Mathematical riddles of COVID-19

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Abstract. We construct a simple model of a coronavirus epidemic by using a recurrence equation. This approach involves rather elementary mathematical tools (like roots of polynomials) but may be instructive both from mathematical and practical points of view, in particular, for prediction of the further course of the epidemic.

1. INTRODUCTION. In 2020, the world was shaken by the coronavirus pandemic. Charts showing the numbers of infected by countries became a symbol of this year. In this note we look aside from the ominous meaning of those diagrams and will deal with them as mathematical objects.

One of such diagrams is presented on Fig 1. We denote here by x_n the number of cases of infection that are detected during the day n in the country in question. The diagram on Fig. 1 shows the subgraph of a piecewise constant function x_n. Such diagrams will be referred to as x-*diagrams*.

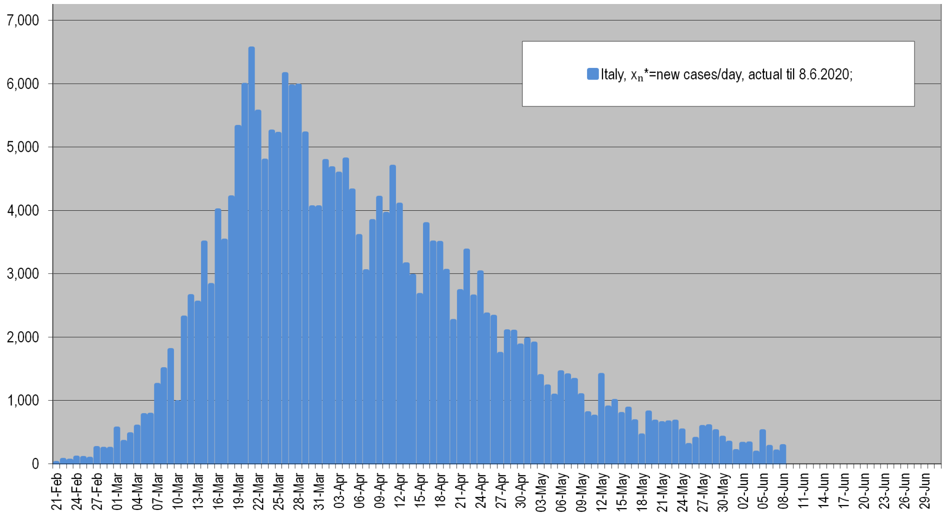

Figure 1. x-diagram for Italy: the numbers of actually registered daily cases

Denote by y_n the cumulative number of detected cases from the beginning of the epidemic by the beginning of the day n; that is,

$$y_{n+1} = y_n + x_n.$$

The graph of a piecewise linear interpolation of the sequence $\{y_n\}$ is shown on Fig. 2. Such diagrams will be referred to as y-*diagrams*.

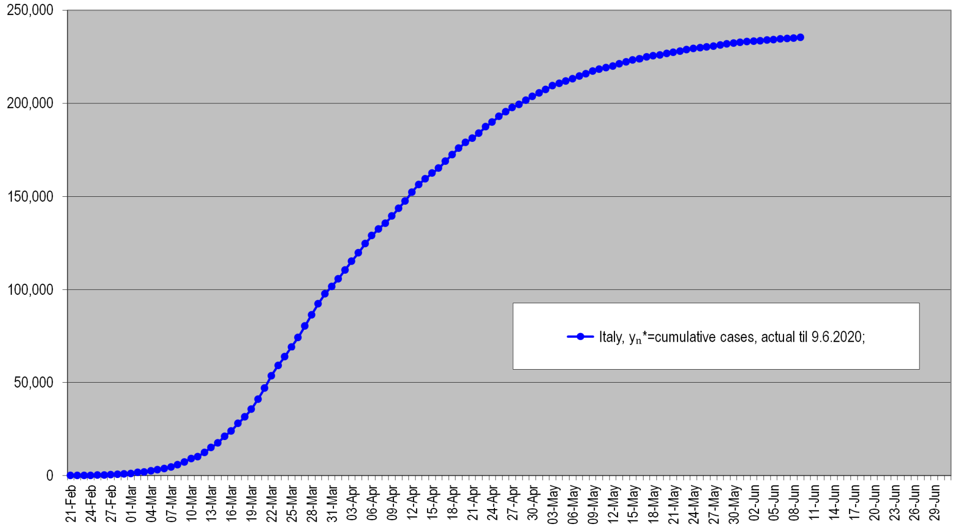

Figure 2. y-diagram for Italy: the cumulative numbers of registered cases

In this note we construct a simple model of a coronavirus epidemic by using a recurrence equation. This involves rather elementary mathematical tools but may be instructive both from mathematical and practical points of view, for example, for prediction of the further course of the epidemic.

The models for individual countries are based on reported numbers x_n of detected cases rather than on the actual number of infected individuals, which is unknown. While this may not give a complete picture, it still gives a good idea of the state of an epidemic.

Of course, there exist comprehensive mathematical models of epidemics created and used by professional epidemiologists, see, for example, [**4**], [**9**], [**10**], [**11**], [**12**], [**13**] and many others sources. However, such models require much more information about the disease, whereas in our model we manage without a priori knowledge and use the information that can be extracted from the x- and y-diagrams *only*. Consequently, our model is accessible to undergraduate students with basic knowledge of Algebra and Analysis.

In Section 2, we present a simple recurrence equation for x_n that models an epidemic for periods of time of invariable quarantine conditions. This equation contains three numerical parameters that can be determined by comparing the model with the actual data for the initial 3-4 weeks of the period in question. Usually the model agrees well with the actual course of the epidemic also after the initial weeks and, hence, can be used for predictions.

In Section 3, we discuss positive solutions of linear recurrence equations with constant coefficients. The long time behavior of such solutions is determined by the *leading root* – a root of the characteristic polynomial with the maximal absolute value. We prove in Theorem 5 that, for the above model, the leading root is always a positive real, say r, and that any positive solution x_n is asymptotically equivalent to $\operatorname{const} r^n$ as $n \to \infty$. This result explains why the decay phase of the epidemic is relatively long: because it is an exponential with the base r close to 1.

In Theorem 7 we give some estimates of r that are useful for numerical computation of r. In particular, we obtain the following relation between the leading root r and the *basic reproductive rate* R_0 that is a main characteristic of an epidemic in epidemiology:

$$r \approx R_0^{\frac{1}{2q}}. \tag{1}$$

Here q is the latent period of the disease and $\approx$ means that the right hand side of (1) can be used as the initial approximation in Newton's method for computation of r. In practice already the first iteration gives a satisfactory value for r.

In Section 4, we consider random perturbations of the basic model. The reported numbers x_n of daily cases are significantly affected by random events in the society, and we try to take them into account by adding to a basic recurrence equation a random term. We use the *Green function* of the recurrence equation in order to solve a randomly perturbed equation and to produce a confidence interval for a random solution (Theorem 15). The results of computations are shown for a number of countries.

In Section 5, we consider a modification of the basic model when the parameters a and b are periodic functions of n. This is motivated by observation that, in some countries, the sequence x_n exhibits clear periodic patterns, probably, due to a weekly rhythm of life. For such countries, the model with periodic parameters provides a better approximation than a basic model.

In Section 6, we discuss a two-phase model that covers two periods of an epidemic with different sets of parameters – the first phase of a fast growth and the second phase of a decay. We provide the two-phase models for a number of countries, where the peak of COVID-19 occured in March-May 2020.

Acknowledgement. All the data of the coronavirus epidemic by countries/territories were taken from the following sources: [**5**], [**6**], [**7**], [**8**].

All numerical computations and diagrams were done by using Microsoft Excel and Scientific Workplace.

I am grateful to Sergey Grigorian for a number of useful conversations on the topic of this paper and for explaining me basics of epidemiology. In particular, Sergey suggested me a way of computation of R_0 for a basic model that is implemented in Lemma 9.

2. A BASIC MODEL.

Let us make the following simple assumptions about spread of an epidemic in a certain county or territory. We use three parameters: $q \in \mathbb{N}$, $a > 0$ and $b \in (0,1)$.

(I) Any infected person becomes ill and infectious on the q-th day after infection.[1]

(A) During each day, each ill person at large infects on average a other persons.

(B) During each day, a fraction b of ill people at large gets isolated (hospitalized or otherwise) and withdrawn from a further spread of the epidemic.

In order to derive the equation of expansion of the epidemic, let us introduce the following notation.

- x_n – the number of infected people that are detected and isolated during the day n;
- y_n – the cumulative number of detected cases from the beginning of epidemic by the beginning of the day n;
- z_n – the number of ill people at large by the beginning of the day n (that is, those who were infected at least q days ago and stay unisolated);
- u_n – the number of people newly infected during the day n.

Clearly, we have

$$y_{n+1} = y_n + x_n.$$

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[1] The number of days before an infected person becomes infectious is called the *latent period*, and before he/she becomes symptomatically ill – the *incubation period*. Here we assume for simplicity that these two periods are equal.

Since bz_n people are isolated during the day n, we have $x_n = bz_n$. Since az_n people get infected during the day n, we have $u_n = az_n$. Observe also that

$$z_{n+1} = z_n - x_n + u_{n-q}. \tag{2}$$

because during the day n the number x_n of ill people get isolated, while new u_{n-q} people become ill (as u_{n-q} is the number of people infected during the day $n - q$).

It follows from the above equations that

$$z_{n+1} = (1 - b)\, z_n + az_{n-q}.$$

Using $x_n = bz_n$ we obtain the following equation for x_n:

$$x_{n+1} = (1 - b)\, x_n + ax_{n-q}. \tag{3}$$

This is a recurrence equation of the order $q + 1$ that is valid for all $n \geq q$. In order to solve it inductively, we need to know the initial conditions for $x_0, \ldots, x_q$.

Denote by x_n^* the actual number of infected people that are detected and isolated during the day n, while the notation x_n will be reserved for a solution of (3), that is, for a model. Then we impose the following initial conditions:

$$x_n = x_n^* \text{ for } n = 0, 1, \ldots, q, \tag{4}$$

which together with (3) allows to determine uniquely the entire sequence $\{x_n\}$.

Denote by y_n^* the reported cumulative number of cases by the day n. Then we determine the model number y_n by

$$y_0 = y_0^* \text{ and } y_{n+1} = y_n + x_n, \;\; n \geq 0.$$

It follows from (4) that $y_n = y_n^*$ for all $n = 0, \ldots, q + 1$.

Note that the numbers x_n^* and y_n^* are observables as their values are widely reported, while the values of the parameters a, b, q cannot be measured directly. Nevertheless, one can determine them at least approximately by comparing the actual data with the model data. For that we use the normalized 1-norm:

$$\|x - x^*\| := \frac{1}{N+1} \sum_{n=0}^{N} |x_n - x_n^*|, \tag{5}$$

where N need to be chosen so that $N \gg q$. Usually N is taken to be the maximal value of n for which x_n^* is available. Similarly one defines $\|y^* - y\|$. One can attempt to determine the values of a, b, q by minimizing the differences

$$\|x - x^*\| \text{ and } \|y - y^*\|. \tag{6}$$

Usually it is impossible to minimize simultaneously two functions at the same point, but some numerical compromise would give a reasonable approximation for a, b, q. Of course, the so determined values of the parameters may depend on N as well as on the choice of the initial date, and adjustment maybe needed later when more data become available.

We show below on some examples how this approach works. Typically an epidemic in a given country has two phases: a phase of an initial fast growth and a phase of decay, after imposing of quarantine measures. Obviously, the values of the parameters a and b

are different for these two phases. Therefore, the present model makes sense only for the periods of time within one phase. A two-phase model will be considered in Section 6.

In practice one can distinguish the two phases by looking at the convexity of the y-diagram: it is convex in the first phase and concave in the second phase. Hence, the borderline between the two phases is around the inflection point.

For most of examples in this paper, the values of a, b, q had been computed in the second half of April 2020. The values of the distances (6) shown on the diagrams below were computed by using the latest available actual data at the beginning of June 2020 when this paper was completed (only minor adjustment of a and b were needed then).

Example 1. One can see on Fig 2 that the second phase in Italy starts around March 26 so that we set $n = 0$ for that day. The results of numerical minimization of the differences (6) are shown on Fig. 3 and 4.

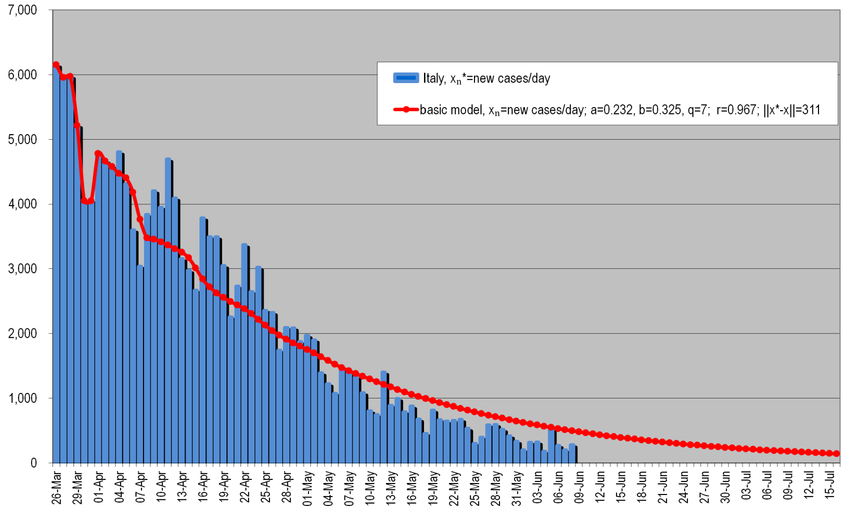

Figure 3. Comparison of the basic model with the actual data, Italy (x-diagram)

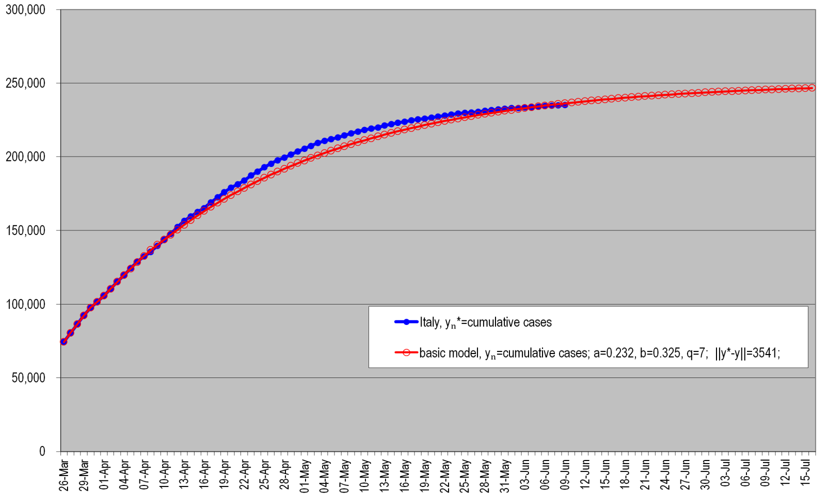

Figure 4. Comparison of the basic model with the actual data, Italy (y-diagram)

Example 2. A similar analysis for the USA gives the results shown on Fig. 5 and 6.

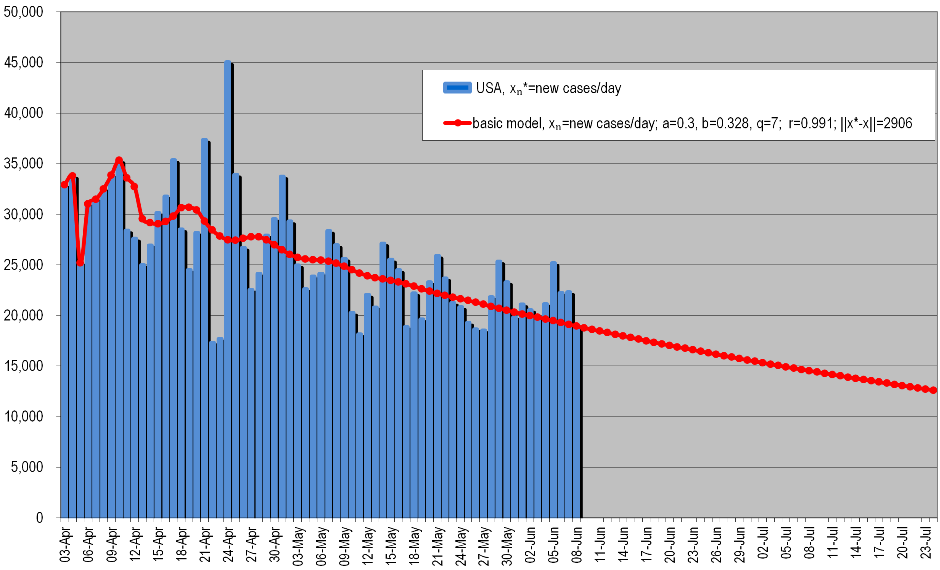

Figure 5. Comparison of the basic model with the actual data, USA (x-diagram)

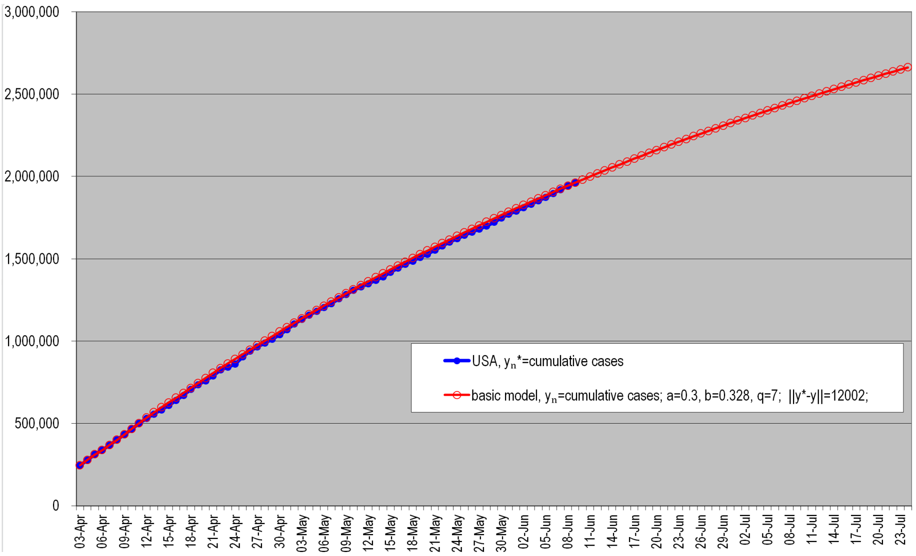

Figure 6. Comparison of the basic model with the actual data, USA (y-diagram)

Here we see a surprisingly good match of y_n and y_n^* with an error less than 1%.

Example 3. The actual data and a model for Germany are shown on Fig 7 and 8.

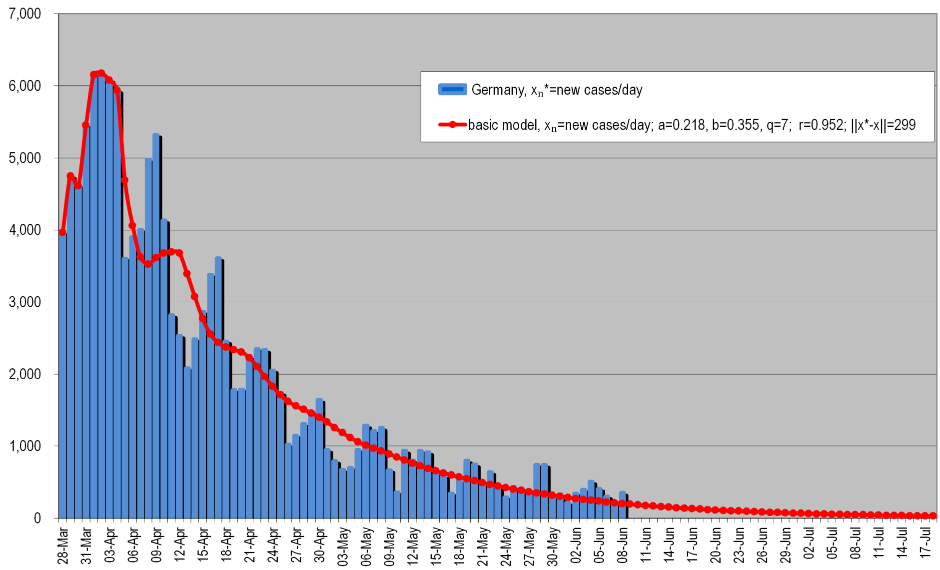

Figure 7. Comparison of the basic model with the actual data, Germany (x-diagram)

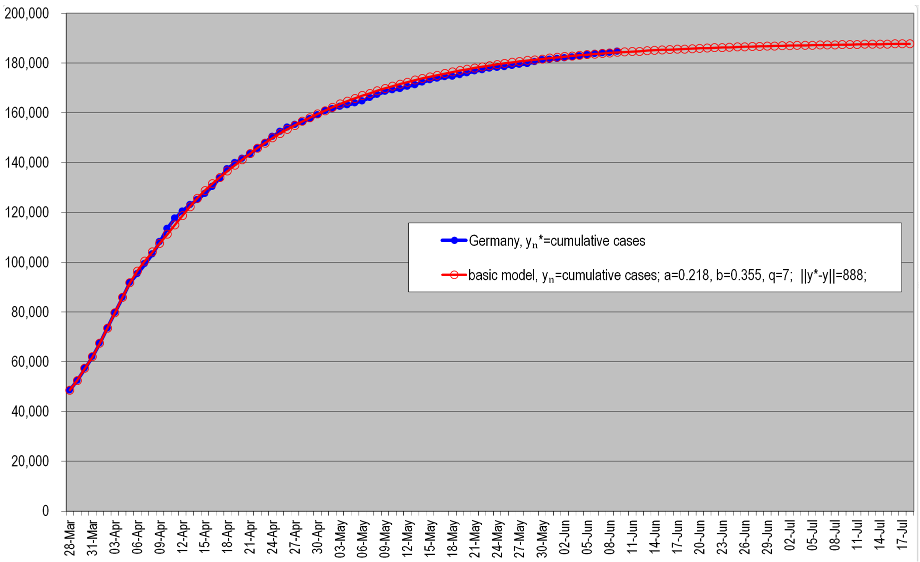

Figure 8. Comparison of the basic model with the actual data, Germany (y-diagram)

In the above x-diagrams, alongside the values of a, b, q, there is one more parameter r. It is a function of a, b, q whose meaning will be explained in the next section.

3. THE LEADING ROOT. Consider a general linear recurrence equation with constant coefficients:

$$x_{n+1} = a_0 x_n + a_1 x_{n-1} + a_2 x_{n-2} + \ldots + a_q x_{n-q}, \tag{7}$$

where q is a positive integer and a_k are non-negative reals, $a_q \neq 0$. The equation (7) represents a model of an epidemic with a distributed latent period. Indeed, let us keep the assumptions (A) and (B) of the basic model of Section 2 and modify the assumption (I) as follows.

(I') Any infected person becomes ill and infectious on the day $k = 1, 2, \ldots, q$ after infection with probability c_k, where $c_1 + c_2 + \ldots + c_q = 1$.

Arguing as in Section 2, we obtain for the number of daily cases x_n the equation (7) with

$$a_0 = 1 - b \text{ and } a_k = ac_k, \; k = 1, \ldots, q.$$

In particular, we have $a_1 + \ldots + a_q = a$.

Let us recall some mathematical facts about the recurrence equation (7) that are valid for arbitrary real coefficients a_k (cf. [1]). Any solution of (7) is uniquely determined by $q + 1$ initial values of $x_0, \ldots, x_q$, so that the set of all solutions of (7) is a $(q + 1)$-dimensional vector space. A basis in this space can be determined with help of the characteristic polynomial of (7):

$$f(\lambda) = \lambda^{q+1} - a_0\lambda^q - a_1\lambda^{q-1} - a_2\lambda^{q-2} - \ldots - a_q. \tag{8}$$

Indeed, any root λ of (8), real or complex, gives a solution $x_n = \lambda^n$ (note that $\lambda \neq 0$ due to $a_q \neq 0$). If all the roots of f are simple then f has $q + 1$ different complex roots $\lambda_0, \ldots, \lambda_q$, and we obtain $q + 1$ linearly independent solutions

$$\lambda_0^n, \; \lambda_1^n, \; \ldots \; , \lambda_q^n \tag{9}$$

of (7). The general solution of of (7) is then

$$x_n = C_0\lambda_0^n + \ldots + C_q\lambda_q^n, \tag{10}$$

where $C_0, \ldots, C_q$ are arbitrary complex constants. If a root λ_k is multiple, say, with multiplicity $m > 1$, then the m instances of λ_k^n in (9) and (10) should be replaced by the following m independent solutions:

$$\lambda_k^n, \; n\lambda_k^n, \; \ldots \; , n^{m-1}\lambda_k^n. \tag{11}$$

We are interested only in real solutions of (7). If λ_k is complex then $\overline{\lambda}_k$ is also a root of f of the same multiplicity, and each pair of the complex solutions $n^j\lambda_k^n$, $n^j\overline{\lambda}_k^n$ can be replaced by real solutions $n^j \operatorname{Re} \lambda_k^n$ and $n^j \operatorname{Im} \lambda_k^n$, thus yielding again $q + 1$ linearly independent real solutions.

A typical solution x_n of (7) contains all the terms (11) with non-zero coefficients. Hence, the long time behavior of x_n is determined by a root λ of f with the maximal absolute value $|\lambda|$ (see Theorem 5 below for a precise statement).

Definition 4. A root λ of f with the maximal absolute value $|\lambda|$ will be referred to as a *leading root* of (7).

From now let us assume that all the coefficients a_k in (7) are non-negative reals and $a_0 > 0$. Then any solution x_n with positive initial values remains positive forever. Determination of the leading root of (7) is in this case of paramount importance for prediction of the course of the epidemic that is modelled by this equation.

Theorem 5. *Let* $a_k \geq 0$ *for all* $k = 0, \ldots, q$ *and* $a_0 > 0$.

(a) (Cauchy, 1829) *The polynomial* $f(\lambda)$ *has exactly one positive real root* r. *Besides, the root* r *is simple and, for any other root* $\lambda \in \mathbb{C}$, *we have* $|\lambda| < r$. *Consequently,* r *is the leading root of* (7).

(b) *For any positive solution* x_n *of* (7), *there exists* $C > 0$ *such that*

$$x_n \sim Cr^n \text{ as } n \to \infty. \tag{12}$$

It follows from (12) that if $r < 1$ then the epidemic fades away, whereas if $r > 1$ then it spreads unlimited.

Proof. (a) Although this statement is not new, we give here the proof as it is quite simple and a part of the argument will be used below. The equation $f(\lambda) = 0$ is equivalent to

$$1 = \frac{a_0}{\lambda} + \frac{a_1}{\lambda^2} + \ldots + \frac{a_q}{\lambda^{q+1}}. \tag{13}$$

Since $a_0 > 0$, the right hand side is strictly monotone decreasing in $\lambda > 0$, tends to $+\infty$ as $\lambda \to 0+$ and to 0 as $\lambda \to +\infty$. Hence, there is exactly one positive value $\lambda = r$ that satisfies this equation, that is,

$$1 = \frac{a_0}{r} + \frac{a_1}{r^2} + \ldots + \frac{a_q}{r^{q+1}}. \tag{14}$$

Let $\lambda \in \mathbb{C} \setminus \{0\}$ be another root of f. We obtain from (13) that

$$1 \leq \frac{a_0}{|\lambda|} + \frac{a_1}{|\lambda|^2} + \ldots + \frac{a_q}{|\lambda|^{q+1}}$$

which implies that $|\lambda| \leq r$. If $|\lambda| = r$ then comparison with (13) and (14) shows that $|\lambda| = \lambda$ and, hence, $\lambda = r$.

Let us verify that the root r is simple. If $q = 0$ then there is nothing to prove. Let $q \geq 1$. Then the polynomial $\frac{1}{q+1} f'(\lambda)$ satisfies the hypotheses of the present theorem and, by the above argument, $f'(\lambda)$ has exactly one positive root. Let us denote it by r' and verify that $r' < r$, which will, in particular, imply that r is simple. If $r' = 0$ then all is clear. If $r' > 0$ then it follows from $f'(r') = 0$ that

$$\begin{aligned} 1 &= \frac{q a_0}{(q+1) r'} + \frac{(q-1) a_1}{(q+1)(r')^2} + \ldots + \frac{a_{q-1}}{(q+1)(r')^q} \\ &< \frac{a_0}{r'} + \frac{a_1}{(r')^2} + \ldots + \frac{a_{q-1}}{(r')^q}, \end{aligned}$$

whence $r' < r$.

(b) Let $\lambda_1, \lambda_2, \ldots$ be all other distinct roots of f apart from r (so that λ_k are negative or imaginary). Any solution x_n of (7) has the form

$$x_n = Cr^n + \widetilde{x}_n, \tag{15}$$

where $\widetilde{x}_n$ is a linear combination of the functions $n^j \lambda_k^n$. Since by (a) we have $|\lambda_k| < r$, it follows that

$$|\widetilde{x}_n| = o(r^n) \text{ as } n \to \infty. \tag{16}$$

Since $x_n > 0$, it follows from (15) and (16) that $C \geq 0$.

Let us verify that $C > 0$, which will settle the claim. It is tempting to say that if $C = 0$ then $x_n = \widetilde{x}_n$ is a linear combination of terms of the form $n^j \rho^n \sin \varphi n$ and $n^j \rho^n \cos \varphi n$ and, therefore, cannot stay positive. However, it is not easy to make this argument rigorous because different roots of f may have the same absolute value ρ and an uncontrollable cancellation of the terms can occur. We employ here a different, simpler approach that takes advantage of nonnegative coefficients a_k.

To that end, consider a new sequence

$$X_n = \frac{x_n}{r^n}$$

that obviously satisfies the equation

$$X_{n+1} = A_0 X_n + A_1 X_{n-1} + \ldots + A_q X_{n-q} \tag{17}$$

with $A_k = a_k / r^{k+1}$. Since r is a root of f, we have

$$A_0 + A_1 + \ldots + A_q = 1. \tag{18}$$

Set $c := \min \left(X_1, \ldots, X_{q+1} \right) > 0$. Then we obtain from (17) and (18) by induction that

$$X_n \geq c \ \text{ for all } n \in \mathbb{N},$$

which implies

$$x_n \geq c r^n.$$

Comparing with (15) and (16), we conclude that $C \geq c > 0$. ■

Let us discuss a numerical procedure for computing of r. Of course, there are many software packages that compute instantaneously all the roots of a polynomial, but a reasonably quick computation of r can be done by Newton's method. Choose some initial value $r_0 > 0$ and define a sequence $\{r_n\}$ by

$$r_{n+1} = r_n - \frac{f(r_n)}{f'(r_n)}, \quad n \geq 0. \tag{19}$$

We will show below that the sequence $\{r_n\}$ converges to r for a simple choice of r_0.

It follows from Theorem 5 that $f(\lambda) < 0$ for $0 < \lambda < r$ and $f(\lambda) > 0$ for $\lambda > r$. As in the proof of Theorem 5, let r' be the largest non-negative root of $f'(\lambda)$, and similarly r'' – the largest non-negative root of $f''(\lambda)$.

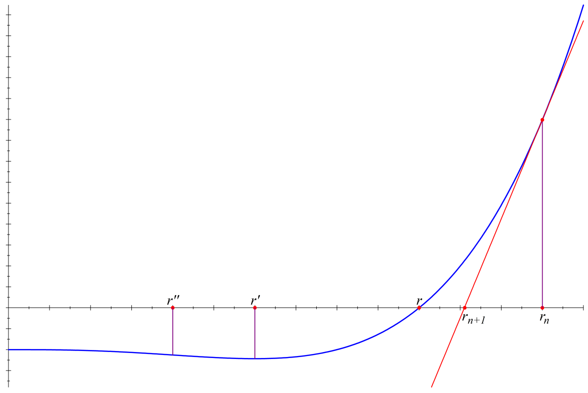

Figure 9. Polynomial $f(\lambda)$

By the argument in the proof of Theorem 5 we have

$$r'' \leq r' < r. \tag{20}$$

Lemma 6. *If $r_0 > r'$ then $r_n \to r$ as $n \to \infty$.*

Proof. It follows from (20) that the function $f(\lambda)$ is monotone increasing and convex in the interval $I = (r', \infty)$. It is known that, in the case of a convex function f, Newton's method converges to r provided both r_0 and r_1 belong to I (cf. [**3**]). Since $r_0 \in I$ by hypotheses, it remains to verify that $r_1 > r'$. If $r_0 \leq r$ then $f(r_0) \leq 0$ and

$$r_1 = r_0 - \frac{f(r_0)}{f'(r_0)} \geq r_0 > r'.$$

Let $r_0 > r$. Then $r_1 < r_0$ and we have for some $\xi \in (r_1, r_0)$ that

$$f(r_1) = f(r_0) + f'(\xi)(r_1 - r_0) = f(r_0) - f'(\xi)\frac{f(r_0)}{f'(r_0)}.$$

Since $f'(\xi) < f'(r_0)$, it follows that $f(r_1) > 0$ and, hence, $r_1 > r > r'$. ■

The next statement gives a simple estimate for the leading root r that can be used to set up the initial value r_0.

Theorem 7. *Let $a_k \geq 0$ for all $k = 0, \ldots, q$. Denote $a = a_1 + \ldots + a_q$, $b = 1 - a_0$ and assume that $a > 0$, $b \in (0,1)$.*

(a) *We have the equivalences: $r < 1 \Leftrightarrow a < b$ and $r > 1 \Leftrightarrow a > b$.*

(b) *Let $m \geq 1$ be such that $a_1 = \ldots = a_{m-1} = 0$ and $a_m > 0$. Then*

$$\min\left(1, \left(\frac{a}{b}\right)^{1/m}\right) \leq r \leq \max\left(1, \left(\frac{a}{b}\right)^{1/m}\right). \tag{21}$$

Remark 8. Although there are in the literature plenty of estimates of the leading roots of polynomial (see, for example, [**2**]), none of them seems to imply (21). The latter is very useful for a basic model as we will see below in an example.

Proof. (a) We have $f(1) = 1 - a_0 - a_1 - \ldots - a_q = b - a$, whence

$$r < 1 \Leftrightarrow f(1) > 0 \Leftrightarrow a < b \quad \text{and} \quad r > 1 \Leftrightarrow f(1) < 0 \Leftrightarrow a > b.$$

(b) The equation $f(r) = 0$ is equivalent to

$$r^{q+1} - r^q = -br^q + a_1 r^{q-1} + \ldots + a_q = -br^q + a_m r^{q-m} + \ldots + a_q.$$

Hence, if $r > 1$ then $r^{q+1} - r^q > 0$ and, hence,

$$br^q < a_m r^{q-m} + \ldots + a_q \leq (a_m + \ldots + a_q)\, r^{q-m} \leq ar^{q-m},$$

whence

$$r < \left(\frac{a}{b}\right)^{1/m}.$$

Similarly, if $r < 1$ then $r > \left(\frac{a}{b}\right)^{1/m}$, which implies (21). ■

In epidemiology the main characteristic of an epidemic is the *basic reproductive rate* R_0 that is defined as an average number of persons infected by one ill person before the latter gets isolated. One of the principles of epidemiology says that the epidemic fades away if and only if $R_0 < 1$.

Lemma 9. *For the model described by equation* (7) *we have*

$$R_0 = \frac{a}{b}.$$

Proof. Let u be the number of people infected on some day, say 0. On the day $k = 1, \ldots, q$ the number $c_k u$ of them become ill and can infect other people. On the day $k+1$ they infect $ac_k u$ people while $bc_k u$ of them get isolated. On the day $k+1$, the remaining $(1-b)\,c_k u$ people infect further $a\,(1-b)\,c_k u$ people. Continuing this way, we obtain that this group of $c_k u$ people infects in total

$$ac_k u + a\,(1-b)\,c_k u + a\,(1-b)^2\,c_k u + \ldots = \frac{a}{b} c_k u.$$

Hence, the initial group of u people infects in total

$$\sum_{k=1}^{q} \frac{a}{b} c_k u = \frac{a}{b} u,$$

so that $R_0 = \frac{a}{b}$. ■

Theorems 5 and 7 imply that the epidemic fades away if and only if $\frac{a}{b} < 1$, which gives for the model (7) a justification of the aforementioned condition $R_0 < 1$. However, for the model (7), a more important and relevant characteristic is the leading root r that determines precisely the dynamics of the epidemic.

Let us return to the equation (3), that is, to

$$x_{n+1} = (1-b)\,x_n + ax_{n-q}, \tag{22}$$

where $b \in (0,1)$ and $a > 0$. The characteristic polynomial is

$$f(\lambda) = \lambda^{q+1} - (1-b)\,\lambda^q - a.$$

Let r be its leading root. By Theorem 7 with $m = q$, we obtain that

$$\min\left(1, \left(\frac{a}{b}\right)^{1/q}\right) \le r \le \max\left(1, \left(\frac{a}{b}\right)^{1/q}\right).$$

Hence, we could take r_0 to be equal to the arithmetic mean of 1 and $\left(\frac{a}{b}\right)^{1/q}$. However, many numerical examples show that a better approximation is generally achieved by using the *geometric mean*, that is, by

$$r_0 = \left(\frac{a}{b}\right)^{1/(2q)} = R_0^{1/(2q)}. \tag{23}$$

The derivative $f'(\lambda) = (q+1)\,\lambda^q - (1-b)\,q\lambda^{q-1}$ has a positive root

$$r' = \frac{q\,(1-b)}{q+1}.$$

By Lemma 6, if $r_0 > r'$ (which is the case in all examples of interest) then $r_n \to r$ as $n \to \infty$. In practice, already r_1 or r_2 provide good enough approximations of r.

Example 10. Let $q = 7$, $a = 0.218$ and $b = 0.355$ as on Fig. 7 modelling the decay phase of the epidemic in Germany. By (23) we obtain $r_0 = 0.96577$. Since $r' = \frac{q(1-b)}{q+1} = 0.56438$, we have $r_0 > r'$, which implies that $r_n \to r$. We obtain by (19)

$$r_1 = 0.95296, \quad r_2 = 0.95219, \quad r_3 = 0.95219,$$

so that $r = 0.95219$. Of course, for practical purposes is enough to have $r \approx 0.95$ which predicts the decay rate of the epidemic 5% per day. On Fig. 10 we show the x-diagram together with a function Cr^n.

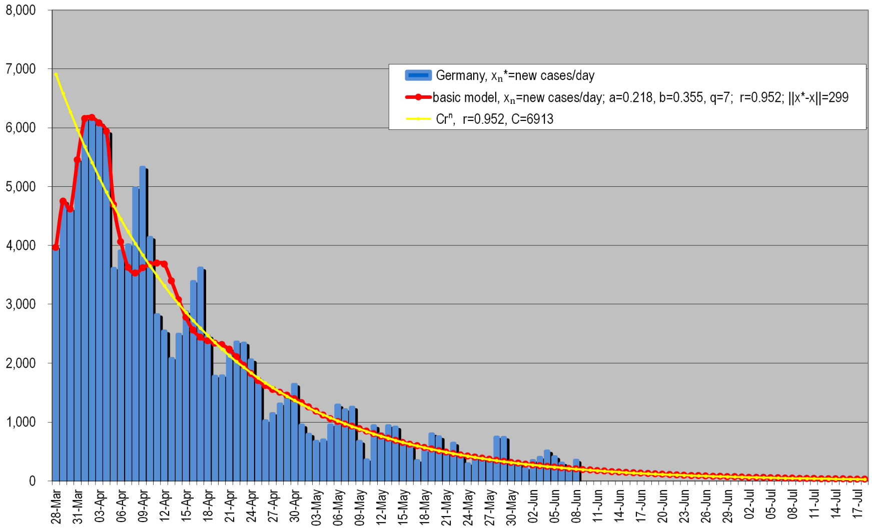

Figure 10. Comparison of x_n^*, x_n and Cr^n, Germany

Example 11. On Fig. 11 we show a model for the initial phase of the epidemic in the USA.

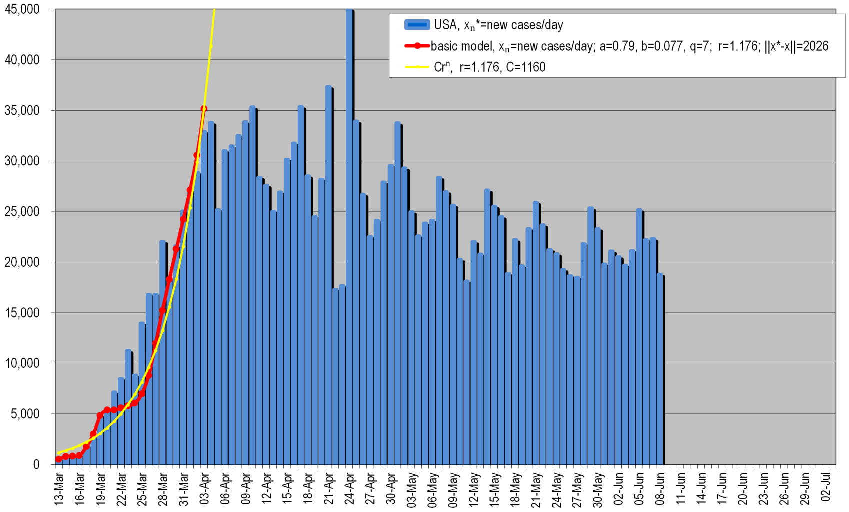

Figure 11. Comparison of x_n^*, x_n and Cr^n, USA

Here $q = 7,\ a = 0.79$ and $b = 0.077$. By (23) we obtain $r_0 = 1.1809$, and then by (19)

$$r_1 = 1.1765, \quad r_2 = 1.1764, \quad r_3 = 1.1764$$

so that $r = 1.1764$, which gives the growth rate 17.6% per day.

Example 12. For comparison, consider a recurrence equation with a *negative* coefficient:

$$x_{n+1} = 1.6x_n + 0.1x_{n-1} - 0.732x_{n-2}. \tag{24}$$

Its characteristic polynomial $f(\lambda) = \lambda^3 - 1.6\lambda^2 - 0.1\lambda + 0.732$ has the roots

$$\lambda_0 = -0.6, \ \ \lambda_1 = 1.1 + 0.1i, \ \ \lambda_2 = 1.1 - 0.1i$$

and, hence, no positive root. Consequently, all solutions x_n are oscillating. In particular, consider a solution

$$x_n = \rho^n \sin n\varphi,$$

where $\rho = |\lambda_1| = 1.1045$ and $\varphi = \arg \lambda_1 = 0.09066$. The graph of this solution is shown on Fig. 12.

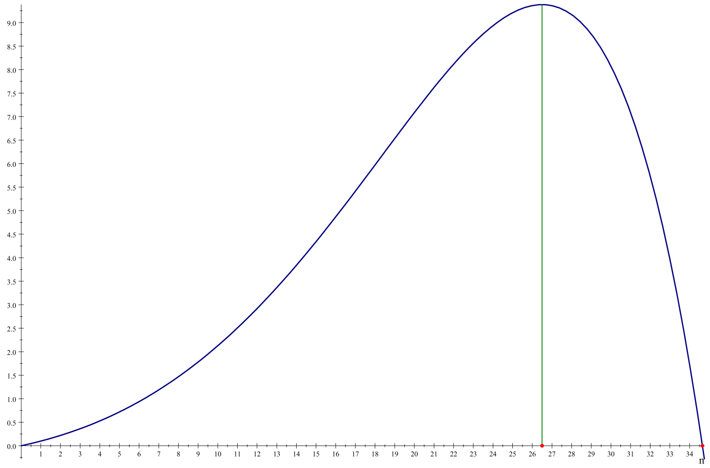

Figure 12. An oscillating solution of (24)

The solution takes its maximum at

$$n = \left(\pi - \arctan \frac{\varphi}{\ln \rho}\right) \frac{1}{\varphi} = 26.496$$

and then vanishes at $n = \pi/\varphi = 34.652$. If (24) were a model of an epidemic then this epidemic would have stopped abruptly, shortly after its peak. Of course, in our models such a situation can never happen, but we do not exclude that this phenomenon might occur for other diseases with a high self-recovery rate.

4. A MODEL WITH RANDOM PERTURBATIONS. Here we consider a random perturbation in the basic model. In fact, the results apply to any recurrence equation with constant coefficients:

$$x_{n+1} = a_0 x_n + a_1 x_{n-1} + a_2 x_{n-2} + \ldots + a_q x_{n-q}, \tag{25}$$

where a_k are reals. Denote by $\{g_n\}_{n\in\mathbb{Z}}$ the sequence that satisfies (25) for all $n \geq q+1$ with the initial conditions

$$g_n = 0 \ \text{ for } n = 0, 1, \ldots, q \quad \text{and} \quad g_{q+1} = 1.$$

The solution g_n is called the *Green function* of the equation (25). An example of the Green function is shown on Fig. 13.

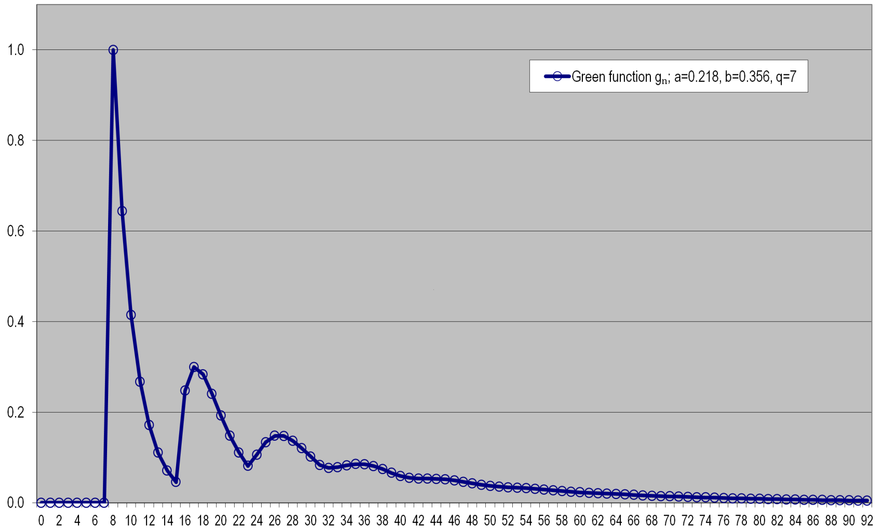

Figure 13. The Green function g_n for the equation $x_{n+1} = (1-b)\,x_n + a x_{n-q}$.

In what follows we use the Kronecker symbol

$$\delta_{nk} := \begin{cases} 1, & k = n, \\ 0, & k \neq n. \end{cases}$$

Lemma 13. *The Green function satisfies for all $n \in \mathbb{Z}$ the equation*

$$g_{n+1} = a_0 g_n + a_1 g_{n-1} + a_2 g_{n-2} + \ldots + a_q g_{n-q} + \delta_{nq}. \tag{26}$$

Proof. If $n < q$ then all the terms in (8) vanish. If $n \geq q+1$ then $\delta_{nq} = 0$ and (26) is satisfied by the definition of the Green function. Finally, if $n = q$ then $g_{n+1} = 1$, $\delta_{nq} = 1$ while all other terms vanish, and the equation is again satisfied. ■

Lemma 14. *Let $\{f_n\}_{n\geq 0}$ be any sequence of reals such that*

$$f_0 = f_1 = \ldots = f_{q-1} = 0.$$

Then the sequence

$$z_n = \sum_{k=0}^{n} g_{n-k+q} f_k \tag{27}$$

satisfies the equation

$$z_{n+1} = a_0 z_n + a_1 z_{n-1} + a_2 z_{n-2} + \ldots + a_q z_{n-q} + f_n, \quad n \geq q \tag{28}$$

and the initial conditions

$$z_0 = z_1 = \ldots = z_q = 0. \tag{29}$$

Proof. Since $f_k = 0$ for $k < q$ and $g_q = 0$, the summands in (27) with $k < q$ and $k = n$ always vanish, so that

$$z_n = \sum_{k=q}^{n-1} g_{n-k+q} f_k. \tag{30}$$

In particular, if $n \leq q$ then the set of summands is empty and, hence, $z_n = 0$, which proves (29).

In order to prove (28), observe that

$$f_n = \sum_{j=q}^{\infty} \delta_{nj} f_j.$$

By linearity, it suffices to prove (28) when $f_n = \delta_{nj}$ for some $j \geq q$. In this case we obtain by (27)

$$z_n = \sum_{k=0}^{n} g_{n-k+q} \delta_{kj} = g_{n-j+q}.$$

If $j = q$ then $z_n = g_n$, and (28) follows from (26). If $j > q$ then set $m = j - q$ and observe that the sequence

$$z_n = g_{n-j+q} = g_{n-m}$$

satisfies by (26) the equation

$$g_{n-m+1} = a_0 g_{n-m} + a_1 g_{n-m-1} + a_2 g_{n-m-2} + \ldots + a_q g_{n-m+q} + \delta_{(n-m)q}.$$

Since

$$\delta_{(n-m)q} = \delta_{n(q+m)} = \delta_{nj},$$

we conclude that $z_n = g_{n-m}$ satisfies the equation

$$z_{n+1} = a_0 z_n + a_1 z_{n-1} + a_2 z_{n-2} + \ldots + a_q z_{n-q} + \delta_{nj},$$

which was to be proved. ■

Consider now the following random perturbation of the equation (25):

$$\mathbf{x}_{n+1} = a_0\mathbf{x}_n + a_1\mathbf{x}_{n-1} + a_2\mathbf{x}_{n-2} + \ldots + a_q\mathbf{x}_{n-q} + \xi_n, \quad n \geq q, \tag{31}$$

where $\{\xi_n\}$ is a sequence of independent random variables with

$$\mathbb{E}\xi_n = 0,$$

and $\{\mathbf{x}_n\}$ is a random sequence satisfying the deterministic initial conditions

$$\mathbf{x}_n = x_n^* \text{ for } n = 0, \ldots, q.$$

Let $\{x_n\}$ solve the unperturbed equation (25) with the same initial conditions

$$x_n = x_n^* \text{ for } n = 0, \ldots, q.$$

Theorem 15. *We have, for all* $n \geq 0$,

$$\mathbb{E}\mathbf{x}_n = x_n \tag{32}$$

and

$$\operatorname{Var}(\mathbf{x}_n) = \sum_{k=q}^{n-1} g_{n-k+q}^2 \operatorname{Var}(\xi_k). \tag{33}$$

Besides, if all ξ_n *are normally distributed then all* $\mathbf{x}_n$ *with* $n > q$ *are also normally distributed.*

Proof. It follows from (31) and $\mathbb{E}\xi_n = 0$ that $e_n := \mathbb{E}\mathbf{x}_n$ satisfies

$$e_{n+1} = a_0 e_n + a_1 e_{n-1} + \ldots + a_q e_{n-q}, \ n \geq q,$$

and the initial conditions $e_n = x_n^*$ for $n \leq q$. Hence, $e_n = x_n$, which proves (32).

Consider now the difference

$$z_n := \mathbf{x}_n - x_n = \mathbf{x}_n - \mathbb{E}\mathbf{x}_n.$$

Clearly, z_n satisfies the equation

$$z_{n+1} = a_0 z_n + a_1 z_{n-1} + \ldots + a_q z_{n-q} + \xi_n, \quad n \geq q,$$

and the initial conditions

$$z_n = 0 \text{ for } n = 0, 1, \ldots, q.$$

By the identity (30) of Lemma 14 we obtain

$$z_n = \sum_{k=q}^{n-1} g_{n-k+q}\xi_k. \tag{34}$$

Using the independence of $\{\xi_k\}$ we obtain that

$$\operatorname{Var}(\mathbf{x}_n) = \operatorname{Var}(z_n) = \sum_{k=q}^{n-1} g_{n-k+q}^2 \operatorname{Var}(\xi_k).$$

If all ξ_n are normally distributed then it follows from (34) that also $\mathbf{x}_n$ with $n > q$ is normally distributed. ■

Let us now specify the choice of the random variables $\{\xi_n\}$. Let $\{\eta_n\}$ be an i.i.d. sequence of random variables with

$$\mathbb{E}\eta_n = 0 \text{ and } \sigma^2 := \mathbb{E}\eta_n^2 < \infty.$$

Fix some $\varepsilon > 0$ and set

$$\xi_n = \varepsilon \eta_n x_n$$

so that

$$\operatorname{Var} \xi_n = \varepsilon^2 \sigma^2 x_n^2.$$

If $\varepsilon\sigma$ is small then ξ_n can be regarded as a small perturbation compared with x_n. Clearly, we have in this case by (33)

$$\operatorname{Var}(\mathbf{x}_n) = \varepsilon^2 \sigma^2 \sum_{k=q}^{n-1} g_{n-k+q}^2 x_k^2.$$

Set

$$v_n = \sqrt{\operatorname{Var}(\mathbf{x}_n)} = \varepsilon\sigma \left(\sum_{k=q}^{n-1} g_{n-k+q}^2 x_k^2 \right)^{1/2}$$

and consider for some $K > 0$ a confidence interval $(x_n - K v_n, x_n + K v_n)$ for $\mathbf{x}_n$.

If η_n are Gaussian then $\mathbf{x}_n \sim \mathcal{N}(x_n, v_n^2)$ and we obtain that

$$\mathbb{P}(\mathbf{x}_n \in (x_n - K v_n, x_n + K v_n)) = 2 \int_0^{K v_n} \frac{1}{\sqrt{2\pi} v_n} \exp\left(-\frac{t^2}{2 v_n^2}\right) dt = \operatorname{erf}\left(K/\sqrt{2}\right),$$

where

$$\operatorname{erf}(s) = \frac{2}{\sqrt{\pi}} \int_0^s e^{-t^2} dt$$

is the error function. For example, for $K = 2$ we have

$$\operatorname{erf}\left(2/\sqrt{2}\right) = 0.95450.$$

However, in numerical experiments it is more convenient to use the random variables η_n that are uniformly distributed in $[-1, 1]$ since η_n is bounded. Then we have

$$\sigma^2 = \frac{1}{2} \int_{-1}^{1} t^2 dt = \frac{1}{3},$$

and we choose $\varepsilon = 0.2$ and $K = 2$.

The numerical computation with these parameters were done in Excel by means of a generator RAND() of random numbers. The results are shown on the next pictures: the blue columns represent the actual data x_n^*, the green and yellow lines are the graphs of

$x_n + Kv_n$ and $x_n - Kv_n$, respectively, and the read line is a sample graph of $\mathbf{x}_n$ (it is random and changes at each instance of computation). The data for Moscow and the rest of Russia are separated because of different dynamics of the epidemic there.

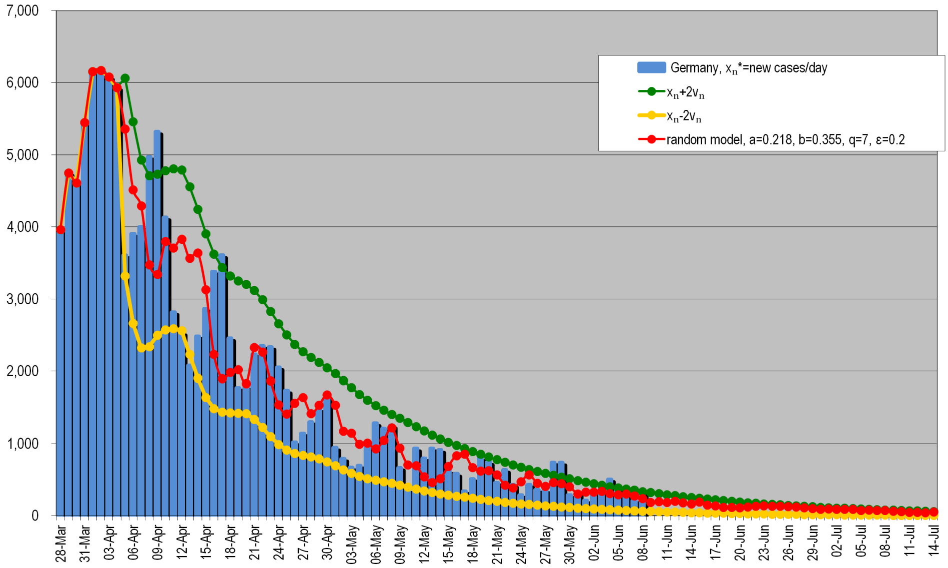

Figure 14. Random simulation, Germany

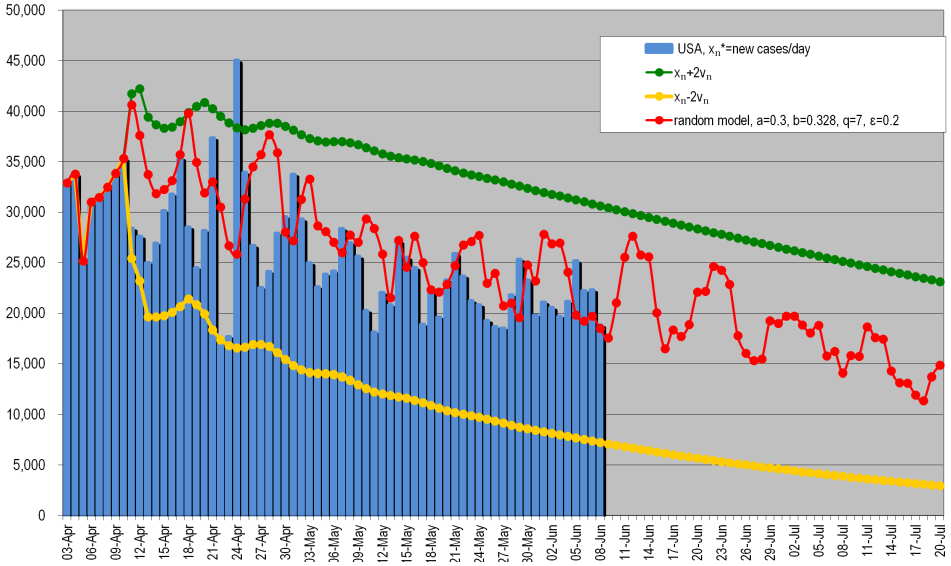

Figure 15. Random simulation, USA

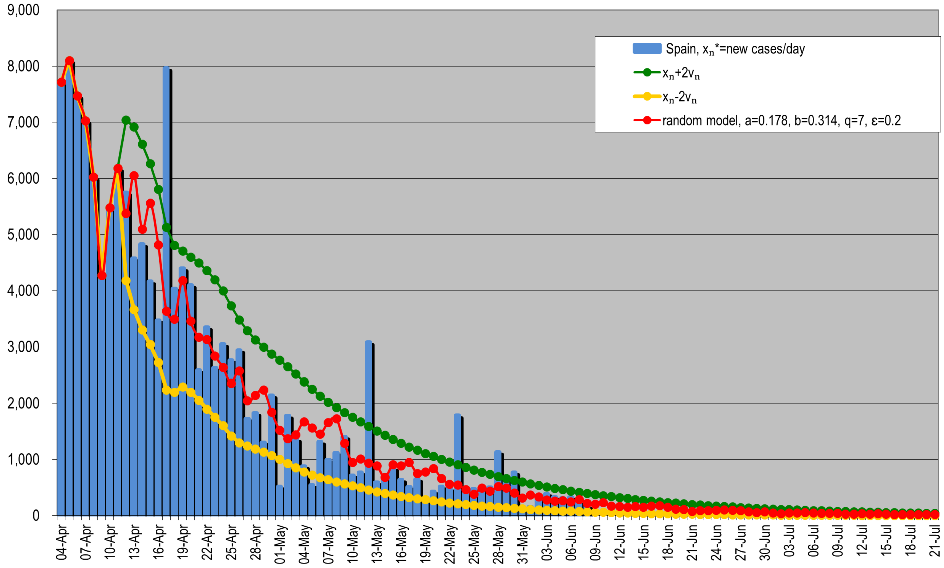

Figure 16. Random simulation, Spain

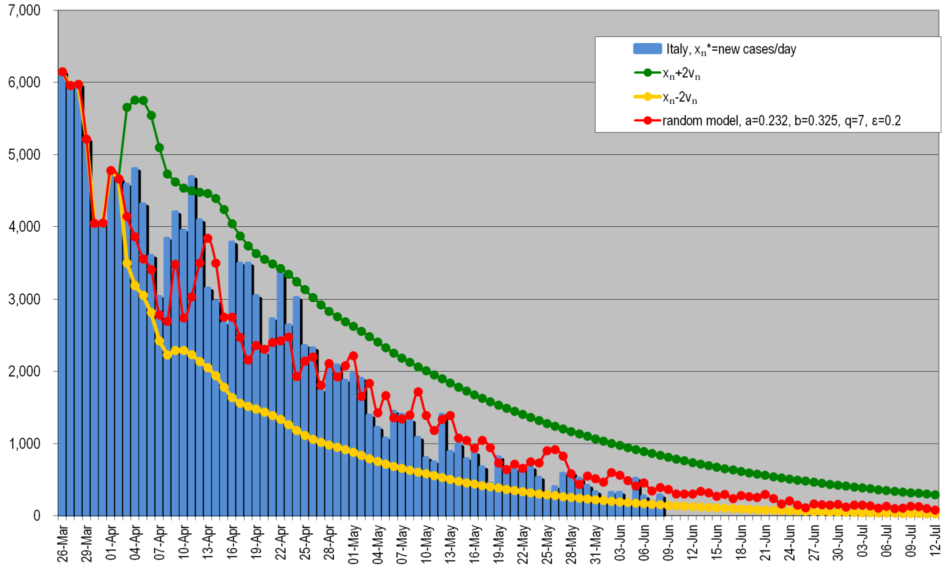

Figure 17. Random simulation, Italy

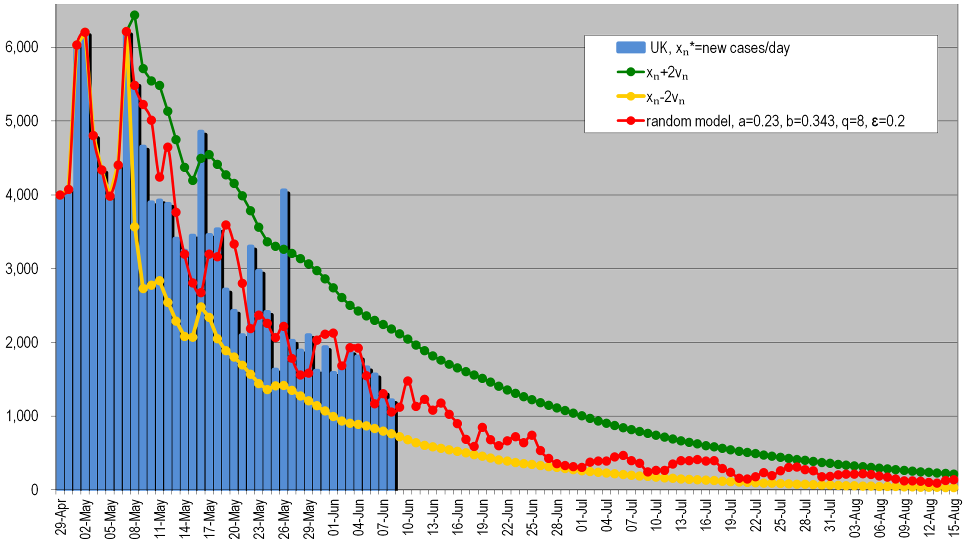

Figure 18. Random simulation, United Kingdom

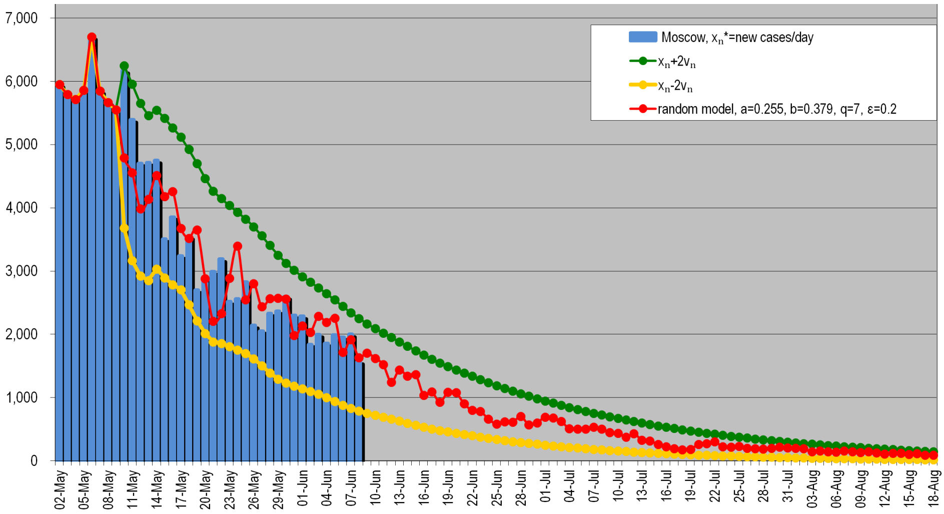

Figure 19. Random simulation, Moscow

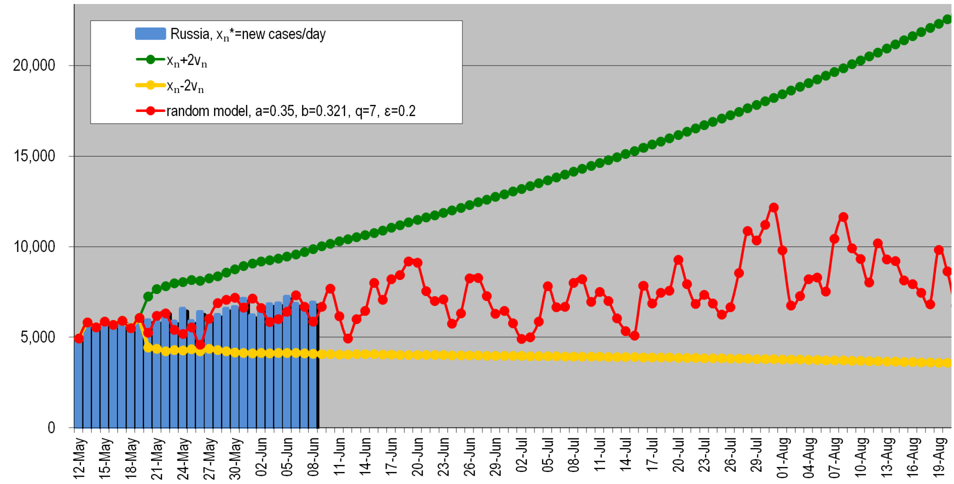

Figure 20. Random simulation, Russia outside Moscow

5. A MODEL WITH VARIABLE COEFFICIENTS. Let us consider a generalization of the basic model where the parameters a and b become variable. More precisely, while keeping the assumption (I) of the basic model, we replace (A) and (B) by the following assumptions.

(A_n) During n-th day each ill person at large infects a_n other persons.

(B_n) During n-th day a fraction b_n of ill people at large gets isolated.

Here $a_n > 0$ and $b_n \in (0,1)$ for all n. Using the same notation as in Section 2, we obtain the following relations: $x_n = b_n z_n$ and $u_n = a_n z_n$. Substituting into (2), we obtain

$$z_{n+1} = (1 - b_n)\, z_n + a_{n-q} z_{n-q}.$$

Using $x_n = b_n z_n$, we obtain the following equation for x_n:

$$x_{n+1} = \frac{b_{n+1}(1 - b_n)}{b_n} x_n + \frac{a_{n-q} b_{n+1}}{b_{n-q}} x_{n-q}. \tag{35}$$

The initial conditions should be the same as above, that is (4).

As an example, consider the case when the coefficients a_n and b_n are periodic:

$$a_n = a\left(1 + c_1 \sin\left(\tfrac{2\pi}{p_1}(n - n_1)\right)\right)$$

and

$$b_n = b\left(1 + c_2 \sin\left(\tfrac{2\pi}{p_2}(n - n_2)\right)\right)$$

where as above $a > 0$, $b \in (0,1)$ while c_i, p_i, n_i are new parameters. By minimizing the differences $\|x - x^*\|$ and $\|y - y^*\|$, we try to obtain the best values for all the parameters involved.

For some countries the sequence x_n^* shows certain periodic patterns. For those countries, the periodic model provides a better match than the basic model. Moreover, the periodic model x_n provides frequently a better approximation to x_n^* than even the *moving averages* do. Denote by $x_n^*\left(1\right)$ a simple moving average of x_n^*, that is,

$$x_n^*\left(1\right) = \frac{x_{n-1}^* + x_n^* + x_{n+1}^*}{3}, \quad n \geq 1$$

and $x_0^*\left(1\right) = \frac{x_0^*+x_1^*}{2}$. Define inductively $x_n^*\left(k\right)$ as a moving average of $x_n^*\left(k-1\right)$. Then $x_n^*\left(3\right)$ is a 7-day moving average of x_n^* that is frequently used as a natural mollification of x_n^*.

On the next diagrams we compare the actual data x_n^* with the basic model, periodic model and the moving averages $x^*\left(3\right)$, where in some cases we have

$$\left\|x - x^*\right\| << \left\|x^*\left(3\right) - x^*\right\|$$

for periodic models x_n. The corresponding y-diagrams are not shown here because y_n and y_n^* in all these cases are practically indistinguishable on the pictures.

It is interesting to observe that, for periodic models, the value of b is usually smaller than that for basic models, that is, a periodic pattern has a positive effect for suppressing the epidemic. A mathematical explanation for that is yet to be found.

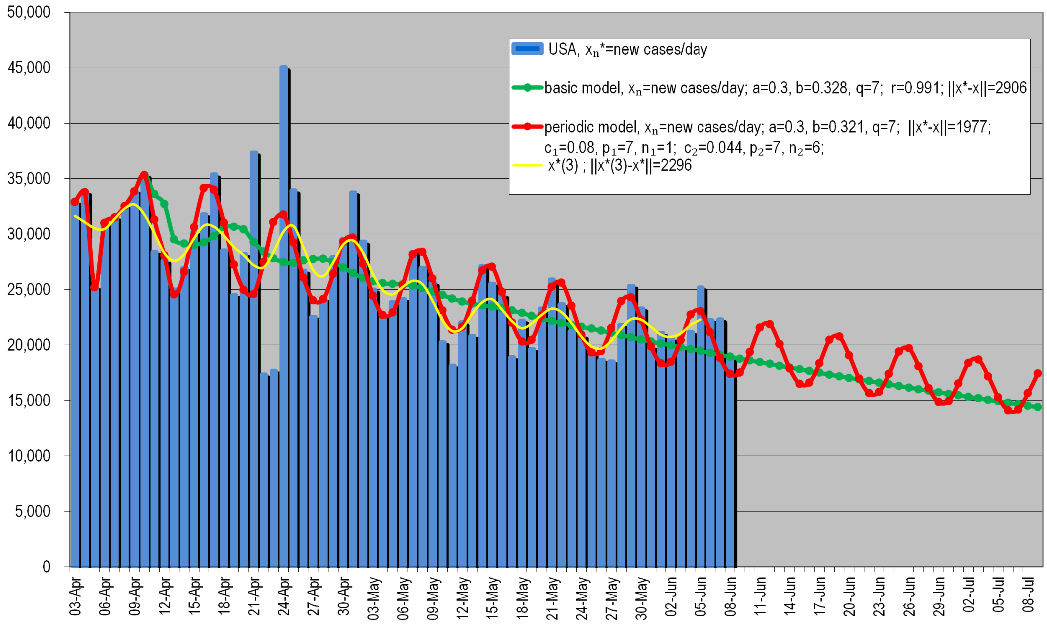

Figure 21. Comparison of basic and periodic models with moving averages, USA

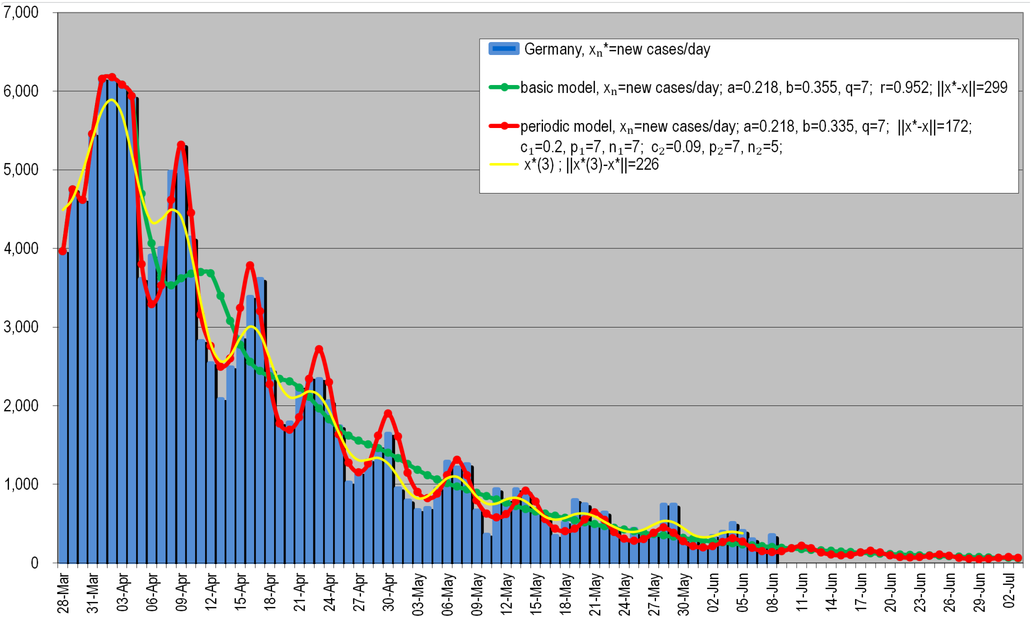

Figure 22. Comparison of basic and periodic models with moving averages, Germany

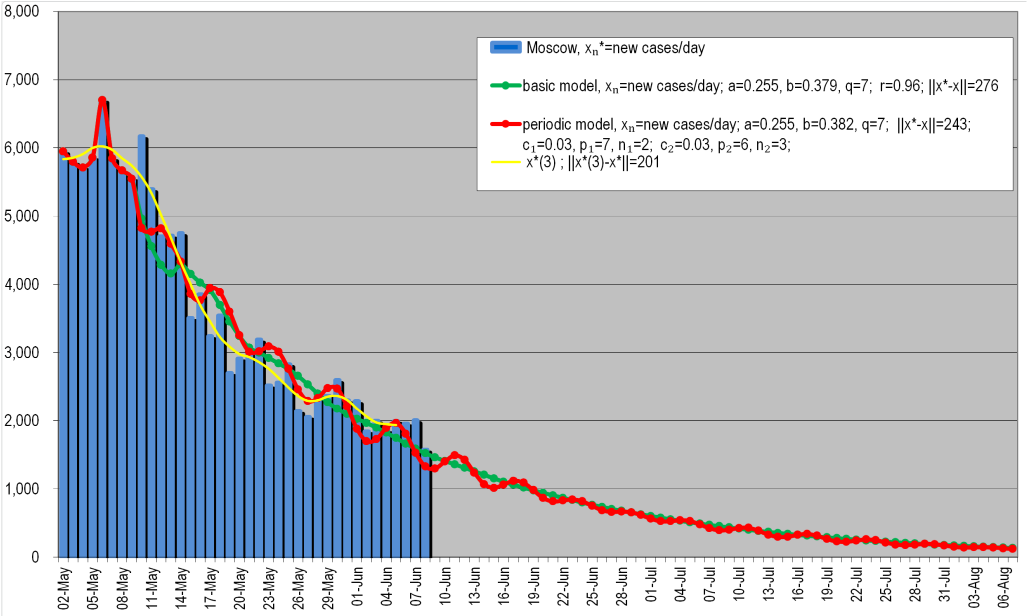

Figure 23. Comparison of basic and periodic models with moving averages, Moscow

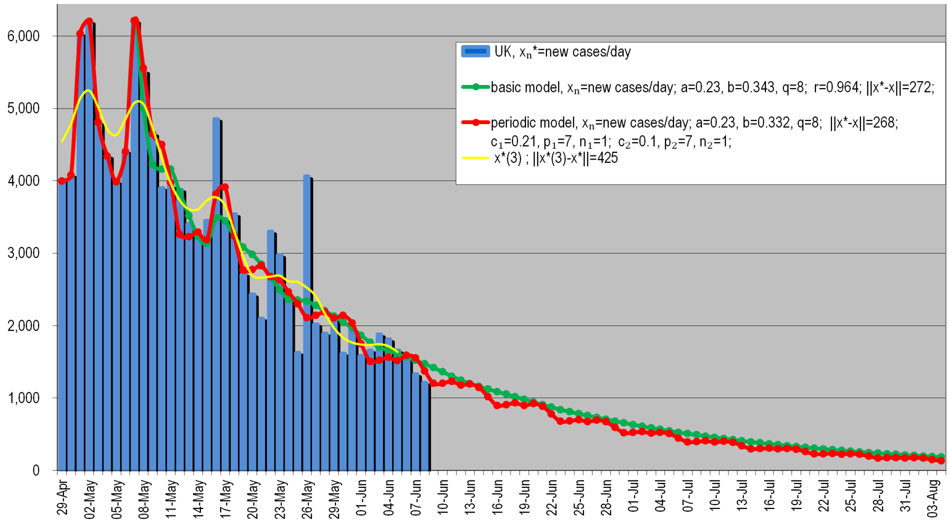

Figure 24. Comparison of basic and periodic models with moving averages, UK

6. A TWO-PHASE MODEL. In the setting of the model with variable coefficients a_n, b_n, assume that

$$a_n = \begin{cases} a', & n < n_0 \\ a, & n \geq n_0 \end{cases} \quad \text{and} \quad b_n = \begin{cases} b', & n < n_0 \\ b, & n \geq n_0 \end{cases}$$

for some $n_0 > 0$, $a, a' > 0$ and $b, b' \in (0, 1)$. In other words, we have two phases of the epidemic with different pairs of parameters (a', b') and (a, b).

The equation (35) becomes as follows:

$$\begin{aligned} x_n &= (1 - b')\, x_{n-1} + a' x_{n-q-1}, \quad q + 1 \leq n < n_0, \\ x_n &= (1 - b)\, x_{n-1} + a x_{n-q-1}, \qquad n \geq n_0 + q + 1, \end{aligned}$$

and

$$\begin{aligned} x_n &= \frac{b}{b'} (1 - b')\, x_{n-1} + \frac{b}{b'} a' x_{n-q-1}, \qquad n = n_0 \\ x_n &= (1 - b)\, x_{n-1} + \frac{b}{b'} a' x_{n-q-1}, \qquad n_0 < n \leq n_0 + q. \end{aligned}$$

Hence, for $n < n_0$ we obtain the equation with coefficients a', b', for $n \geq n_0 + q + 1$ we obtain the equation with coefficients a, b, whereas for transition values of n between n_0 and $n_0 + q$ the coefficients may be quite wild because the ratio $\frac{b}{b'}$ may be very large. This may be a reason why this model does not give good match of x_n and x_n^* within the transition period.

In practice, the change of the values of the parameters a, b occurs not overnight but during some period. Therefore, it is necessary to do some smoothing of the coefficients in the transition period. This is done by capping them by certain values, say, by 1 and by replacing them by the moving averages. On top of that, we apply some weighted averaging of the initial values of x_n in the first phase, towards increasing their values. Indeed, the epidemic is caused at the initial stage by external sources that are not accounted for in the equation. To compensate for that and to improve a match with x_n^*, we increase appropriately the initial data.

Finally, in order to take into account periodic patterns, we make a periodic perturbation of the equation (35) as follows. Rewrite (35) in the form

$$x_{n+1} = (1 - B_n)\, x_n + A_n x_{n-q}$$

and replace A_n by $A_n\,(1 + \varepsilon_1 \sin(n\varphi_1 + \psi_2))$ and B_n by $B_n\,(1 + \varepsilon_2 \sin(n\varphi_2 + \psi_2))$, where the new parameters φ_j, ψ_j and ε_j are also to be determined in the process of minimization of $\|x - x^*\|$ and $\|y - y^*\|$.

Without going into further details, let us show the final results for two-phase periodic models for various countries. The dates are shown in the formats $dd.mm$ and dd-mmm.

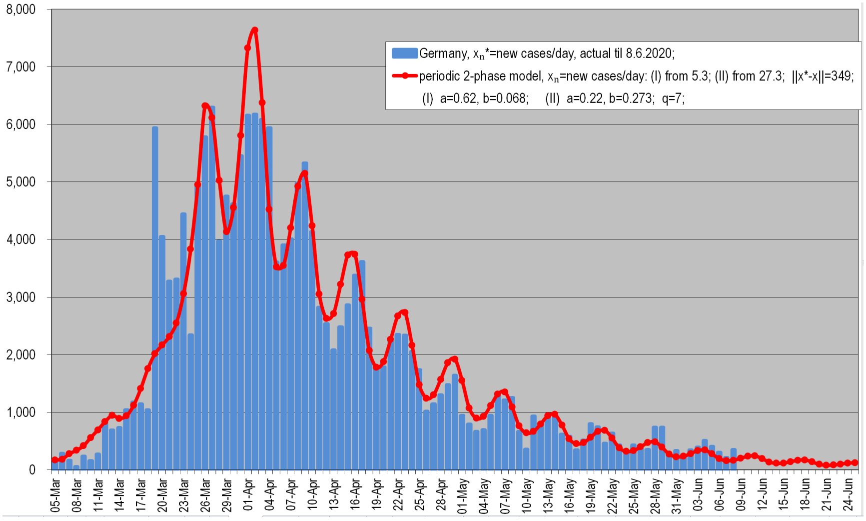

Figure 25. A two-phase periodic model, Germany (x-diagram)

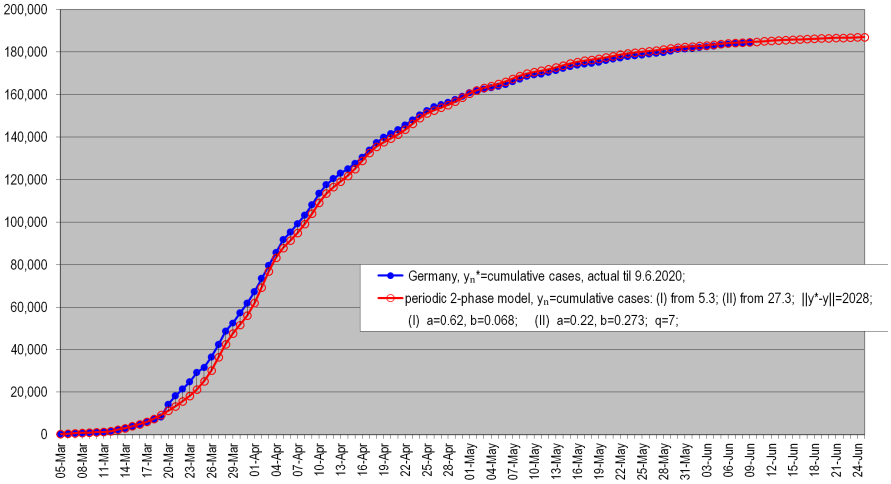

Figure 26. A two-phase periodic model, Germany (y-diagram)

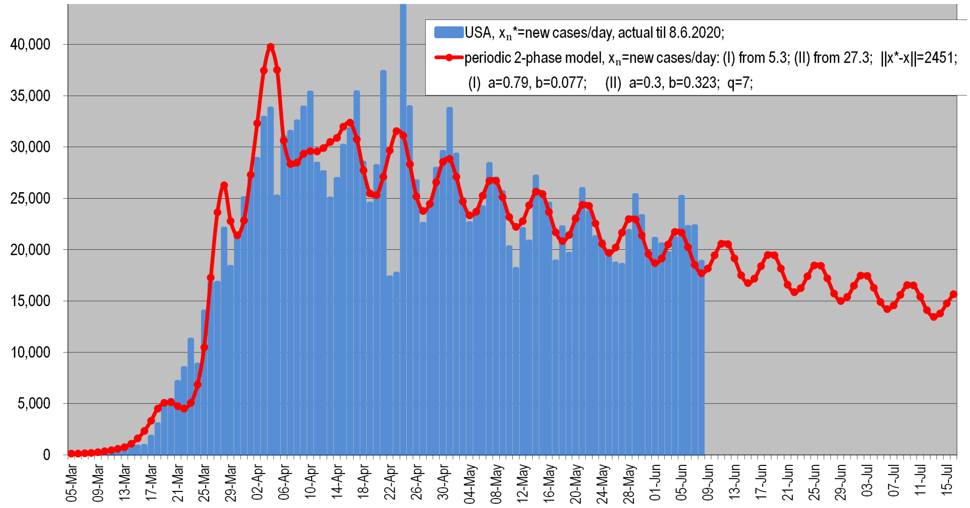

Figure 27. A two-phase periodic model for the USA (x-diagram)

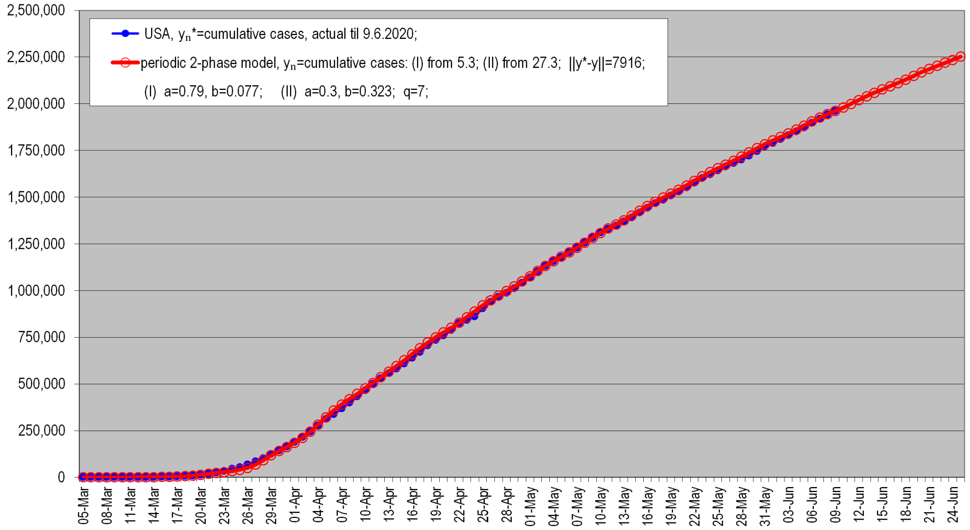

Figure 28. A two-phase periodic model, USA (y-diagram)

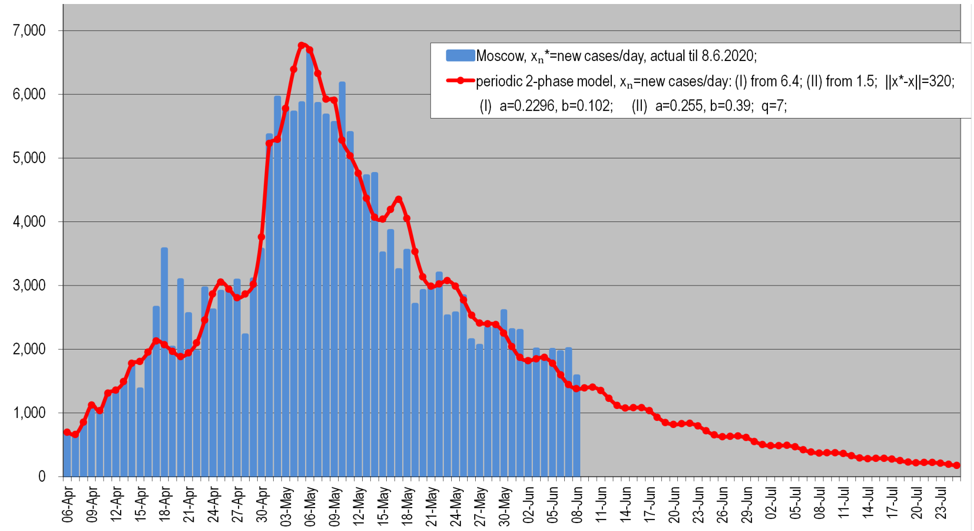

Figure 29. A two-phase periodic model, Moscow (x-diagram)

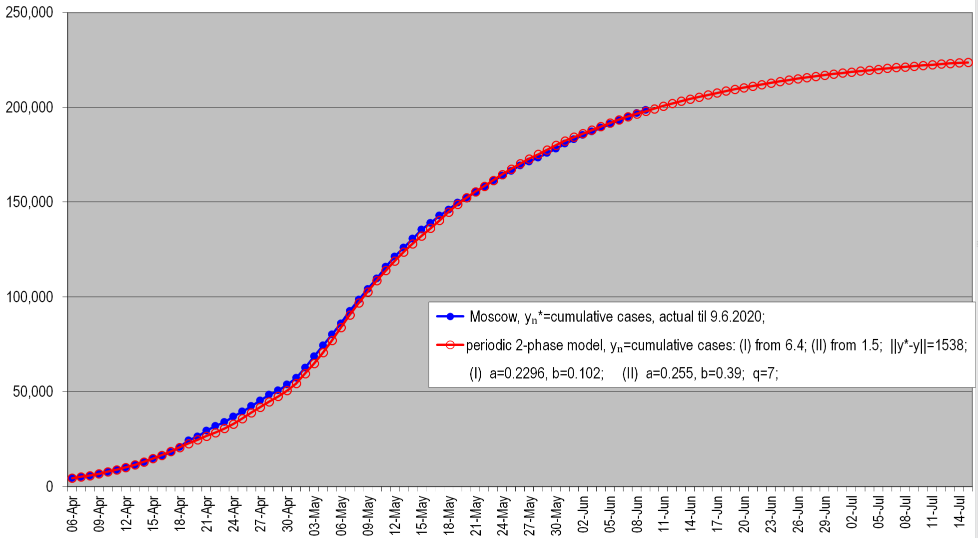

Figure 30. A two-phase periodic model, Moscow (y-diagram)

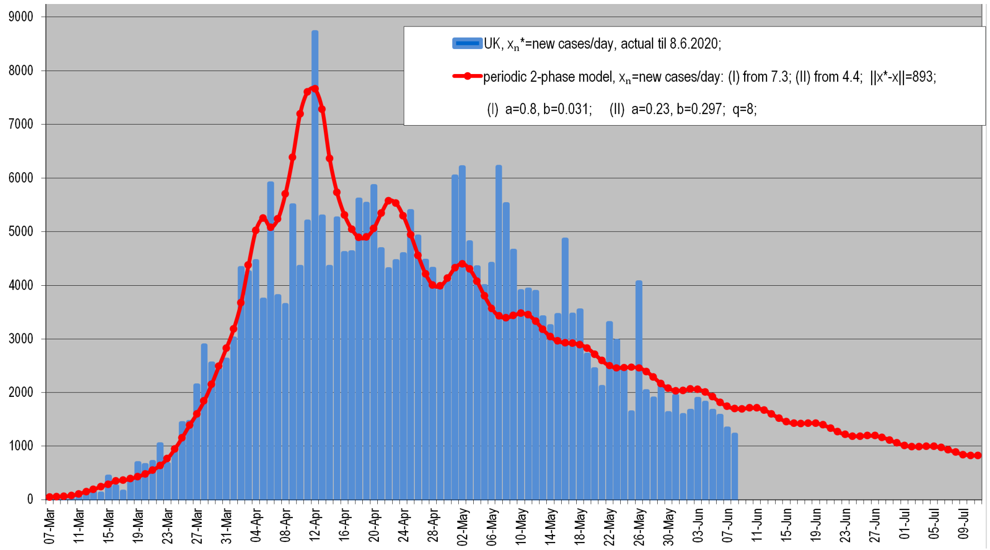

Figure 31. A two-phase periodic model, UK (x-diagram)

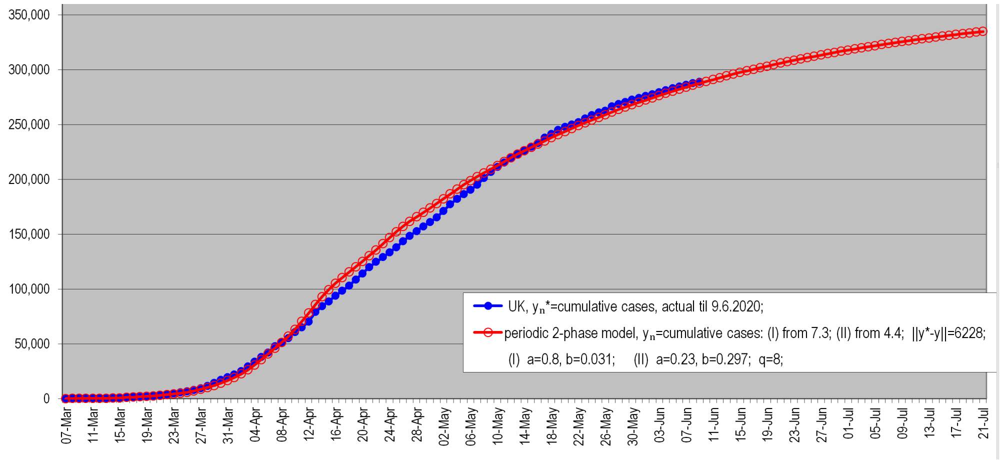

Figure 32. A two-phase periodic model, UK (y-diagram)

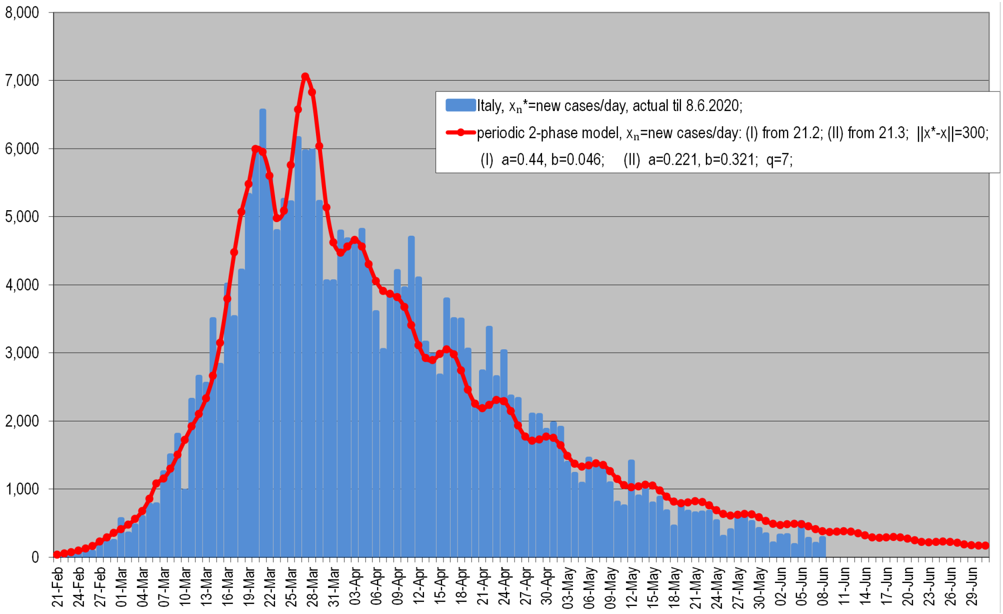

Figure 33. A two-phase periodic model, Italy (x-diagram)

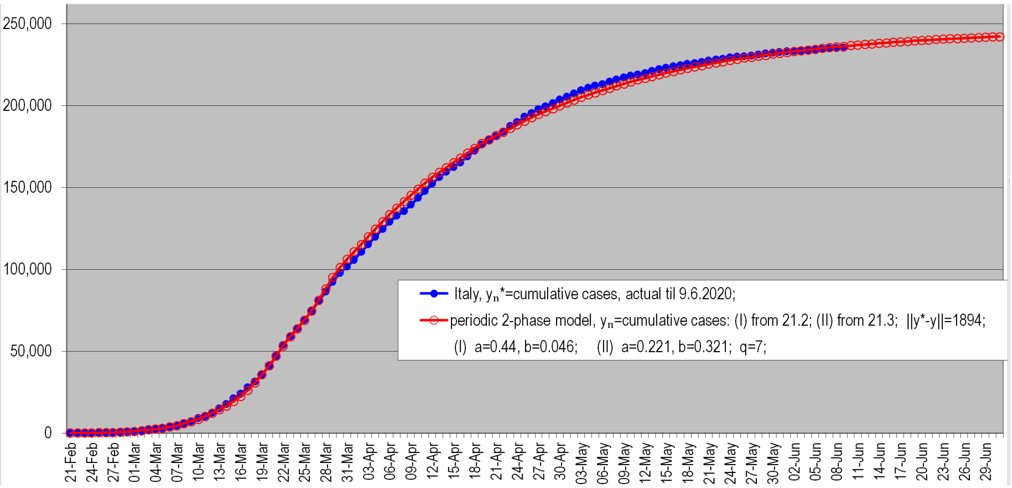

Figure 34. A two-phase periodic model, Italy (y-diagram)

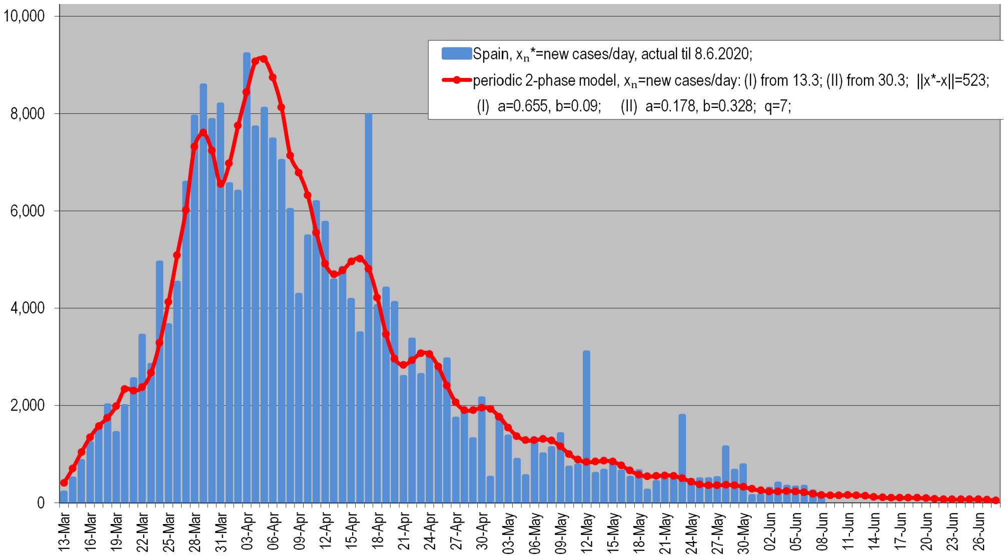

Figure 35. A two-phase periodic model, Spain (x-diagram)

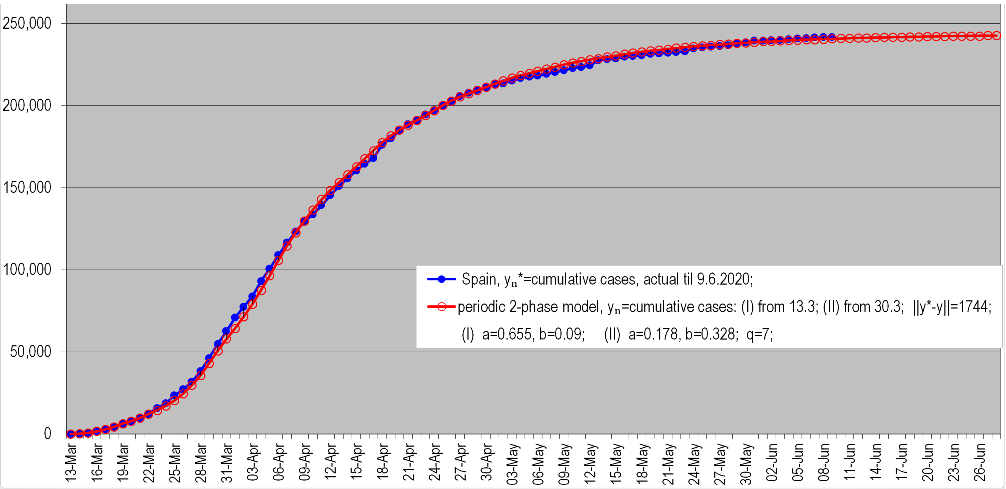

Figure 36. A two-phase periodic model, Spain (y-diagram)

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