

Comments on the Half Logistic Inverse Rayleigh (HLIR) cdf with “Polynomial Variable Transfer”. Some Applications

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Abstract: *On the base of the Half Logistic – G family of distributions proposed by Cordeiro, Alizadeh and Marinho [2] some mathematical properties are investigated by Almarashi et al. [1]. We study the “saturation” to the horizontal asymptote: $t=1$ by the new growth function $M(t)$ in the Hausdorff sense. Similar to our previous studies [3-6], in this article we will define and analyze in detail the new family. We will call this family the “Half-Logistic-Inverse-Rayleigh cdf with Polynomial Variable Transfer” (HLIRPVT) cdf. Section 3 shows the potentiality of proposed new model under four real data sets. Some numerical examples using CAS MATHEMATICA are given.*

Keywords: *Half-Logistic-Inverse-Rayleigh (HLIR) cdf, Half-Logistic-Inverse-Rayleigh cdf with Polynomial Variable Transfer (HLIRPVT) cdf, “Saturation” in Hausdorff sense, Hausdorff distance, Upper and lower bounds.*

1. Introduction and preliminaries

Definition 1. In [1] authors proposed the following new Half-Logistic-Inverse-Rayleigh (HLIR) cdf:

$$(1) \quad M(t) = \frac{1 - \left(1 - e^{-\left(\frac{\alpha}{t}\right)^2}\right)^\lambda}{1 + \left(1 - e^{-\left(\frac{\alpha}{t}\right)^2}\right)^\lambda},$$

where $t > 0, \alpha > 0, \lambda > 0$, and proved the following inequalities for any, $t, \alpha, \lambda > 0$:

$$(2) \quad M_{**}(t) < M(t) < M_*(t),$$

$$M_*(t) = 1 - \left(1 - e^{-\left(\frac{\alpha}{t}\right)^2} \right)^\lambda; \quad M_{**}(t) = \frac{t^{2\lambda}}{t^{2\lambda} + \alpha^{2\lambda}} M_*(t),$$

where $M_*(t)$ is the Exponentiated Inverted Rayleigh cdf, and $M_{**}(t)$ is a weighted version of it, which remains a valid cdf.

During the last two decades or so, various approaches of determining new families of distributions have been introduced for increasing chances of modeling practical data that come from a wide variety of disciplines.

The reader can find a detailed bibliography in article [7].

In this paper we study some properties of the new family.

When studying the intrinsic properties of the $M(t)$, it is also appropriate to study the “saturation” to the horizontal asymptote.

Definition 2. Similar to our previous studies [3-6], in this article we will define and analyze in detail the following new family:

$$(3) \quad M_1(t; a_1, \dots, a_n) = \frac{1 - \left(1 - e^{-\left(\frac{\alpha}{F(t)}\right)^2} \right)^\lambda}{1 + \left(1 - e^{-\left(\frac{\alpha}{F(t)}\right)^2} \right)^\lambda},$$

$$F(t) = \sum_{i=1}^n a_i t^i.$$

We will call this family the “Half-Logistic-Inverse-Rayleigh cdf with Polynomial Variable Transfer” (HLIRPVT) cdf.

The rest of the paper is structured as follows. In Section 2 we study the “saturation” to the horizontal asymptote: $t = 1$ by the growth functions (1) and (3) in the Hausdorff sense [19].

Section 3 shows the potentiality of proposed new model based on the insertion of “correcting amendments” of polynomial-type (3) for the estimation procedure under two real data sets.

2. Main results

1. For the “saturation” d_1 to the horizontal asymptote: $t = 1$ by the growth function (1) in the Hausdorff sense we have

$$(4) \quad M(d_1) = \frac{1 - \left(1 - e^{-\left(\frac{\alpha}{d_1}\right)^2}\right)^\lambda}{1 + \left(1 - e^{-\left(\frac{\alpha}{d_1}\right)^2}\right)^\lambda} = 1 - d_1,$$

or, equivalently,

$$(5) \quad G(d_1) := \frac{1}{\left(1 - e^{-\left(\frac{\alpha}{d_1}\right)^2}\right)^\lambda} + 1 - \frac{2}{d_1} = 0.$$

The following theorem gives upper bound for d_1 .

Theorem 1. The “saturation” d_1 satisfies the following inequality for $\alpha > 0, \lambda > 0$:

$$(6) \quad d_1 < \left(2\alpha^{2\lambda}\right)^{\frac{1}{1+2\lambda}} := d_{1,r}.$$

Proof: We consider the interval $[0, +\infty)$.

Clearly, $G' > 0$ and $G(t)$ is increasing function of $t \in [0, +\infty)$ (Fig. 1).

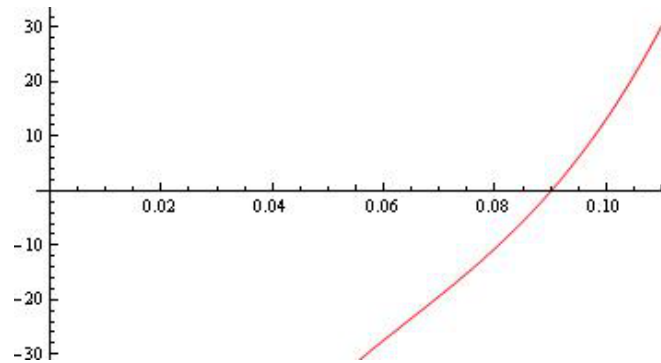


Fig. 1. The function G for $\lambda = 2.3$ and $\alpha = 0.05$; the “saturation” $d_1 = 0.090098$

Hence, if (5) has a root, then it is unique.

Using the inequalities

$$1 \leq 1 + \left(1 - e^{-\left(\frac{\alpha}{t}\right)^2}\right)^\lambda < 1 + \left(\frac{\alpha}{t}\right)^{2\lambda}; \quad e^\beta \geq 1 + \beta, \quad \beta \in \mathbb{R},$$

we have

$$G(d_1) > \left(\frac{d_1}{\alpha}\right)^{2\lambda} - \frac{2}{d_1} = \frac{d_1^{2\lambda+1} - 2\alpha^{2\lambda}}{\alpha^{2\lambda} d_1}.$$

The positive root of the expression in the numerator is

$$\left(2\alpha^{2\lambda}\right)^{\frac{1}{1+2\lambda}} := d_{1,r},$$

Then $G(d_{1,r}) > 0$.

This completes the proof of the theorem.

2. The one-sided Hausdorff distance d between the Heaviside function $h_{t_0}(t)$ and the model (1) satisfies the relation

$$(7) \quad M(t_0 + d) = 1 - d,$$

where t_0 is the “median level”, i.e., $M(t_0) = \frac{1}{2}$. Some computational examples using model (1) are presented in Figs 2 and 3.

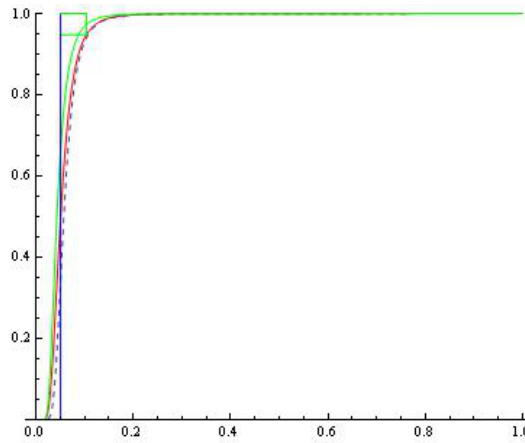


Fig. 2. The model (1) and two-sided estimations (2) for fixed $\alpha = 0.05$, $\lambda = 2.3$, and $t_0 = 0.0508144$, Hausdorff distance $d = 0.0526852$

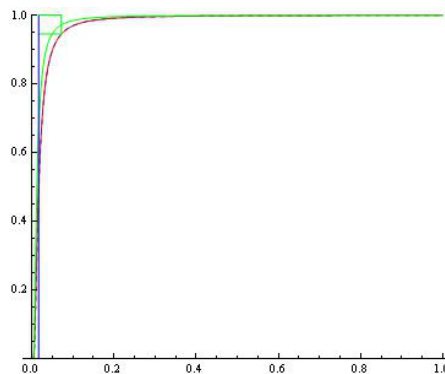


Fig. 3. The model (1) and two-sided estimations (2) for fixed $\alpha = 0.01$, $\lambda = 0.9$, and $t_0 = 0.0169128$, Hausdorff distance $d = 0.0551343$

From Figs 2, 3 it can be seen that the characteristic d and estimations (2) can be used as “confidence bounds”, which are extremely useful for the specialists in the choice of model for cumulative data approximating in areas of Biostatistics, Population dynamics, Growth theory, Debugging and Test theory, Computer viruses propagation, Insurance mathematics and Financial Mathematics.

3. Investigations on the “Half-Logistic-Inverse-Rayleigh cdf with Polynomial Variable Transfer” (HLIRPVT) cdf (3).

Let t_0 is the “median level”. The one-sided Hausdorff distance d_2 between Heaviside function h_{t_0} and cumulative function (3) satisfies

$$M_1(d_2; a_1, \dots, a_n) = 1 - d_2.$$

The question of finding precise two-sided estimates for the magnitude of the Hausdorff approximation [19] of the Heaviside function with classes of the indicated family $M_1(t; a_1, \dots, a_n)$ 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 [20, 21].

In some of cases when only a part of all zeros of polynomial are necessary to be known methods given in [22] can be used.

Below we look at some comparisons (Fig. 4) between the Half-Logistic-Inverse-Rayleigh (HLIR) cdf and the “Half-Logistic-Inverse-Rayleigh with Polynomial Variable Transfer” (HLIRPVT) cdf, as well as the ability to approximate specific dynamics data.

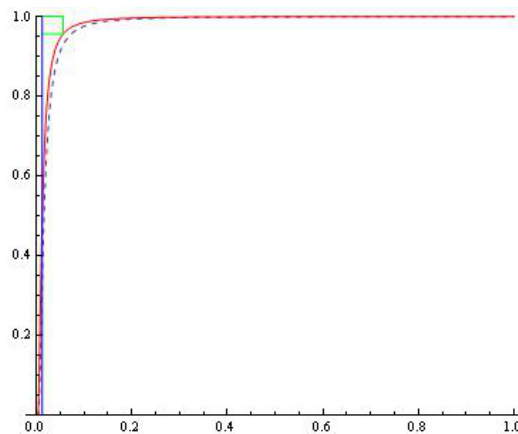


Fig. 4. Comparison between the model (1) (dashed) and the new model (3) (red) at fixed $\alpha = 0.001$, $\lambda = 0.95$, $n = 3$, $a_1 = -1.3$, $a_2 = 0.03$, $a_3 = -0.00001$. For the model (3) $t_0 = 0.0125191$, Hausdorff distance $d_2 = 0.0439798$

We conclude that the proposed model $M_1(t; a_1, \dots, a_n)$ has some free parameters leading to greater flexibility in modeling various data types.

3. Some applications

Example 1. The model explored here can be successfully used for approximating propagation data of computer viruses [10-18, 25].

As an example we will approximate Stuxnet spreading. Stuxnet is world's first cyberweapon. On 20 July 2010 Symantec initiate to monitor traffic to the Stuxnet Command and Control (C&C) servers [9]. The worm infected over 200,000 computers.

For the cumulative data from Fig. 5 the fitted model

$$M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n) \text{ for } \lambda = 0.41, \alpha = 0.00157998, n = 5,$$

$$A = 209000, a_1 = -0.00589269, a_2 = 0.00630298, a_3 = -0.00371303,$$

$$a_4 = 0.000861294, a_5 = -0.0000764171$$

is presented on Fig. 6.

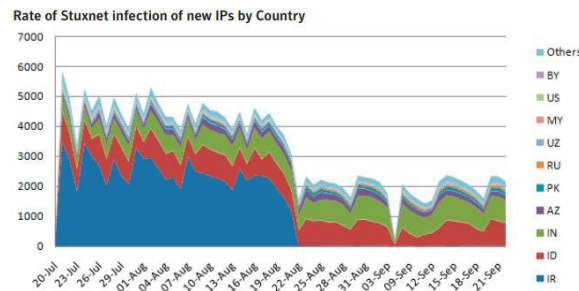


Fig. 5. Stuxnet propagation from 20 July 2010 to 21 September 2010 [9]

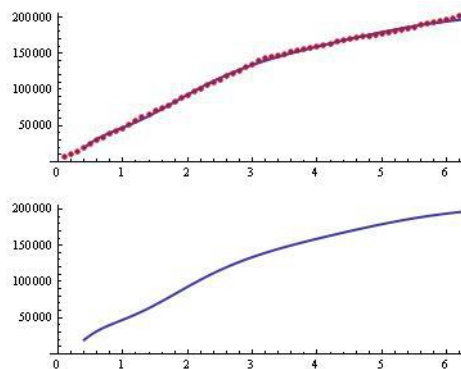


Fig. 6. The fitted model $M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n)$ for the cumulative data from Fig. 5

Example 2. Approximation of the data “Data Zika Virus Infection” [44, 45].

The number of these M&CD diagnoses to be confirmed with a Zika virus infection also grows (green dots; left-hand axis) by 1 new detection (green bars; right-hand axis) to 208 this EW.

Those confirmed Zika virus infections represent 15% of all confirmed M&CD diagnoses and 3% of all suspect diagnoses.

For the cumulative data (Fig. 7) the fitted model

$$M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n)$$

for $n = 3$, $\lambda = 0.91$, $\alpha = 8318.88$, $A = 220$,
 $a_1 = 3134.48$, $a_2 = -416.973$, $a_3 = 25.9594$

is depicted in Fig. 8.

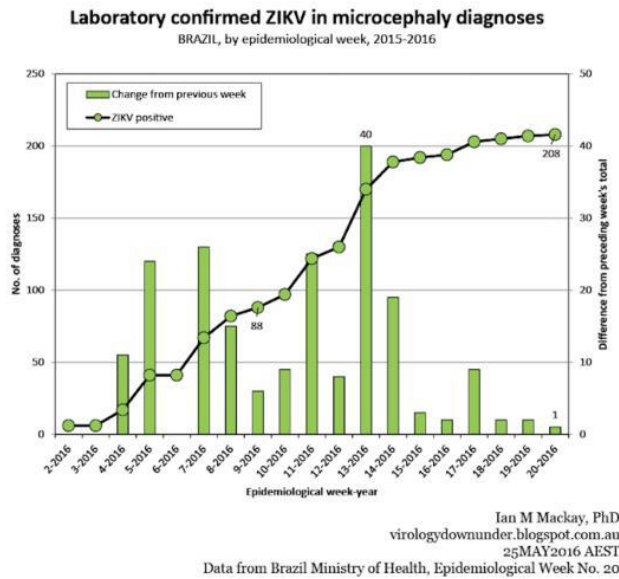


Fig. 7. Laboratory confirmed ZIKV in microcephaly diagnoses [44, 45]

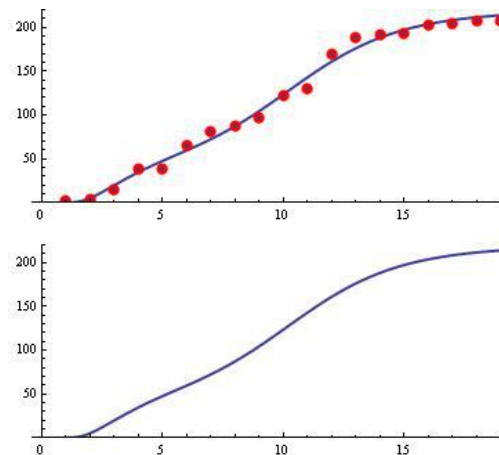


Fig. 8. The fitted model $M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n)$ for the data “Data Zika Virus Infection” [44, 45]

From the attached graph, it can be seen that at the degree of the polynomial $n = 3$, some specific distortions typical of the model analyzed are very well approximated.

Example 3. Approximation of the data "Influenza A(H1N1) (also known as Swine influenza)" [46].

In April 2009 scientific laboratories discover an influenza virus known as H1N1. This virus seems like a combination of viruses from birds, humans and pigs. Later, in 2010 The World Health Organization (WHO) reported the infection caused by H1N1 as a global pandemic. In August 2010 the WHO reported the finishing of pandemic. Since that scientists changed the name of infection and H1N1 virus is now H1N1v.

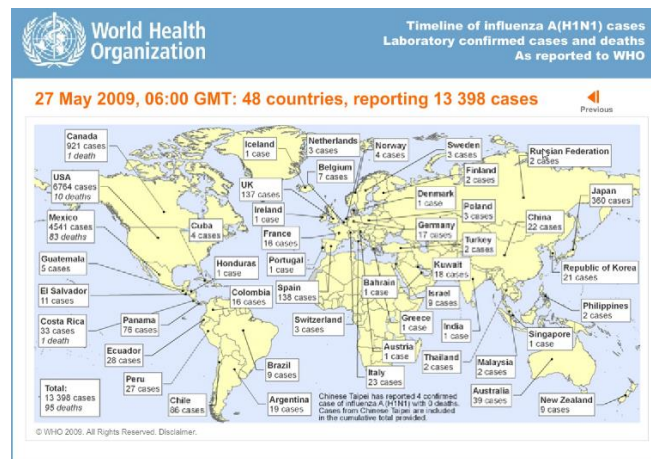


Fig. 9. Influenza A(H1N1) cases [46]

For the cumulative data from Fig. 9 the fitted model $M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n)$ for $\lambda = 1.5$, $\alpha = 21021.1$, $n = 6$, $A = 13398$, $a_1 = 2777.7$, $a_2 = -69.8471$, $a_3 = -26.6675$, $a_4 = 3.21043$, $a_5 = -0.131274$ is presented on Fig. 10.

A detailed discussion of the topic the reader can find in the monographic study [5]. For other results, see [23-41, 42, 43].

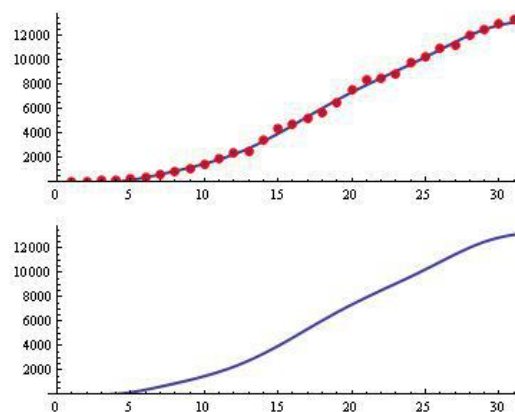


Fig. 10. The fitted model $M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n)$ for the data "Influenza A(H1N1)" (also known as "Swine influenza") [46]

Example 4. Approximation of the data “Data South Korea: Total Cases COVID-19” from 15.02.2020 to 26.04.2020 [8].

For the cumulative data from Fig. 11 the fitted model $M_1^*(t; a_1, \dots, a_n)$ for

$$\lambda = 1.7109099, \alpha = 1039.51, n = 5, A = 10728, a_1 = 17.2212,$$

$$a_2 = 6.32739, a_3 = -0.267302, a_4 = 0.00374985, a_5 = -0.0000123795$$

is presented on Fig. 12.

Total Coronavirus Cases in South Korea

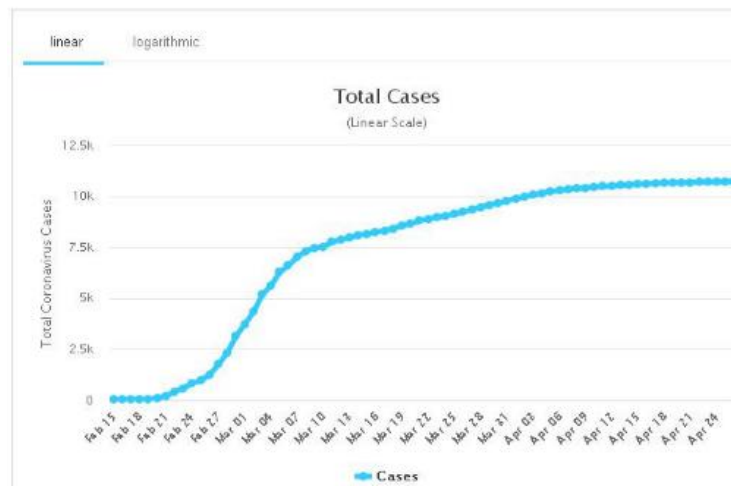


Fig. 11. “Data South Korea: Total Cases COVID-19” from 15 February 2020 to 26 April 2020 [8]

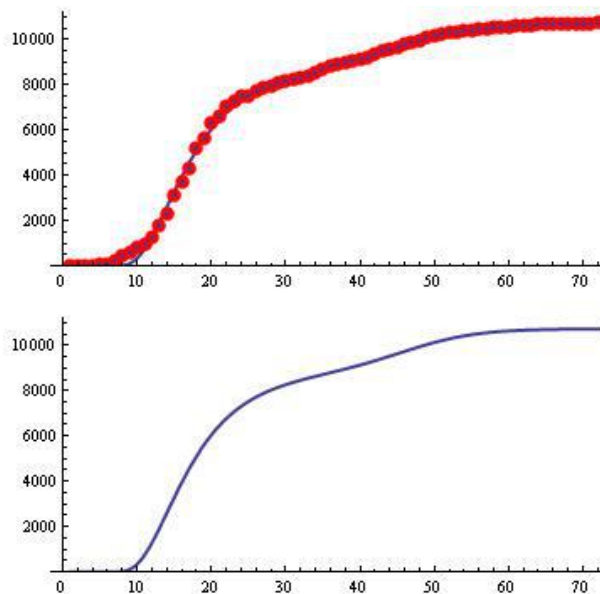


Fig. 12. The fitted model $M_1^*(t; a_1, \dots, a_n) = AM_1(t; a_1, \dots, a_n)$

for the “Data South Korea: Total Cases COVID-19” from 15 February 2020 to 26 April 2020 [8]

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