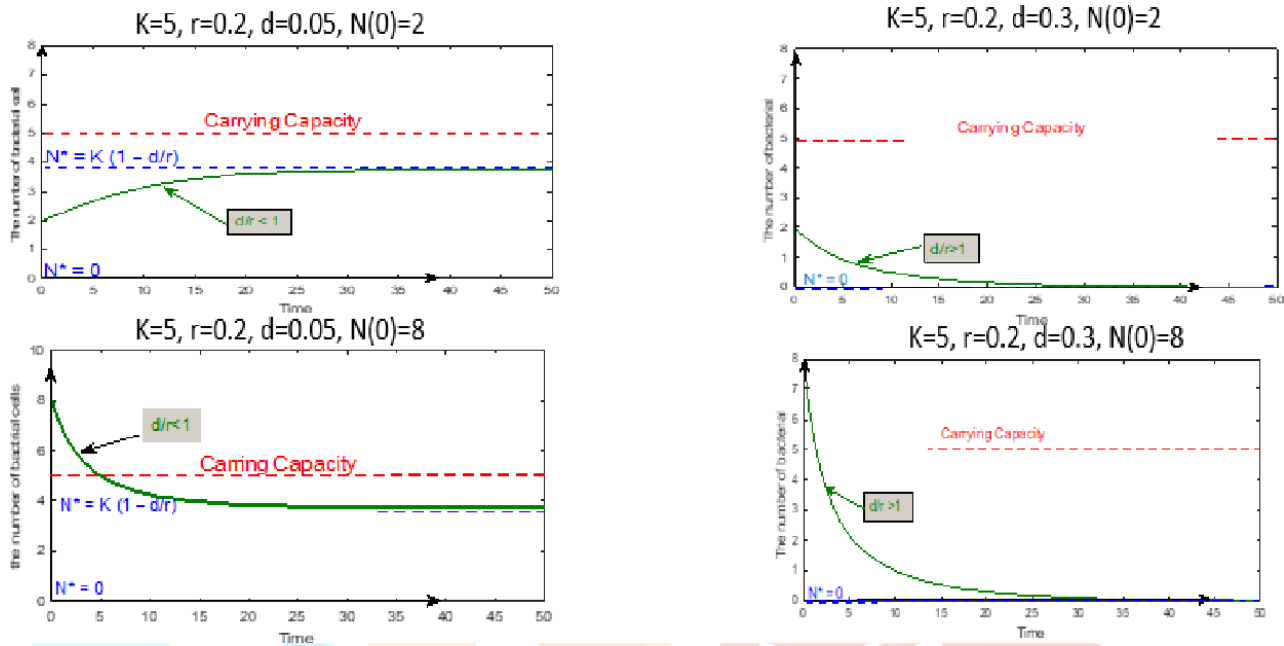

Fig.2: Numerical simulations of model (7). When a=b=1 d/r<1, and d/r >1.

From the Fig.2 the solution converges to zero, otherwise the solution reaches to the positive equilibrium.

For the biological interpretation we will summarize the equilibrium solution and their asymptotic stability with respect to the ration d/r in the following table- 2

Equilibrium	Condition	Out come	Biological Interpretation
N*=0	d/r > 1	Asymptotically stable	The bacterial population will go extinct
N*=0	d/r<1	Unstable	The bacterial population will establish
N*=K(1-d/r)	d/r>1	Impossible	No biological meaning
N*=K(1-d/r)	d/r<1	Asymptotically stable	The bacterial population will go extinct

Analysis at the reduced model case 2: a ≥0, b≥0

In this case the rate of change of the population equal to zero

$$r\, N(t)^{a} \left\{ 1 - \frac{N(t)}{K} \right\}^{b} - d\,N = 0$$

Imply, $Dn = rN(t)^a \left\{ 1 - \dfrac{N(t)}{K} \right\}^b \dfrac{}{} \, dN = 0$

As illustrated in Fig.2 the intersections of the line d N and the function

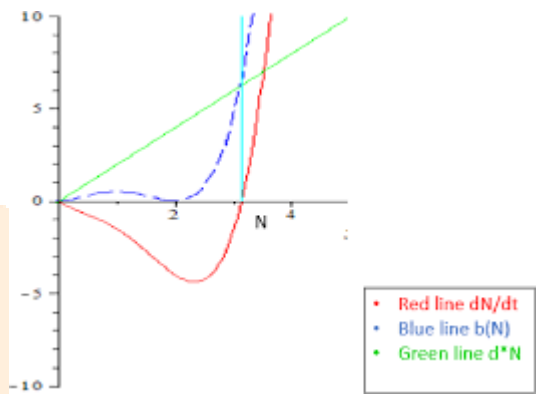b (N) = r N(t) ^{a} [1- N(t)/k] ^{b} are the equilibrium solution of the model.

Fig 3 : Numerical simulations of model (7). When a≥0 and b≥0

Moreover, if we let b (N) = rN(t)^a, and N* be an equilibrium solution of the model. Then by the derivative test the sign of b' (N*) –d determines the stability for N* . But note that b' (N*) is the slope of the b(N) at N* and d is the slope of the dN everywhere including N*. Hence, the difference between the slope of b (N) at each intersection point and the decontamination rate d determines the asymptotic stability of the equilibrium solution.

For additional analysis we will only consider four selected combinations of powers a and b which are (1) a>1 and b add ; (2) a>1 and b even ; (3) a≤ 1 and b odd; a≥ 1 and b even, those possible cases have been summarized in Fig 3, where survival or extinction –survial may occur based on the values of a&b.

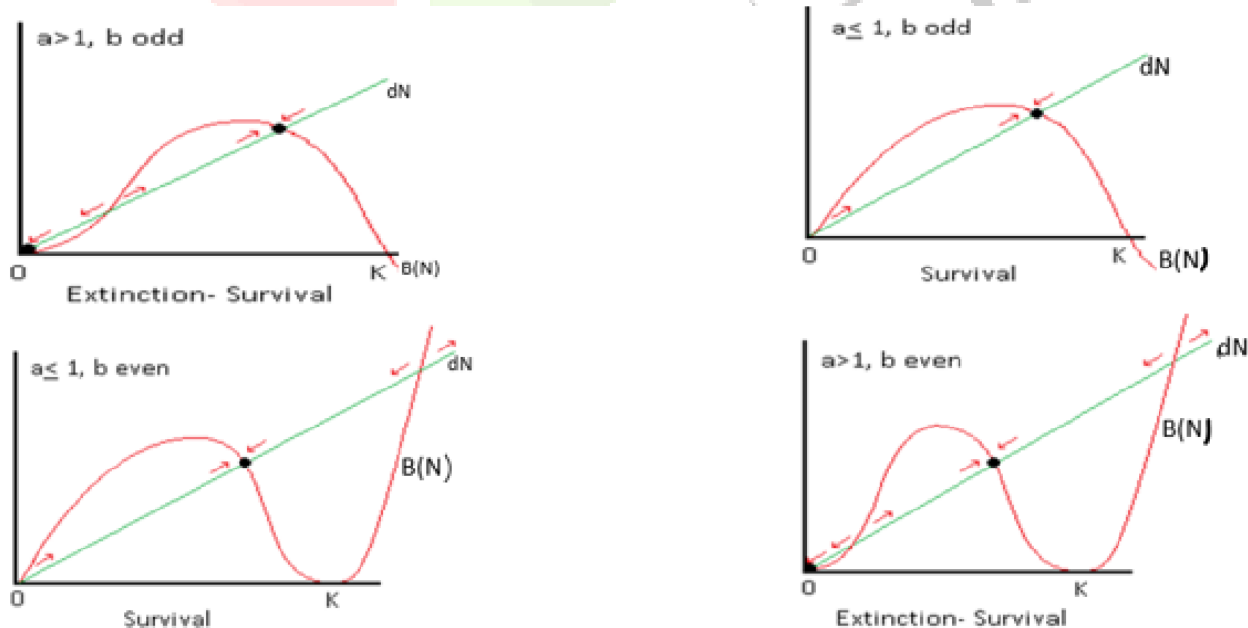Fig 4: Numerical simulations of model (7) when a>1 and b odd a>1 and b even ; a≤1 and b odd ≥1 and b even.

Table -3 For the biological interpretation we will summarize the equilibrium solution and their asymptotic stability in the following table:

Condition	Maximum Number of equilibrium	Out come	Biological Interpretation
a>1 b odd	Three	1. Stable 2. Unstable 3. Stable	The bacterial population will go extinct or survival depending on population initial number.
a≤1 b odd	Two	1. Unstable 2. stable	The bacterial population will survival
a≤1 b even	Thee	1. unstable 2. stable 3. Unstable	The bacterial population will survival
a>1 b even	Four	1. Stable 2. Unstable 3. Stable 4. Unstable	The bacterial population will go extinct or survival depending on population initial number

Conclusion : It is our goal to analyze the general model, using the same method provided in this paper , in a conclusion , analysis of delayed Logistic growth models can provide a mathematical frame work for a better understanding of bacterial growth and survival affected by different decontamination policies. Investigation of microbial growth provides excellent possibilities laboratory exercises, mathematical modeling , and model-based data analysis , application of mathematics proved to be very fruitful in getting deeper insight in to processes of microbial growth. The step-by-step modeling resulted in an extended model of the growth covering conventional lag and exponential and stationary phases. In contrast to known models (differential equations that can be solved only numerically), the present model expressed symbolically as a finite combination of elementary functions. The approach can be applied in other areas of modern biology and applied sciences.

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