



On a Logistic Differential Model. Some Applications

Nikolay Kyurkchiev¹ and Svetoslav Markov²

¹Faculty of Mathematics and Informatics,
University of Plovdiv Paisii Hilendarski,
24, Tzar Asen Str., 4000 Plovdiv, Bulgaria,
nkyurk@uni-plovdiv.bg,

²Institute of Mathematics and Informatics,
Bulgarian Academy of Sciences,
Acad. G. Bonchev Str., Bl. 8, 1113 Sofia, Bulgaria,
smarkov@bio.bas.bg

Abstract. In this article we will consider the possibility of approximating the input function $s(t)$ (the nutrient supply for cell growth) of the form $s(t) = \frac{1}{1+mt}e^{-mt}$ where $m > 0$ is parameter.

We prove upper and lower estimates for the one-sided Hausdorff approximation of the shifted Heaviside function $h_{t^*}(t)$ by means of the general solution of the differential equation $y'(t) = ky(t)s(t)$ with $y(t_0) = y_0$.

We will illustrate the evolution of the solution $y(t)$ for approximating and modelling of three data sets: i) "data on the development of the *Drosophila melanogaster* population", published by Pearl in 1920,, ii) dataStormIdentifications (Storm worm was one of the most biggest cyber threats of 2008, and "cancer data" [49]–[50].

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Numerical examples using *CAS Mathematica*, illustrating our results are given.

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1 Introduction

Sigmoidal functions find multiple applications to population dynamics, analysis of nutrient supply for cell growth in bioreactors, population survival functions, classical predator–prey models, debugging theory and others [19]–[47].

Evidently, the Verhulst model can be considered as a prototype of models used in bioreactor modelling. In batch growth, the rate of biomass production is given by $\frac{dx}{dt} = \kappa x$, where: x = biomass concentration; κ = specific growth rate; t = time.

The rate κ is a function of nutrient supply and therefore can be a function of time (i.e., if nutrient supply is changing with time).

In general, $\kappa = F(S, P, I, X, T, \textit{osmotic pressure})$; S = substrate concentration; P = product concentration; I = inhibitor concentration.

There, especially in the case of continuous bioreactor, the nutrient supply is considered as an input function $s(t)$ as follows:

$$\frac{dy(t)}{dt} = ky(t)s(t) \tag{1}$$

where s is additional specified.

To the role and choice of nutrient supply for cell growth in bioreactors are devoted to a number of studies [1]–[16].

Following the ideas given in [13], in this paper we consider the following differential model:

$$\begin{cases} \frac{dy(t)}{dt} = ky(t) \frac{1}{1+mt} e^{-mt} \\ y(t_0) = y_0 \end{cases} \quad (2)$$

where k and m are parameters.

We prove upper and lower estimates for the one-sided Hausdorff approximation of the shifted Heaviside function $h_{t^*}(t)$ by means of the general solution of this differential equation.

We will illustrate the advances of the solution $y(t)$ for approximating and modelling of:

- "data on the development of the *Drosophila melanogaster* population", published by biologist Raymond Pearl in 1920 (see, also Alpatov, Pearl [17]);
- *data_Storm_Identifications* [48], [47]);
- "cancer data" [49]–[50].

2 Preliminaries

Definition 1. *The shifted Heaviside step function is defined by*

$$h_{t^*}(t) = \begin{cases} 0, & \text{if } t < t^*, \\ [0, 1], & \text{if } t = t^*, \\ 1, & \text{if } t > t^*. \end{cases} \quad (3)$$

Definition 2. [18] *The Hausdorff distance (the H-distance) $\rho(f, g)$ between two interval functions f, g on $\Omega \subseteq \mathbb{R}$, is the distance between their completed graphs $F(f)$ and $F(g)$ considered as closed subsets of $\Omega \times \mathbb{R}$.*

More precisely,

$$\rho(f, g) = \max\left\{ \sup_{A \in F(f)} \inf_{B \in F(g)} \|A - B\|, \sup_{B \in F(g)} \inf_{A \in F(f)} \|A - B\| \right\}, \quad (4)$$

wherein $\|\cdot\|$ is any norm in \mathbb{R}^2 , e. g. the maximum norm $\|(t, x)\| = \max\{|t|, |x|\}$; hence the distance between the points $A = (t_A, x_A)$, $B = (t_B, x_B)$ in \mathbb{R}^2 is $\|A - B\| = \max(|t_A - t_B|, |x_A - x_B|)$.

3 Main Results

3.1 A New Model

The general solution of the differential equation (2) is of the following form:

$$y(t) = y_0 e^{\frac{ek}{m} Ei(-1-mt) - \frac{ek}{m} Ei(-1-mt_0)}, \quad (5)$$

where $Ei(\cdot)$ is the exponential integral function defined by

$$Ei(z) = - \int_{-z}^{\infty} \frac{e^{-t}}{t} dt$$

(for $z > 0$), where the principal value of the integral is taken.

It is important to study the characteristic - "supersaturation" of the model to the horizontal asymptote.

In this Section we prove upper and lower estimates for the one-sided Hausdorff approximation of the Heaviside step-function $h_{t^*}(t)$ by means of families (5).

Without loss of generality, we consider the following class of this family for:

$$t_0 = 0; \quad y_0 = e^{\frac{ek}{m} Ei(-1)}$$

$$M(t) = e^{\frac{ek}{m} Ei(-1-mt)}. \quad (6)$$

The function $M(t)$ and the "input function" $s(t)$ are visualized on Fig. 1.

Denoting by t^* the unique positive solution of the nonlinear equation:

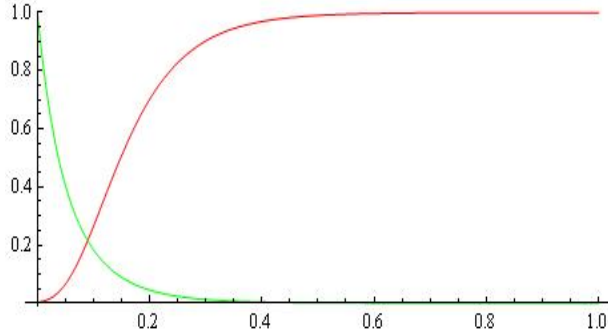


Figure 1: The functions $M(t)$ –(red) and $s(t)$ –(green) for $k = 100$; $m = 10$.

$$e^{\frac{ek}{m} Ei(-1-mt^*)} - \frac{1}{2} = 0. \quad (7)$$

The one–sided Hausdorff distance d between the function $h_{t^*}(t)$ and the sigmoid - (6) satisfies the relation

$$M(t^* + d) = 1 - d. \quad (8)$$

The following theorem gives upper and lower bounds for d

Theorem 1. Let

$$\begin{aligned} \alpha &= -\frac{1}{2}, \\ \beta &= 1 + \frac{k}{2} \frac{1}{1+mt^*} e^{-mt^*} \\ \gamma &= 2.1\beta. \end{aligned} \quad (9)$$

For the one–sided Hausdorff distance d between $h_{t^*}(t)$ and the sigmoid (6) the following inequalities hold for the condition: $\gamma > e^{1.05}$:

$$d_l = \frac{1}{\gamma} < d < \frac{\ln \gamma}{\gamma} = d_r. \quad (10)$$

Proof. Let us examine the function:

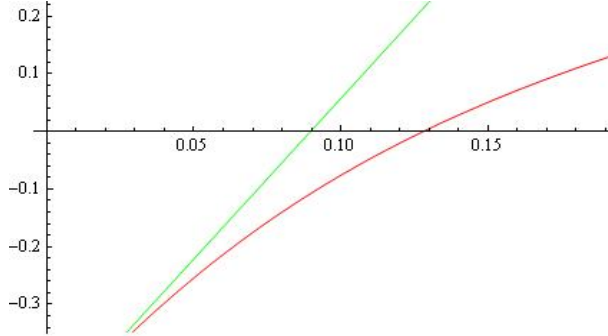


Figure 2: The functions $F(d)$ and $G(d)$ for $k = 100$; $m = 10$.

$$F(d) = M(t^* + d) - 1 + d. \quad (11)$$

From $F'(d) > 0$ we conclude that function F is increasing. Consider the function

$$G(d) = \alpha + \beta d. \quad (12)$$

From Taylor expansion we obtain $G(d) - F(d) = O(d^2)$. Hence $G(d)$ approximates $F(d)$ with $d \rightarrow 0$ as $O(d^2)$ (see Fig. 2). In addition $G'(d) > 0$. Further, for $\gamma > e^{1.05}$ we have

$$G(d_l) < 0; \quad G(d_r) > 0.$$

This completes the proof of the theorem.

Approximations of the $h_{t^*}(t)$ by model (6) for various k , m and L are visualized on Fig. 3–Fig. 4.

4 Some applications

The proposed model can be successfully used to approximating data from Population Dynamics, Debugging Theory and Theory of Computer Viruses Proppagation. .

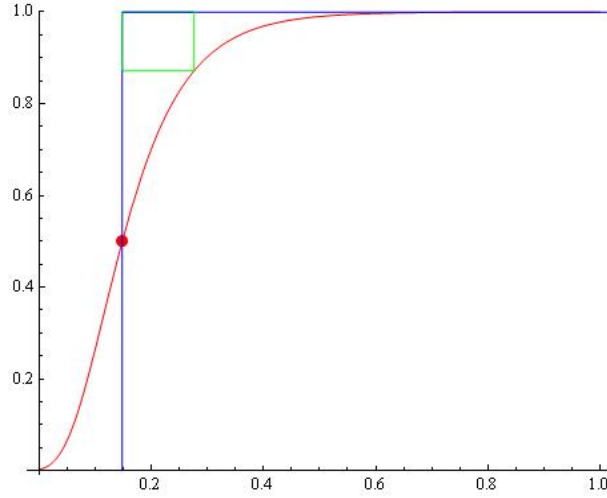


Figure 3: The model (6) for $k = 100$; $m = 10$; $t^* = 0.148284$; Hausdorff distance $d = 0.128078$; $d_l = 0.0854317$; $d_r = 0.210165$.

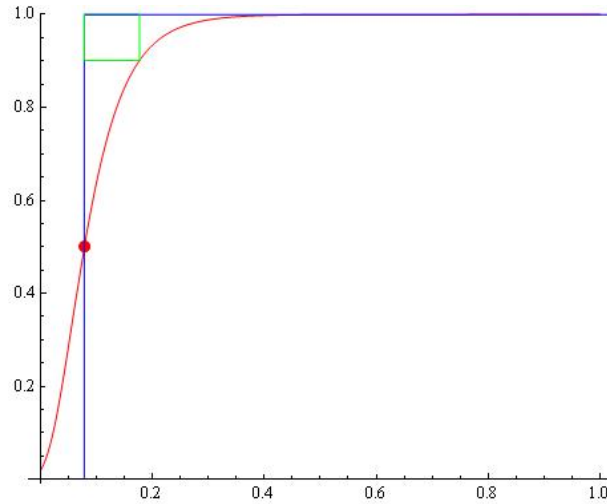


Figure 4: The model (6) for $k = 100$; $m = 15$; $t^* = 0.0786205$; Hausdorff distance $d = 0.0986342$; $d_l = 0.059118$; $d_r = 0.1672$.

4.1 Approximating the "data on the development of the *Drosophila melanogaster* population"

We will illustrate the advances of the solution $y(t)$ for approximating and modelling of "data on the development of the *Drosophila melanogaster* population", published by biologist Raymond Pearl in 1920 (see, also [17]).

We consider the following data:

data_Pearl

$:= \{\{9, 39\}, \{12, 105\}, \{15, 152\}, \{18, 225\}, \{21, 390\}, \{25, 547\},$
 $\{29, 618\}, \{33, 791\}, \{36, 877\}, \{39, 938\}\}.$

After that using the model

$$M^*(t) = \omega e^{\frac{ek}{m}} Ei(-1-mt)$$

for $\omega = 1040.42$, $k = 2.37757$ and $m = 0.09$ we obtain the fitted model (see, Fig. 5).

4.2 Approximating the *data_Storm_Identifications* [48], [47])

Storm worm was one of the most biggest cyber threats of 2008. In [48] are noticed particular periods during which their Storm specimen published different IDs every 10 minutes, that behavior cannot account for the very large number of IDs.

We analyze the following data:

data_Storm_Identifications $:=$

$\{\{1, 0.843\}, \{4, 0.926\}, \{5, 0.954\}, \{6, 0.967\}, \{7, 0.976\},$
 $\{8, 0.981\}, \{9, 0.985\}, \{10, 0.991\}, \{22, 0.995\}, \{38, 0.997\},$
 $\{51, 0.998\}, \{64, 0.9985\}, \{74, 0.999\}, \{83, 1\}, \{100, 1\}\}.$

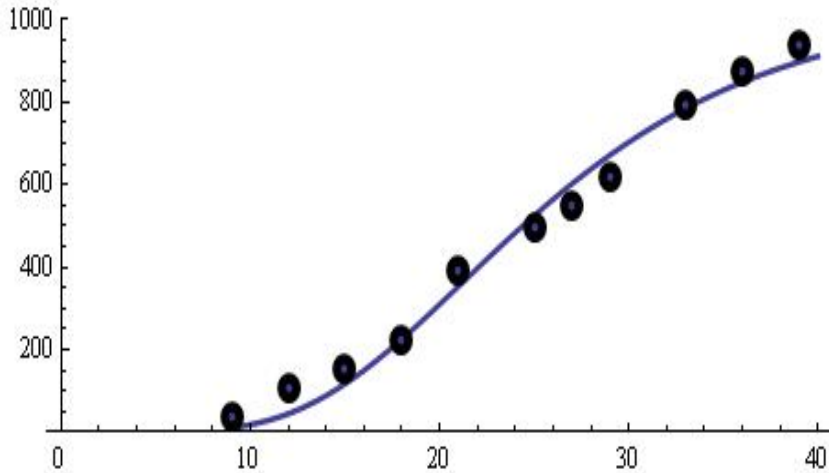


Figure 5: The fitted model $M^*(t)$.

After that using the model $M^*(t)$ for $\omega = 1$, $k = 0.0583363$ and $m = 0.169$ we obtain the fitted model (see, Fig. 6).

4.3 Application of the new cumulative sigmoid for analysis of the "cancer data"

We will illustrate the advances of the modified inverse Rayleigh cumulative sigmoid for approximation and modelling of "cancer data" (for some details see, [49]–[50]).

<i>days</i>	4	7	10	12	14	17	19	21
$R(t)$	0.415	0.794	1.001	1.102	1.192	1.22	1.241	1.3

Table 1: The "cancer data" [49]–[50]

The model $M^*(t)$ based on the data from Table 1 for the estimated parameters:

$$\omega = 1.38611; m = 0.13; k = 0.522489$$

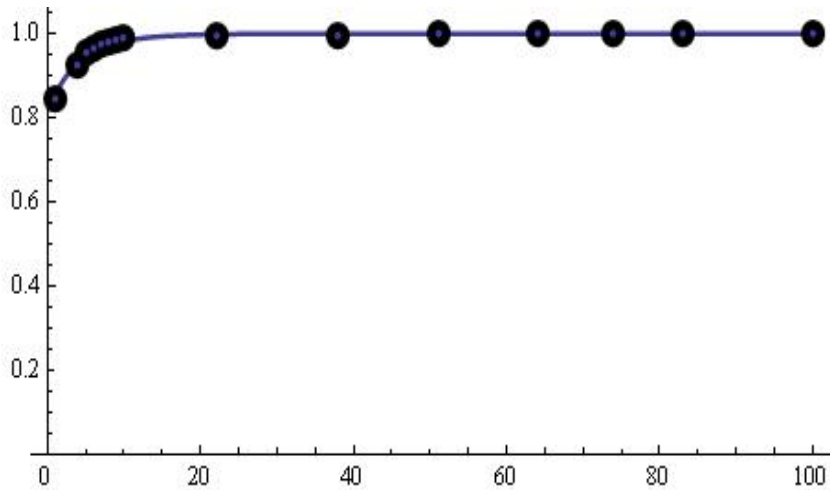


Figure 6: The fitted model $M^*(t)$.

is plotted on Fig. 7.

As should be expected, the experiments conducted (see, Sections 4.1 - 4.3) show a very good approximation of data from the field of population dynamics and computer viruses propagation, with suggested in this article, modified logistic model.

5 Conclusion.

A special choice of nutrient supply for cell growth in a continuous bioreactor is introduced.

We prove upper and lower estimates for the one-sided Hausdorff approximation of the shifted Heaviside function $h_{t^*}(t)$ by means of the general solution of the differential equation $y'(t) = ky(t)s(t)$ with $y(t_0) = y_0$, where $s(t) = \frac{1}{1+mt}e^{-mt}$.

We propose a software module within the programming environment *CAS Mathematica* for the analysis of the considered family of functions.

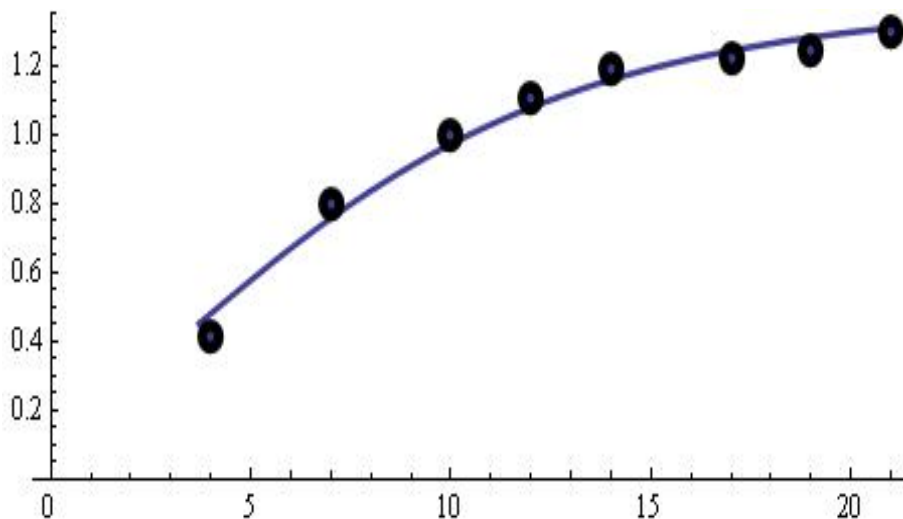


Figure 7: The model $M^*(t)$ based on the "cancer data".

The module offers the following possibilities:

- calculation of the H-distance between the h_{t^*} and the model $M(t)$ (6);
- generation of the functions under user defined values of the parameters k and m ;
- numerical solution of the differential model (2) and opportunities for comparison with other logistics models;
- software tools for animation and visualization.

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