

ON THE HALF-LOGISTIC MODEL WITH "POLYNOMIAL
VARIABLE TRANSFER". APPLICATION TO APPROXIMATE
THE SPECIFIC "DATA CORONA VIRUS"

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ABSTRACT: Verhulst model [1] makes an extensive use of the logistic sigmoidal function $S(t) = \frac{a}{1+e^{-kt}}$. Studying "Canteloup growth", Pearl et al. [2]–[3] empirically found that one should generalize the logistic map in order to reproduce better the data. The Half-Logistic cumulative sigmoid can be written as $x(t) = \frac{1-e^{-kt}}{1+e^{-kt}}$. We consider a new class of growth curves, generated by reaction networks, based on the insertion of "correcting amendments" of polynomial-type: $M(t) = \frac{1-e^{-F(t)}}{1+e^{-F(t)}}$ where $F(t) = \sum_{i=0}^n a_i t^i$. We will call this family the "**Half-Logistic curve of growth with polynomial variable transfer**" (**HLCGPVT**). The new coronavirus [28], SARS-CoV-2, is the reason for a new disease, Covid-19. Below we look at some comparisons between the Verhulst model and the new model (HLCGPVT), as well as the ability to approximate specific population dynamics data, including "Data Corona Virus". Illustrating our results the following datasets are fitted [27] using *CAS MATHEMATICA*: "Corona virus–Total Deaths" and "Corona virus–Total Deaths"- up to: 15.03.2020, 21.03.2020, 25.03.2020; Total Coronavirus Cases in China (22.01.2020 – 16.03.2020); Total Coronavirus Cases in Bulgarian (8.03.2020 – 28.03.2020).

AMS Subject Classification: 41A46

Key Words: Verhulst logistic model, Half-Logistic curve of growth with polynomial variable transfer, Heaviside step-function, Hausdorff distance

Received: April 1, 2020

Revised: April 3, 2020

Published: April 5, 2020

doi: 10.12732/ijdea.v19i1.4

Academic Publications, Ltd.

<https://acadpubl.eu>

1. INTRODUCTION

Verhulst model [1] makes an extensive use of the logistic sigmoidal function

$$s(t) = \frac{a}{1 + e^{-kt}}. \quad (1)$$

Studying "Canteloup growth", Pearl et al. [2]–[3] empirically found that one should generalize the logistic map in order to reproduce better the data. Rather than the mere logistic, they propose a form like

$$y(t) = \frac{r}{1 + e^{a_0 + a_1 t + a_2 t^2 + \dots}},$$

where y , is the number of seedlings of the canteloups. An extensive overview on the topic can be found in [4], see also [5]–[6]).

The logistic model is generated by the following reaction network:



where $k = \text{const}$. In [7] we consider the reaction network



where $k(t) = \sum_{i=0}^n b_i t^i$. For example, let $n = 2$. Reaction network (3) induces the following differential system

$$\begin{cases} \frac{ds}{dt} = -(b_0 + b_1 t + b_2 t^2) s x \\ \frac{dx}{dt} = (b_0 + b_1 t + b_2 t^2) x s. \end{cases} \quad (4)$$

with $s(0) = s_0$; $x(0) = x_0$. For $s(0) = s_0 = \frac{1}{2}$; $x(0) = x_0 = \frac{1}{2}$ from $s' + x' = 0$ we get $s + x = C$, $C = s_0 + x_0 = 1$ and

$$\begin{cases} \frac{ds}{dt} = -(b_0 + b_1 t + b_2 t^2) s(1 - s) \\ \frac{dx}{dt} = (b_0 + b_1 t + b_2 t^2) x(1 - x). \end{cases} \quad (5)$$

Hence, the new model can be written in the form:

$$s(t) = \frac{e^{-(b_0 t + \frac{b_1}{2} t^2 + \frac{b_2}{3} t^3)}}{1 + e^{-(b_0 t + \frac{b_1}{2} t^2 + \frac{b_2}{3} t^3)}}; \quad x(t) = \frac{1}{1 + e^{-(b_0 t + \frac{b_1}{2} t^2 + \frac{b_2}{3} t^3)}}. \quad (6)$$

Apparently, for arbitrary n we have

$$s(t) = \frac{e^{-(b_0t + \frac{b_1}{2}t^2 + \dots + \frac{b_n}{n+1}t^{n+1})}}{1 + e^{-(b_0t + \frac{b_1}{2}t^2 + \dots + \frac{b_n}{n+1}t^{n+1})}}; \quad x(t) = \frac{1}{1 + e^{-(b_0t + \frac{b_1}{2}t^2 + \dots + \frac{b_n}{n+1}t^{n+1})}}. \quad (7)$$

The Half-Logistic cumulative sigmoid can be written as

$$x(t) = \frac{1 - e^{-kt}}{1 + e^{-kt}}. \quad (8)$$

In this paper we consider a class of Half-Logistic growth curves, generated by reaction networks, based on the insertion of "correcting amendments" of polynomial-type.

2. MAIN RESULTS

1. Formally, we will define the following class of growth curves:

$$M(t) = \frac{1 - e^{-F(t)}}{1 + e^{-F(t)}} \quad (9)$$

where

$$F(t) = \sum_{i=0}^n a_i t^i. \quad (10)$$

We will call this family the "**Half-Logistic curve of growth with formally polynomial variable transfer**" (**HLCGFPVT**).

The question of finding precise two-sided estimates for the magnitude of the Hausdorff approximation [8] of the Heaviside function with classes of the indicated family $M(t)$ remains open.

The task is greatly complicated by the intrinsic properties of the generated class of functions, as well as by the type and location of zeros of polynomial $F(t)$.

Methods for simultaneous approximation of all roots of a given polynomial of degree n can be found in [11]–[12].

Below we look at some comparisons between the Half-Logistic model and the new model (HLCGFPVT), as well as the ability to approximate specific population dynamics data.

Some comparisons between Half-Logistic model $x(t)$ - (8) and the model (HLCGFPVT) - (9) are visualized on Fig. 1.

Let us consider the our new model with fixed $a_0 = 0$. In this case we will call this family the "**Half-Logistic curve of growth with polynomial variable transfer**" (**HLCGPVT**).

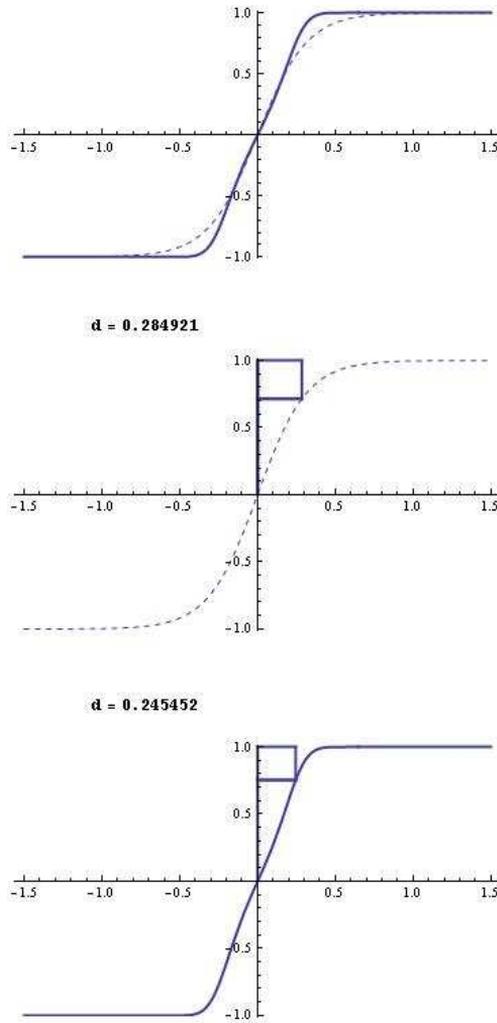


Figure 1: a) Comparison between Half-Logistic model $x(t)$ - (8) – (dashed) and model (HLCGFPVT) - (thick) at fixed $k = 6.3$, $n = 4$, $a_0 = -0.002$, $a_1 = 5.1$, $a_2 = -0.1$, $a_3 = 48.9$, $a_4 = -0.01$; b) Hausdorff distance $d = 0.284921$ for the model (8); c) Hausdorff distance $d = 0.245452$ for the model (9).

Example 1. We will show how it can be modelled data in [9] for Malicious and High-Risk Android App Volume Growth, see Fig. 2.

$$\begin{aligned} \text{Malicious_data} &:= \{ \{1, 11000\}, \{2, 21000\}, \{3, 28000\}, \\ &\{4, 41000\}, \{5, 156000\}, \{6, 175000\} \} \end{aligned}$$

The fitted model $M^*(t) = \omega M(t)$ for $n = 8$, $\omega = 175000$ and $a_1 = 0.0752877$; $a_2 = 0.0525465$; $a_3 = 0.0203803$; $a_4 = -0.0131301$; $a_5 = -0.022312$; $a_6 = 0.0168824$; $a_7 =$

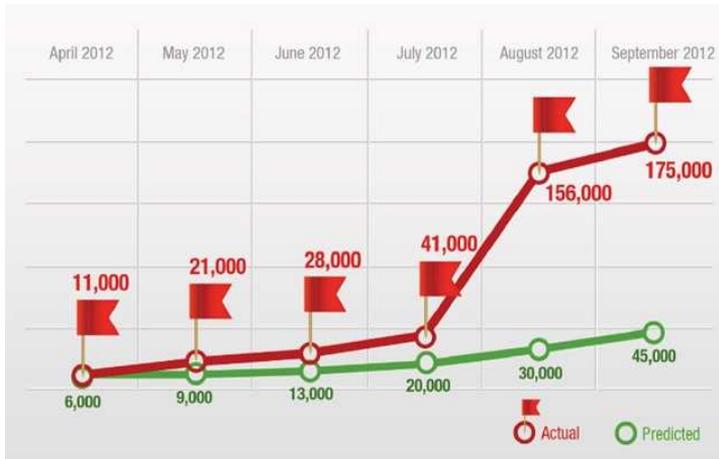


Figure 2: Malicious and High-Risk Android App Volume Growth [9].

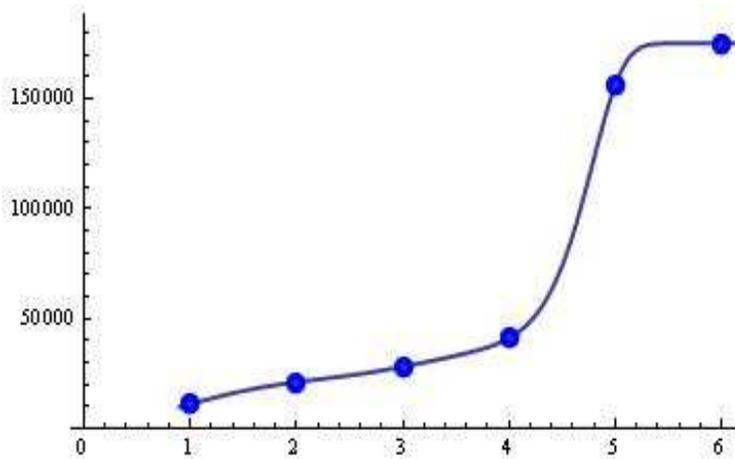


Figure 3: The fitted model $M^*(t) = \omega M(t)$ for the data in Fig. 2.

-0.00411904 ; $a_8 = 0.000344485$ is depicted on Fig. 3.

Example 2. We analyze the following data

data_Paecilomyces_Sinclairii_Ascomycota :=
 $\{\{0.5, 0.625\}, \{0.75, 3.125\}, \{1, 5.417\}, \{1.25, 7.5\}, \{1.5, 11.25\},$
 $\{1.75, 16.875\}, \{2, 17.5\}, \{2.25, 23.75\}, \{2.5, 30.833\}, \{2.75, 31.771\},$
 $\{3.25, 31.25\}, \{3.5, 32.292\}, \{3.75, 32.708\}, \{4.25, 31.771\}\}$

The fitted models $M^*(t) = \omega M(t)$ for $n = 4$; $\omega = 32.1935$, $a_1 = -0.721707$; $a_2 =$

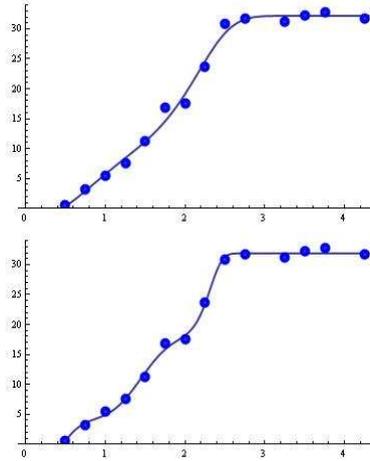


Figure 4: The fitted model $M^*(t) = \omega M(t)$ for the data *Paecilomyces_Sinclairii_Ascomycota* ; a) $n = 4$; b) $n = 6$.

-2.16146 ; $a_3 = -1.43265$; $a_4 = 0.351626$ and for $n = 6$; $\omega = 31.8907$, $a_1 = -4.72847$; $a_2 = 21.7584$; $a_3 = -36.2242$; $a_4 = 28.7694$; $a_5 = -10.8188$; $a_6 = 1.55322$ are depicted on Fig. 4

We conclude that, the proposed model $M(t)$ has some free parameters leading to greater flexibility in modeling various data types.

Example 3. We will demonstrate this with another example - approximating the specific "Cancer Stem Cell data" (see, [10]):

Empirical_cdf :=

$\{ \{0.3253, 0\}, \{0.58, 0\}, \{0.5964, 0.013\}, \{0.73, 0.013\}, \{0.747, 0.031\},$
 $\{0.76, 0.031\}, \{0.7711, 0.048\}, \{0.79, 0.048\}, \{0.91, 0.084\},$
 $\{0.9277, 0.093\}, \{1.035, 0.1022\}, \{1.036, 0.111\}, \{1.11, 0.1289\},$
 $\{1.127, 0.1422\}, \{1.23, 0.1422\}, \{1.3012, 0.2356\}, \{1.3614, 0.2356\},$
 $\{1.4819, 0.2844\}, \{1.5422, 0.4756\}, \{1.6084, 0.5244\}, \{1.6386, 0.6178\},$
 $\{1.699, 0.7911\}, \{1.7831, 0.8756\}, \{1.8916, 0.9511\}, \{2.006, 0.9822\},$
 $\{2.2349, 0.9822\}, \{2.241, 1\}, \{2.4458, 1\} \}$.

After that using the model $M^*(t) = \omega M(t)$ for $n = 4$; $\omega = 1/00042$, $a_1 = -1.53012$; $a_2 = -5.22393$; $a_3 = -5.44352$; $a_4 = 1.9267$ and for $n = 5$; $\omega = 0.9866624$, $a_1 = 1.31229$; $a_2 =$

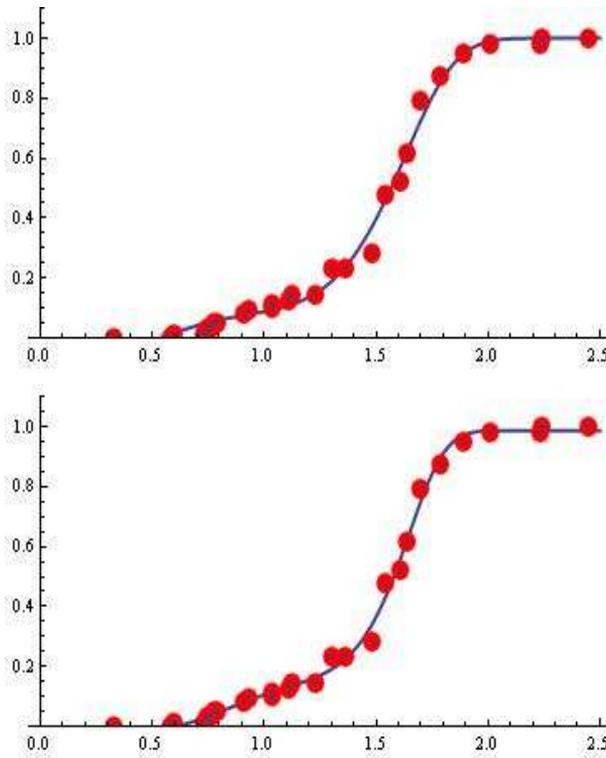


Figure 5: The fitted model $M^*(t) = \omega M(t)$ for the data *Empirical_cdf*; a) $n = 4$; b) $n = 5$.

-7.64499 ; $a_3 = 14.7455$; $a_4 = -11.2552$; $a_5 = 3.05828$ we obtain the fitted models (see, Fig. 5).

Example 4. Approximation of the data "Corona virus–Total Deaths" [27].

The new coronavirus [28], SARS-CoV-2, is the reason for a new disease, Covid-19. Up to now it is not exactly sure how SARS-CoV-2 is spread. The new virus is part of the coronavirus family which includes the common cold and SARS. These viruses are spread by cough and sneeze droplets.

For the data "Corona virus–Total Deaths"- 15.03.2020 [27] (see, Fig. 6) the fitted model $M^*(t)$ for

$$n = 7, \omega = 8000, a_1 = 0.0869701, a_2 = -0.0813959, a_3 = 0.0121497,$$

$$a_4 = -0.0510479, a_5 = 0.0152609, a_6 = -0.003324, a_7 = 0.000310136$$

is depicted on Fig. 7.

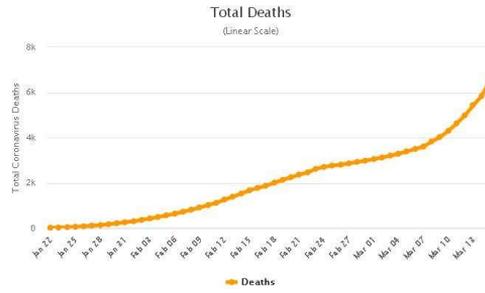


Figure 6: Total Deaths - 15.03.2020 [27].

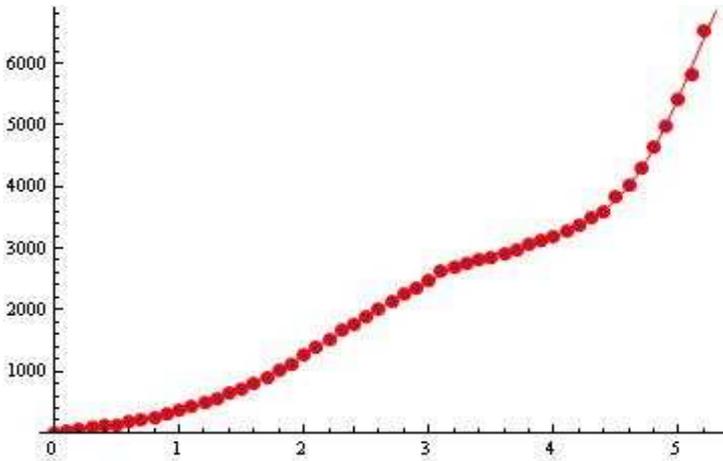


Figure 7: The fitted model $M^*(t)$ ($n = 7$, $\omega = 8000$, $a_1 = 0.0869701$, $a_2 = -0.0813959$, $a_3 = 0.0121497$, $a_4 = -0.0510479$, $a_5 = 0.0152609$, $a_6 = -0.003324$, $a_7 = 0.000310136$) for the data "Corona virus-Total Deaths"- 15.03.2020.

For the data "Corona virus-Total Cases"- 15.03.2020 [27] (see, Fig. 8) the fitted model $M^*(t)$ for

$$n = 7, \omega = 310000, a_1 = 0.157458, a_2 = -0.415101,$$

$$a_3 = 0.575543, a_4 = -0.297136, a_5 = 0.073664,$$

$$a_6 = -0.00901115, a_7 = 0.000446717$$

is depicted on Fig. 9.

For the data "Corona virus-Total Deaths"- 21.03.2020 [27] (see, Fig. 10) the fitted

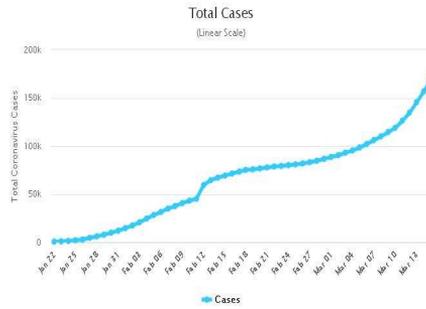


Figure 8: Total Cases - 15.03.2020 [27].

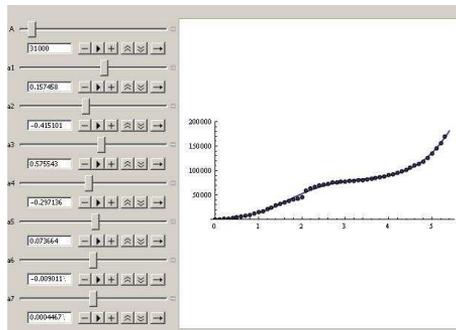


Figure 9: The fitted model $M^*(t)$ for the data "Corona virus–Total Cases"- 15.03.2020.

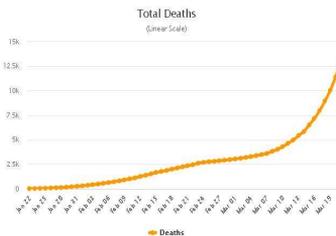


Figure 10: Total Deaths - 21.03.2020 [27].

model $M^*(t)$ for

$$n = 7, \omega = 15400, a_1 = 0.146886, a_2 = -0.394889, a_3 = 0.480165,$$

$$a_4 = -0.25367, a_5 = 0.0698155, a_6 = -0.00987805, a_7 = 0.000570169$$

is depicted on Fig. 11.

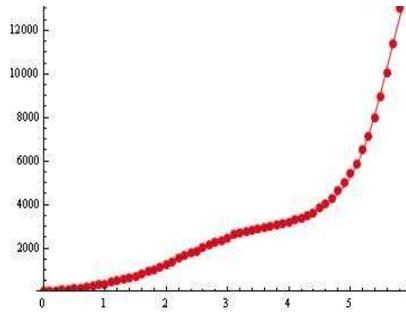


Figure 11: The fitted model $M^*(t)$ ($n = 7$, $\omega = 15400$, $a_1 = 0.146886$, $a_2 = -0.394889$, $a_3 = 0.480165$, $a_4 = -0.25367$, $a_5 = 0.0698155$, $a_6 = -0.00987805$, $a_7 = 0.000570169$) for the data "Corona virus-Total Deaths"- 21.03.2020.

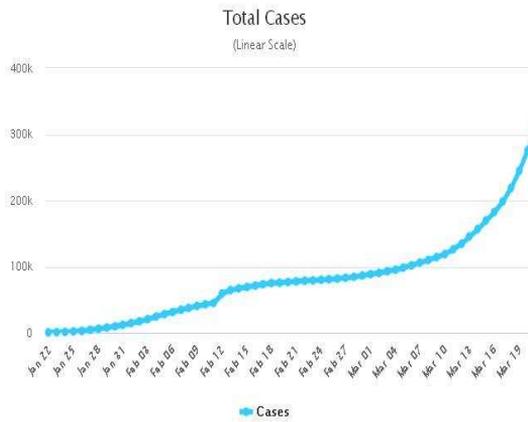


Figure 12: Total Cases - 21.03.2020 [27].

For the data "Corona virus-Total Cases"- 21.03.2020 [27] (see, Fig. 12) the fitted model $M^*(t)$ for

$$n = 7, \omega = 420000, a_1 = 0.177205, a_2 = -0.520648,$$

$$a_3 = 0.683653, a_4 = -0.364756, a_5 = 0.0957228,$$

$$a_6 = -0.012417, a_7 = 0.000642424$$

is depicted on Fig. 13.

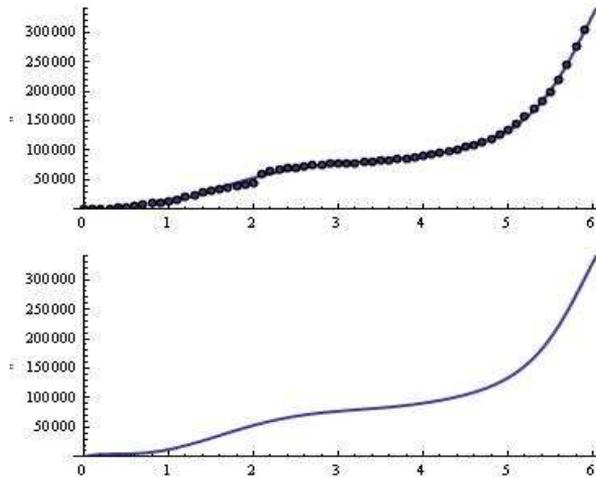


Figure 13: The fitted model $M^*(t)$ for the data "Corona virus-Total Cases"- 21.03.2020.

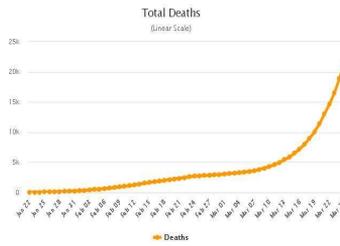


Figure 14: Total Deaths - 25.03.2020 [27].

For the data "Corona virus-Total Deaths"- 25.03.2020 [27] (see, Fig. 14) the fitted model $M^*(t)$ for

$$n = 7, \omega = 23440, a_1 = 0.17055, a_2 = -0.495183, a_3 = 0.571664,$$

$$a_4 = -0.295082, a_5 = 0.0781644, a_6 = -0.010426, a_7 = 0.000558001$$

is depicted on Fig. 15.

For the data "Corona virus-Total Cases"- 25.03.2020 [27] (see, Fig. 16) the fitted model $M^*(t)$ for

$$n = 7, \omega = 620000, a_1 = 0.117151, a_2 = -0.336726,$$

$$a_3 = 0.43737, a_4 = -0.22924, a_5 = 0.0588024,$$

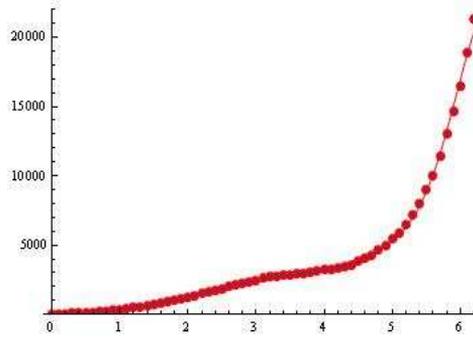


Figure 15: The fitted model $M^*(t)$ ($n = 7, \omega = 23440, a_1 = 0.17055, a_2 = -0.495183, a_3 = 0.571664, a_4 = -0.295082, a_5 = 0.0781644, a_6 = -0.010426, a_7 = 0.000558001$) for the data "Corona virus-Total Deaths"- 25.03.2020.

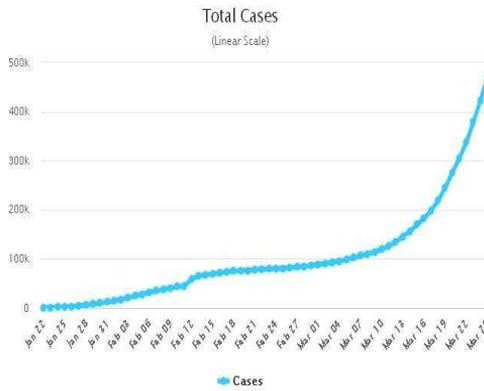


Figure 16: Total Cases - 25.03.2020 [27].

$$a_6 = -0.00743038, a_7 = 0.000374042$$

is depicted on Fig. 17.

From the attached graph, it can be seen that at the degree of the polynomial $n = 7$, some specific distortions typical of the model analyzed are very well approximated.

Total Coronavirus Cases in China (22.01.2020 – 16.03.2020)

For the data "Total Coronavirus Cases in China (22.01.2020 – 16.03.2020) [27] (see, Fig. 18) the fitted model $HLM(t)$ for

$$n = 5, A = 81000, a_1 = 0.076611, a_2 = 0.189088, a_3 = -0.022776,$$

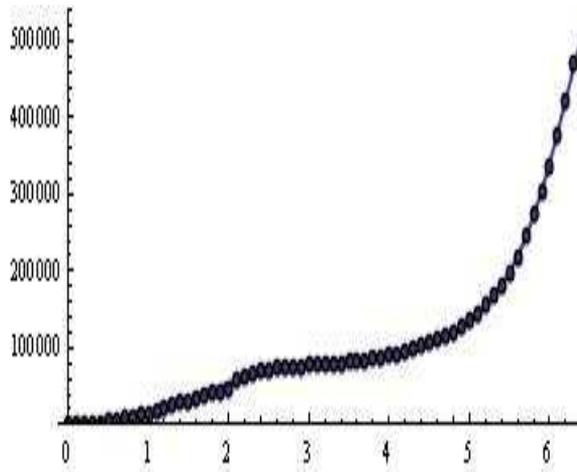


Figure 17: The fitted model $M^*(t)$ for the data "Corona virus-Total Cases"-25.03.2020.

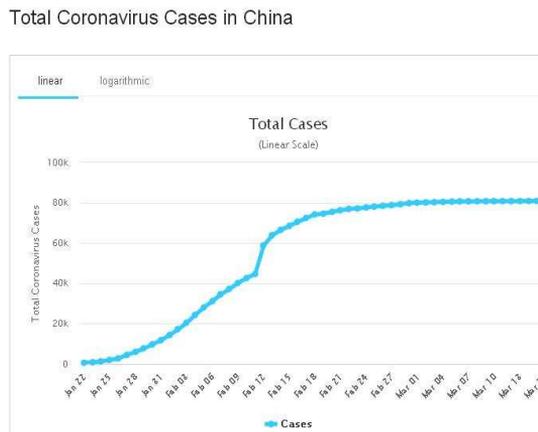


Figure 18: Total Coronavirus Cases in China (22.01.2020 – 16.03.2020) [27].

$$a_4 = 0.0573498, a_5 = -0.00981958$$

is depicted on Fig. 19.

Total Coronavirus Cases in Bulgarian (8.03.2020 – 28.03.2020)

For the data "Total Coronavirus Cases in Bulgaria (8.03.2020 – 28.03.2020) the fitted model $HLM(t)$ for

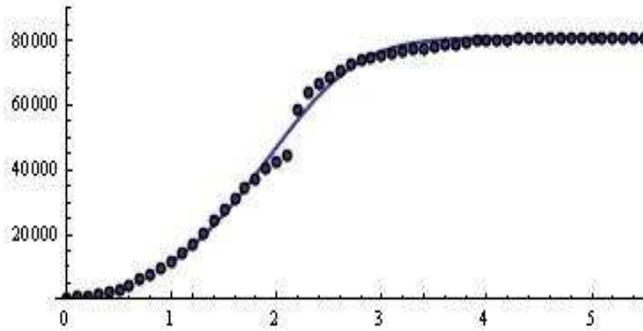


Figure 19: The fitted model $HLM(t)$ ($n = 5$, $A = 81000$, $a_1 = 0.076611$, $a_2 = 0.189088$, $a_3 = -0.022776$, $a_4 = 0.0573498$, $a_5 = -0.00981958$) for the data "Total Coronavirus Cases in China (22.01.2020 – 16.03.2020)".

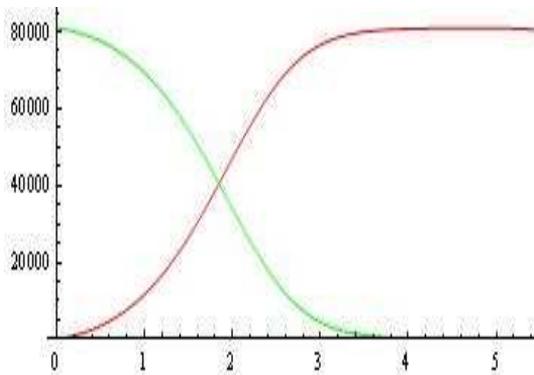


Figure 20: The solutions $HLM(t)$ and $S(t)$ of the "reaction differential system" yielding Half-Logistic model.

$$n = 7, A = 560, a_1 = 9.83785, a_2 = -33.5389, a_3 = 46.1045,$$

$$a_4 = -32.8261, a_5 = 12/8295, a_6 = -2.60911, a_7 = 0.215908$$

is depicted on Fig. 21.

A detailed discussion of the topic the reader can find in the monographic study [31].

For other results, see [13]–[26], [29]–[30].

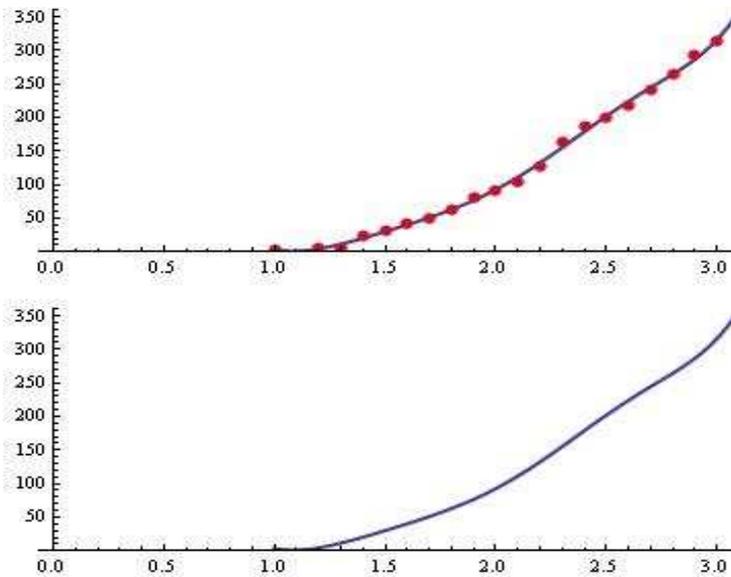


Figure 21: The fitted model $HLM(t)$.

ACKNOWLEDGMENTS

This paper is supported by the National Scientific Program "Information and Communication Technologies for a Single Digital Market in Science, Education and Security (ICTinSES)", financed by the Ministry of Education and Science.

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